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(54) Title: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC STRESS RESPONSE AND PLANT GROWTH AND YIELDS WITH INCREASED TOLERANCE TO ENVIRONMENTAL STRESS

(57) Abstract: This invention relates generally to nucleic acid sequences encoding proteins that are associated with abiotic stress responses and abiotic stress tolerance in plants. This invention further relates to a transformed plant cell with altered metabolic activity compared to a corresponding non-transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) encoding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.

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**NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH
ABIOTIC STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH
INCREASED TOLERANCE TO ENVIRONMENTAL STRESS**

5 **0001.0.1** This invention relates generally to nucleic acid sequences encoding proteins that are associated with abiotic stress responses and abiotic stress tolerance in plants.

0002.0.1 This invention further relates to transformed plant cells with altered metabolic activity compared to a corresponding non transformed wild type plant cell,
10 wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.

0003.0.1 In particular, this invention relates to nucleic acid sequences encoding
15 proteins that confer drought, heat, cold, and/or salt tolerance and/or resistance to plants, especially by altering the metabolic activity leading to drought, heat, cold, and/or salt tolerance and/or resistance to plants. The invention also deals with methods of producing, screening for and breeding such plant cells or plants and method of detecting stress in plants cells or plants.

20 **0004.0.1** Abiotic environmental stresses such as drought stress, salinity stress, heat stress and cold stress, are major limiting factors of plant growth and productivity (Boyer, 1982, *Science* 218, 443-448). Crop losses and crop yield losses of major crops such as rice, maize (corn) and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages in many underdeveloped
25 countries.

0005.0.1 Plants are typically exposed during their life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of low water or desiccation (drought). However, if the severity and duration of the drought conditions are too great, the effects on plant
30 development, growth and yield of most crop plants are profound. Continuous exposure to drought causes major alterations in the plant metabolism. These great changes in metabolism ultimately lead to cell death and consequently yield losses.

0006.0.1 Developing stress-tolerant plants is a strategy that has the potential to solve or mediate at least some of these problems (McKersie and Leshem, 1994, *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). However,
35 traditional plant breeding strategies to develop new lines of plants that exhibit resistance (tolerance) to these types of stresses are relatively slow and require specific resistant lines for crossing with the desired line. Limited germplasm resources for

stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Additionally, the cellular processes leading to drought, cold and salt tolerance are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). This multi-component nature of stress tolerance has not only made breeding for tolerance largely unsuccessful, but has also limited the ability to genetically engineer stress tolerance plants using biotechnological methods.

0007.0.1 Drought, heat, cold and salt stresses have a common theme important for plant growth and that is water availability. Plants are exposed during their entire life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions. However, if the severity and duration of the drought conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Since high salt content in some soils result in less available water for cell intake, its effect is similar to those observed under drought conditions. Additionally, under freezing temperatures, plant cells lose water as a result of ice formation that starts in the apoplast and withdraws water from the symplast (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). Commonly, a plant's molecular response mechanisms to each of these stress conditions are similar.

0008.0.1 The results of current research indicate that drought tolerance is a complex quantitative trait and that no real diagnostic marker is available yet. High salt concentrations or dehydration may cause damage at the cellular level during drought stress but the precise injury is not entirely clear (Bray, 1997. *Trends Plant Sci.* 2, 48-54). This lack of a mechanistic understanding makes it difficult to design a transgenic approach to improve drought tolerance. However, an important consequence of damage may be the production of reactive oxygen radicals that cause cellular injury, such as lipid peroxidation or protein and nucleic acid modification. Details of oxygen free radical chemistry and their reaction with cellular components such as cell membranes have been described (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers).

0009.0.1 It is the object of this invention to identify new, unique genes capable of conferring stress tolerance to plants upon expression or over-expression.

0010.0.1 It is further object of this invention to identify, produce and breed new, unique stress tolerant and/or resistant plant cells or plants and methods of inducing and detecting stress tolerance and/or resistance in plants or plant cells. It is a further object to identify new methods to detect stress tolerance and/or

resistance in plants or plant cells. It is also the object of this invention to identify new, unique genes capable of conferring stress tolerance to plants upon expression or over-expression.

- 0011.0.1 The present invention provides a transformed plant cell with altered metabolic activity compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.
- 10 0012.0.2 The present invention provides a transgenic plant cell transformed by Stress-Related Protein (SRP) coding nucleic acid, selected from the group consisting of:
- a) nucleic acid molecule encoding one of the polypeptides shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
 - 15 b) nucleic acid molecule comprising one of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;
 - c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;
 - 20 d) nucleic acid molecule which encodes a polypeptide which has at least 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;
 - 25 e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
 - f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers as shown in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
 - 30 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
 - 35

- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring an altered metabolic activity in an organism or a part thereof.

or comprising a sequence which is complementary thereto.

0013.0.1 As used herein, the term "metabolite" refers to intermediate substances, preferably such of low molecular weight, which occur during anabolism and catabolism in a cell or plant, in other words a substance produced or consumed by metabolism.

0014.0.1 The term "altered metabolic activity" refers to the change (increase or decrease) of the amount, concentration or activity (meaning here the effective concentration for the purposes of chemical reactions and other mass action) of a metabolite in a specific volume relative to a corresponding volume (e.g. in an organism, a tissue, a cell or a cell compartment) of a control, reference or wild type, including the de novo creation of the activity or expression, measured for example by one of the methods described herein below, which is changed (increased or decreased) as compared to a corresponding non transformed wild type plant cell.

0015.0.2 The terms "increased", "raised", "extended", "enhanced", "improved" or "amplified" relate to a corresponding change of a property in an organism, a part of an organism such as a tissue, seed, root, leave, flower etc. or in a cell and are interchangeable. Preferably, the overall activity in the volume is increased or enhanced in cases if the increase or enhancement is related to the increase or enhancement of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is increased or enhanced or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is increased or enhanced. The terms "reduction", "decrease" or "deletion" relate to a corresponding change of a property in an organism, a part of an organism such as a tissue, seed, root, leave, flower etc. or in a cell. Preferably, the overall activity in the volume is reduced, decreased or deleted in cases if the reduction, decrease or deletion is related to the reduction, decrease or deletion of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is reduced, decreased or

deleted or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is reduced, decreased or deleted.

0016.0.2 The terms "increase" or "decrease" relate to a corresponding change of a property in an organism or in a part of an organism, such as a tissue, seed, root, leave, flower etc. or in a cell. Preferably, the overall activity in the volume is increased in cases the increase relates to the increase of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is increased or generated or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is increased.

0017.0.2 Under "change of a property" it is understood that the activity, expression level or amount of a gene product or the metabolite content is changed in a specific volume relative to a corresponding volume of a control, reference or wild type, including the de novo creation of the activity or expression.

0018.0.2 The terms "increase" or "decrease" include the change of said property in only parts of the subject of the present invention, for example, the modification can be found in compartment of a cell, like a organelle, or in a part of a plant, like tissue, seed, root, leave, flower etc. but is not detectable if the overall subject, i.e. complete cell or plant, is tested. Preferably, the increase or decrease is found cellular, thus the term "increase of an activity" or "increase of a metabolite content" relates to the cellular increase compared to the wild typ cell.

0019.0.2 Accordingly, the term "increase" or "decrease" means that the specific activity of an enzyme as well as the amount of a compound or metabolite, e.g. of a polypeptide, a nucleic acid molecule or of the line chemical of the invention or an encoding mRNA or DNA, can be increased or decreased in a volume.

0020.0.2 The terms "wild type", "control" or "reference" are exchangeable and can be a cell or a part of organisms such as an organelle or a tissue, or an organism, in particular a microorganism or a plant, which was not modified or treated according to the herein described process according to the invention. Accordingly, the cell or a part of organisms such as an organelle or a tissue, or an organism, in particular a microorganism or a plant used as wild typ, control or reference corresponds to the cell, organism or part thereof as much as possible and is in any other property but in the result of the process of the invention as identical to the subject matter of the invention as possible. Thus, the wild type, control or reference is treated identically or as identical as possible, saying that only conditions or properties might be different which do not influence the quality of the tested property.

0021.0.2 Preferably, any comparison is carried out under analogous conditions. The term "analogous conditions" means that all conditions such as, for example, culture or growing conditions, assay conditions (such as buffer composition, temperature, substrates, pathogen strain, concentrations and the like) are kept identical between the experiments to be compared.

0022.0.2 The "reference", "control", or "wild type" is preferably a subject, e.g. an organelle, a cell, a tissue, an organism, in particular a plant or a microorganism, which was not modified or treated according to the herein described process of the invention and is in any other property as similar to the subject matter of the invention as possible.

The reference, control or wild type is in its genome, transcriptome, proteome or metabolome as similar as possible to the subject of the present invention. Preferably, the term "reference-" "control-" or "wild type"-organelle, -cell, -tissue or -organism, in particular plant or microorganism, relates to an organelle, cell, tissue or organism, in particular plant or microorganism, which is nearly genetically identical to the organelle, cell, tissue or organism, in particular microorganism or plant, of the present invention or a part thereof preferably 95%, more preferred are 98%, even more preferred are 99,00%, in particular 99,10%, 99,30%, 99,50%, 99,70%, 99,90%, 99,99%, 99,999% or more. Most preferable the "reference", "control", or "wild type" is a subject, e.g. an organelle, a cell, a tissue, an organism, which is genetically identical to the organism, cell or organelle used according to the process of the invention except that the responsible or activity conferring nucleic acid molecules or the gene product encoded by them are amended, manipulated, exchanged or introduced according to the inventive process.

0023.0.2 Preferably, the reference, control or wild type differs from the subject of the present invention only in the cellular activity of the polypeptide of the invention, e.g. as result of an increase in the level of the nucleic acid molecule of the present invention or an increase of the specific activity of the polypeptide of the invention, e.g. by or in the expression level or activity of an protein having the activity of an Stress-Related Protein (SRP) or its homologs, its biochemical or genetical causes and the altered metabolic activity.

0024.0.2 In case, a control, reference or wild type differing from the subject of the present invention only by not being subject of the process of the invention can not be provided, a control, reference or wild type can be an organism in which the cause for the modulation of an activity conferring the altered metabolic activity or expression of the nucleic acid molecule of the invention as described herein has been switched back or off, e.g. by knocking out the expression of responsible gene product, e.g. by antisense inhibition, by inactivation of an activator or agonist, by activation of an

inhibitor or antagonist, by inhibition through adding inhibitory antibodies, by adding active compounds as e.g. hormones, by introducing negative dominant mutants, etc. A gene production can for example be knocked out by introducing inactivating point mutations, which lead to an enzymatic activity inhibition or a destabilization or an inhibition of the ability to bind to cofactors etc.

0025.0.2 Accordingly, preferred reference subject is the starting subject of the present process of the invention. Preferably, the reference and the subject matter of the invention are compared after standardization and normalization, e.g. to the amount of total RNA, DNA, or protein or activity or expression of reference genes, like housekeeping genes, such as ubiquitin, actin or ribosomal proteins.

0026.0.2 A series of mechanisms exists via which a modification of the a protein, e.g. the polypeptide of the invention can directly or indirectly affect the yield, production and/or production efficiency of the amino acid.

0027.0.2 For example, the molecule number or the specific activity of the polypeptide or the nucleic acid molecule may be increased. Larger amounts of the fine chemical can be produced if the polypeptide or the nucleic acid of the invention is expressed *de novo* in an organism lacking the activity of said protein. However, it is also possible to increase the expression of the gene which is naturally present in the organisms, for example by modifying the regulation of the gene, or by increasing the stability of the corresponding mRNA or of the corresponding gene product encoded by the nucleic acid molecule of the invention, or by introducing homologous genes from other organisms which are differently regulated, eg. not feedback sensitive.

0028.0.2 This also applies analogously to the combined increased expression of the nucleic acid molecule of the present invention or its gene product with that of further enzymes of the amino acid biosynthesis pathways, e.g. which are useful for the synthesis of the fine chemicals.

0029.0.2 The increase, decrease or modulation according to this invention can be constitutive, e.g. due to a stable permanent transgenic expression or to a stable mutation in the corresponding endogenous gene encoding the nucleic acid molecule of the invention or to a modulation of the expression or of the behaviour of a gene conferring the expression of the polypeptide of the invention, or transient, e.g. due to an transient transformation or temporary addition of a modulator such as a agonist or antagonist or inducible, e.g. after transformation with a inducible construct carrying the nucleic acid molecule of the invention under control of a induceable promoter and adding the inducer, e.g. tetracycline or as described herein below.

0030.0.2 The increase in activity of the polypeptide amounts in a cell, a tissue, a organelle, an organ or an organism or a part thereof preferably to at least 5%,

preferably to at least 20% or at least 50%, especially preferably to at least 70%, 80%, 90% or more, very especially preferably are to at least 200%, most preferably are to at least 500% or more in comparison to the control, reference or wild type.

- 0031.0.2** The specific activity of a polypeptide encoded by a nucleic acid molecule of the present invention or of the polypeptide of the present invention can be tested as described in the examples. In particular, the expression of a protein in question in a cell, e.g. a plant cell or a microorganism and the detection of an increase the fine chemical level in comparison to a control is an easy test and can be performed as described in the state of the art.
- 10 **0032.0.2** The term "increase" includes, that a compound or an activity is introduced into a cell *de novo* or that the compound or the activity has not been detectable before, in other words it is "generated".
- 0033.0.2** Accordingly, in the following, the term "increasing" also comprises the term "generating" or "stimulating". The increased activity manifests itself in an increase of the fine chemical.
- 15 **0034.0.1** The transformed plant cells are compared to the corresponding non-transformed wild type of the same genus and species under otherwise identical conditions (such as, for example, culture conditions, age of the plants and the like). In this context, a change in metabolic activity of at least 10%, advantageously of at least 20%, preferably at least 30%, especially preferably of at least 40%, 50% or 60%, very especially preferably of at least 70%, 80%, 90%, 95% or even 100% or more, in comparison with the non-transformed organism is advantageous.
- 20 **0035.0.1** Preferably the change in metabolite concentration of the transformed plant cells is the changed compared to this corresponding non-transformed wild type.
- 25 Preferably the change in metabolite concentration is measured by HPLC and calculated by dividing the peak height or peak area of each analyte (metabolite) through the peak area of the respective internal standards. Data is normalised using the individual sample fresh weight. The resulting values are divided by the mean values found for wild type plants grown under control conditions and analysed in the same
- 30 sequence, resulting in the so-called ratios, which represent values independent of the analytical sequence. These ratios indicate the behavior of the metabolite concentration of the transformed plants in comparison to the concentration in the wild type control plants.
- 0036.0.1** According to this method, the change in at least one metabolite concentration of the transformed plant cells compared to the corresponding non-transformed wild type is at least 10%, advantageously of at least 20%, preferably at
- 35

least 40%, 60% or 80%, especially preferably of at least 90%, 100% or 200%, very especially preferably of at least 700%, 800%, 900% 1000% or more.

0037.0.1 Data significance can be determined by all statistical methods known by a person skilled in the art, preferably by a t-test, more preferably by the student t-test.

0038.0.1 Altered metabolic activity also refers to metabolites that, compared to a corresponding non transformed wild type plant cell, are not produced after transformation or are only produced after transformation.

0039.0.1 Preferred metabolites of the invention are 2,3-dimethyl-5-phytylquinol or 2-hydroxy-palmitic acid or 3,4-dihydroxyphenylalanine (= dopa) or 3-hydroxy-palmitic acid or 5-oxoproline or alanine or alpha linolenic acid (c18:3 (c9, c12, c15)) or alpha-tocopherol or aminoadipic acid or anhydroglucose or arginine or aspartic acid or beta-apo-8' carotenal or beta-carotene or beta-sitosterol or beta-tocopherol or (delta-7-cis,10-cis)-hexadecadienic acid or hexadecatrienic acid or margaric acid or delta-15-cis-tetradecenoic acid or ferulic acid or campesterol or cerotic acid (c26:0) or citrulline or cryptoxanthine or eicosenoic acid (20:1) or fructose or fumarate or galactose or gamma-aminobutyric acid or gamma-tocopherol or gluconic acid or glucose or glutamic acid or glutamins or glycerate or glyceraldehyde or glycerol or glycerol-3-phosphate or glycine or homoserine or inositol or isoleucine or iso-maltose or isopentemyl pyrophosphate or leucine or lignoceric acid (c24:0) or linoleic acid (c18:2 (c8, c12)) or luteine or lycopene or malate or mannose or methionine or methylgalactofuranoside or methylgalactopyranoside or methylgalactopyranoside or palmitic acid (c16:0) or phenylalanine or phosphate or proline or putrescine or pyruvate or raffinose or ribonic acid or serine or shikimate or sinapic acid or stearic acid (c18:0) or succinate or sucrose or threonine or triacontanoic acid or tryptophane or tyrosine or ubiquinone or udp-glucose or valine or zeaxanthine.

0040.0.1 Metabolic activity may also be altered concerning one or more derivatives of one or more of the above metabolites.

0041.0.1 Preferably metabolic activity is altered concerning one or more metabolites selected from the group consisting of all of the above metabolites.

0042.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of mannose, inositol, phosphate, aspartic acid, isoleucine, leucine, gamma-aminobutyric acid, glyceraldehyde, sucrose, campesterol, valine, beta-tocopherol, ubiquinone, palmitic acid (c16:0), 2-hydroxy-palmitic acid, 2,3-dimethyl-5-phytylquinol, beta-carotene, alpha-linolenic acid (c18:3 (c9, c12, c15)), lycopene.

0043.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of methylgalactofuranoside, beta-sitosterol, delta-15-cis-tetracosenic acid (c24:1 me), margarinic acid (c17:0 me), stearic acid (c18:0), methylgalactopyranoside, gamma-tocopherol, linoleic acid (c18:2 (c9, c12)), hexadecatrienic acid (c18:3 me), shikimate, raffinose, glutamic acid, glutamine, 5 udp-glucose, proline, threonine, isopentenyl pyrophosphate, 5-oxoproline, ferulic acid, sinapine acid.

0044.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of tryptophane, citrulline, serine, alanine, glycerate, arginine, 3-hydroxy-palmitic acid, putrescine, 3,4-dihydroxyphenylalanine (=dopa), alpha-tocopherol, aminoadipic acid, anhydroglucose, beta-apo-8' carotenol, delta-7-cis,10-cis-hexadecadienic acid (c18:2 me), cerotic acid (c26:0), cryptoxanthine, eicosenolic acid (20:1), fructose, fumarate.

0045.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of galactose, gluconic acid, glucose, glycerol, glycerol-3-phosphate, glycine, homoserine, iso-maltose, lignoceric acid (c24:0), luteins, malate, triacontanoic acid, methionine, phenylalanine, pyruvate, ribonic acid, succinate, tyrosine, zeaxanthine.

0046.0.1 The present invention provides a transgenic plant cell, wherein expression of said nucleic acid sequence in the plant cell results altered metabolic activity leading to increased tolerance and/or resistance to environmental stress as compared to a corresponding non-transformed wild type plant cell. One preferred wild type plant cell is a non-transformed *Arabidopsis* plant cell. An example here is the *Arabidopsis* wild type C24 (Nottingham Arabidopsis Stock Centre, UK; NASC Stock 25 N906).

0047.0.1 Other preferred wild type plant cells are a non-transformed from plants selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, 30 potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass and forage crops.

0048.0.1 More preferred wild type plant cells are a non-transformed *Linum* plant cell, preferably *Linum usitatissimum*, more preferably the variety Brigitta, Golda, Gold Merchant, Helle, Juliet, Olpina, Livia, Martin, Maedgold, Sporpion, Serenade, Linus, 35 Taurus, Lifax or Liviola, a non-transformed *Helianthus* plant cell, preferably *Helianthus annuus*, more preferably the variety Aurasol, Capella, Flavia, Flores, Jazzy, Paluto, Pegasol, PIR64A54, Rigasol, Sariuca, Sideral, Sunny, Alenka, Candisol or Floyd, or a

non-transformed Brassica plant cell, preferably Brassica napus, more preferably the variety Dorothy, Evita, Heros, Hyola, Kimbar, Lambada, Licolly, Liconira, Licosmos, Lisorna, Mistral, Passat, Serator, Siapula, Sponsor, Star, Caviar, Hybridol, Baical, Olga, Lara, Doublol, Karola, Falcon, Spirit, Olymp, Zeus, Libero, Kyola, Licord, Lion, Lirajet, Lisbeth, Magnum, Maja, Mendel, Mica, Mohican, Olpop, Ontarion, Panthar, Prince, Pronio, Susanna, Talani, Titan, Transfer, Wilking, Wolan, Zenlah, Artus, Contact or Smart.

0049.0.1 The expression of said nucleic acid sequence in the plant cell may directly or indirectly influence the metabolic activity of the transformed plant cells.

10 **Preferably they influence the activity of the above metabolites.**

0050.0.1 Preferably metabolic activity may be altered by transformation with one or more Stress-Related Protein (SRP) coding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c homologs of the afore mentioned sequences.

15 **0051.0.1** It is within the scope of the invention to identify the genes encoded by a nucleic acid sequence selected from the group consisting of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs thereof in target plants, especially crop plants, and then express the corresponding gene to achieve the altered metabolic activity resulting in increased tolerance and/or resistance to environmental stress. Consequently the
20 invention is not limited to a specific plant.

0052.0.2 A protein having an activity conferring an altered metabolic activity preferably has the structure of the polypeptide described herein, in particular of the polypeptides comprising the consensus sequence shown in Fig. 2 or of the polypeptide as shown in Fig. 1a, 1b or 1c or the functional homologues thereof as described herein,
25 or is encoded by the nucleic acid molecule characterized herein or the nucleic acid molecule according to the invention, for example by the nucleic acid molecule as shown in Fig. 1a, 1b or 1c or its herein described functional homologues and has the herein mentioned activity.

0053.0.1 It is further possible to detect environmental stress in plant cells or plants
30 by screening the plant cells for altered metabolic activity as compared to non-stress conditions. This allows for monitoring of stress levels in plants, even when no symptoms are visible. Therefore counter action can be taken earlier and e.g. crop losses minimized by timely watering.

0054.0.1 It is also within the scope of the invention to screen plant cells or plants
35 for increased tolerance and/or resistance to environmental stress by screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions. This allows selection of plants with increased tolerance and/or

resistance to environmental stress without the identification of genes or visual symptoms.

0055.0.1 With the invention it is further possible to breed plant cells or plants towards increased tolerance and/or resistance to environmental stress by screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress. The screening for metabolite activity is faster and easier than e.g. screening for genes.

0056.0.1 Screening is well known to those skilled in the art and generally refers to the search for a particular attribute or trait. In the invention this trait in a plant or plant cell is preferably the concentration of a metabolite, especially preferred the concentration of the above metabolites. The methods and devices for screening are familiar to those skilled in the art and include GC (gas chromatography), LC (liquid chromatography), HPLC (high performance (pressure) liquid chromatography), MS (mass spectrometry), NMR (nuclear magnetic resonance) spectroscopy, IR (infra red) spectroscopy, photometric methods etc and combinations of these methods.

0057.0.1 Breeding is also customary knowledge for those skilled in the art. It is understood as the directed and stable incorporation of a particular attribute or trait into a plant or plant cell.

0058.0.1 The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Different breeding measures can be taken, depending on the desired properties. All the techniques are well known by a person skilled in the art and include for example, but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, Interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also can include the sterilization of plants to yield male or female sterile plants by mechanical, chemical, or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both of the parental lines. The transgenic seeds and plants according to the invention can therefore be used for the breeding of improved plant lines, which can increase the effectiveness of conventional methods such as herbicide or pesticide treatment or which allow one to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance, preferably drought and temperature, can be obtained, which, due to their optimized genetic "equipment", yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

0059.0.1 The invention provides that the environmental stress can be salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof, preferably drought and/or temperature.

5 **0060.0.1** The object of the invention is a transgenic plant cell, wherein the SRP (=stress related protein) is selected preferably from yeast, preferably *Saccharomyces cerevisiae*, or *E. coli* or a plant, preferably *Brassica napus*, *Glycine max*, or *Oryza sativa*.

0061.0.1 Object of the invention is also a transgenic plant cell, wherein the SRP coding nucleic acid is at least about 50 % homologous to one of the nucleic acid of Fig. 10 1a, 1b or 1c.

0062.0.1 In the transgenic plant cell of the invention, the expression of said nucleic acid results in increased tolerance to an environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type plant cell. Herein, the environmental stress is selected from 15 the group consisting of salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof, preferably drought and/or temperature.

0063.0.2 The term "expression" refers to the transcription and/or translation of a codogenic gene segment or gene. As a rule, the resulting product is an mRNA or a protein. However, expression products can also include functional RNAs such as, for 20 example, antisense, nucleic acids, tRNAs, snRNAs, rRNAs, RINAI, siRNA, ribozymes etc. Expression may be systemic, local or temporal, for example limited to certain cell types, tissue, organs or time periods.

0064.0.2 Unless otherwise specified, the terms "polynucleotides", "nucleic acid" and "nucleic acid molecule" are interchangeably in the present context. Unless 25 otherwise specified, the terms "peptide", "polypeptide" and "protein" are interchangeably in the present context. The term "sequence" may relate to polynucleotides, nucleic acids, nucleic acid molecules, peptides, polypeptides and proteins, depending on the context in which the term "sequence" is used. The terms "gene(s)", "polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic 30 acid molecule(s)" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. The terms refer only to the primary structure of the molecule.

0065.0.2 Thus, the terms "gene(s)", "polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic acid molecule(s)" as used herein include double- 35 and single-stranded DNA and RNA. They also include known types of modifications, for example, methylation, "caps", substitutions of one or more of the naturally occurring

nucleotides with an analog. Preferably, the DNA or RNA sequence of the invention comprises a coding sequence encoding the herein defined polypeptide.

0066.0.2 A "coding sequence" is a nucleotide sequence, which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include, but is not limited to mRNA, cDNA, recombinant nucleotide sequences or genomic DNA, while introns may be present as well under certain circumstances.

0067.0.2 For the purposes of the invention, as a rule the plural is intended to encompass the singular and vice versa.

0068.0.1 Further, the transgenic plant cell is derived from a monocotyledonous plant. Alternatively, the transgenic plant cell is derived from a dicotyledonous plant. Preferably, the transgenic plant cell is selected from the group consisting of maize, wheat, rice, oat, trifoliate, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, popper, sunflower, flax, borage, sunflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass, forage crops and *Arabidopsis thaliana*. Moreover, the transgenic plant cell of the present invention can be derived from a gymnosperm plant. Preferably, the plant is selected from the group of spruce, pine and fir.

0069.0.1 The invention further provides a seed produced by a transgenic plant transformed by a SRP coding nucleic acid, wherein the plant is true breeding for increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant cell. The transgenic plant might be a monocot, a dicot or a gymnosperm plant. The invention further provides a seed produced by a transgenic plant expressing an SRP wherein the plant is true breeding for increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant cell. The invention pertains to a seed produced by a transgenic plant, wherein the seed is genetically homozygous for a transgene conferring an increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant.

0070.0.1 The invention further provides an agricultural product produced by any of the below-described transgenic plants, plant parts such as leaf, petal, anther, roots, tubers, stems, buds, flowers or seeds. The invention further provides a isolated recombinant expression vector comprising a SRP encoding nucleic acid.

0071.0.1 The invention further provides a method of producing a transgenic plant with a SRP coding nucleic acid, wherein expression of the nucleic acid in the plant results in increased tolerance and/or resistance to an environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type plant cell, comprising

- a) transforming a plant cell with an expression vector including a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs or parts thereof and
- b) generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.

0072.0.1 With regard to invention described here, "transformed or transgene" means all those plants or parts thereof which have been brought about by genetic manipulation methods and in which either

- c) one or more genes, preferably encoded by one or more nucleic acid sequences as depicted in Fig. 1a, 1b or 1c and/or a homolog thereof, or
- d) a genetic regulatory element, for example a promoter, which is functionally linked c.g. to the nucleic acid sequence as depicted in Fig. 1a, 1b or 1c and/or a homolog thereof, or
- e) (a) and (b)

is/are not present in its/their natural genetic environment or has/have been modified by means of genetic manipulation methods, it being possible for the modification to be, by way of example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide radicals.

0073.0.1 "Natural genetic environment" means the natural chromosomal locus in the organism of origin or the presence in a genomic library. In the case of a genomic library, the natural, genetic environment of the nucleic acid sequence is preferably at least partially still preserved. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, particularly preferably at least 1000 bp, very particularly preferably at least 5000 bp.

0074.0.1 In said method for producing a transgenic plant comprising an SRP, the SRP coding nucleic acid is selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences. Further, the SRP coding nucleic acid used in the said method is at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c.

- 0075.0.1 A plant or plant cell is considered "true breeding" for a particular trait if it is genetically homozygous for that trait to the extent that, when the true-breeding plant is self-pollinated, a significant amount of independent segregation of the trait among the progeny is not observed. In the present invention, the trait arises from the transgenic expression of one or more DNA sequences introduced into a plant cell or plant.
- 0076.0.1 The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the level of expression of a SRP nucleic acid in the plant. The invention provides one method of producing a transgenic plant with a synthetic, novel or modified transcription factor that acts by increasing the transcription of a SRP gene. Theoretically it is also possible to obtain a decrease in expression of the gene.
- 0077.0.1 A method of detecting environmental stress in plant cells or plants comprising screening the plant cells for altered metabolic activity as compared to non-stress conditions is also in the scope of the invention.
- 0078.0.1 Further a method of screening plant cells or plants for increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions is encompassed in the invention.
- 0079.0.1 The present invention also encompasses a method of breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress.
- 0080.0.1 In these methods metabolic activity is preferably altered concerning the above metabolites and groups of metabolites.
- 0081.0.1 The present invention also encompasses the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants or plant cells with increased tolerance to environmental stress.
- 0082.0.1 The present invention further encompasses the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for detection of stress in plants or plant cells.
- 0083.0.1 The present invention also provides methods of modifying stress tolerance of a crop plant comprising utilizing a SRP coding nucleic acid sequence to

identify individual plants in populations segregating for either increased or decreased environmental stress tolerance (DNA marker).

0084.0.1 In the said method of modifying stress tolerance of a plant the SRP encoding nucleic acid may be selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences. Further the SRP coding nucleic acid used therein may at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c. Also an expression vector as described in the present invention might be used in the said method.

0085.0.1 In a variant method of said method of modifying stress tolerance, the plant is transformed with an inducible promoter that directs expression of the SRP. For example, the promoter is tissue specific. In a variant method, the used promoter is developmentally regulated.

0086.0.2 In a further embodiment, the method of modifying stress tolerance comprises one or more of the following steps:

- a) stabilizing a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- b) stabilizing a mRNA conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or its homologs or of a mRNA encoding the polypeptide of the present invention having the herein-mentioned activity of altering the metabolic activity;
- c) increasing the specific activity of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the present invention or decreasing the inhibitory regulation of the polypeptide of the invention;
- d) generating or increasing the expression of an endogenous or artificial transcription factor mediating the expression of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- e) stimulating activity of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the present invention or a polypeptide of the present invention having the herein-mentioned activity of altering the metabolic activity by adding one or more exogenous inducing factors to the organismus or parts thereof;

- f) expressing a transgenic gene encoding a protein conferring the increased expression of a polypeptide encoded by the nucleic acid molecule of the present invention or a polypeptide of the present invention, having the herein-mentioned activity of altering the metabolic activity; and/or
- 5 g) increasing the copy number of a gene conferring the increased expression of a nucleic acid molecule encoding a polypeptide encoded by the nucleic acid molecule of the invention or the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- 10 h) increasing the expression of the endogenous gene encoding the polypeptide of the invention or its homologs by adding positive expression or removing negative expression elements, e.g. homologous recombination can be used to either introduce positive regulatory elements like for plants the 35S enhancer into the promoter or to remove repressor elements from regulatory regions. Further gene conversion methods can be used to
- 15 disrupt repressor elements or to enhance to activity of positive elements-positive elements can be randomly introduced in plants by T-DNA or transposon mutagenesis and lines can be identified in which the positive elements have been integrated near to a gene of the invention, the expression of which is thereby enhanced;
- 20 and/or
- i) modulating growth conditions of the plant in such a manner, that the expression or activity of the gene encoding the protein of the invention or the protein itself is enhanced;
- j) selecting of organisms with especially high activity of the proteins of the invention from natural or from mutagenized resources and breeding them
- 25 into the target organisms, e.g. the elite crops.

0087.0.2 Preferably, said mRNA is the nucleic acid molecule of the present invention and/or the protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the present invention or the polypeptide having the

30 herein mentioned activity is the polypeptide of the present invention, e.g. conferring increased tolerance to environmental stress by altering the metabolic activity.

0088.0.2 In general, the amount of mRNA, polynucleotide or nucleic acid molecule in a cell or a compartment of an organism correlates with the amount of encoded protein and thus with the overall activity of the encoded protein in said

35 volume. Said correlation is not always linear, the activity in the volume is dependent on the stability of the molecules, the degradation of the molecules or the presence of

activating or inhibiting co-factors. Further, product and educt inhibitions of enzymes are well known, e.g. Zinser et al. "Enzyminhibitoren / Enzyme inhibitors".

0089.0.2 The activity of the abovementioned proteins and/or polypeptide encoded by the nucleic acid molecule of the present invention can be increased in various ways.

- 5 For example, the activity in an organism or in a part thereof, like a cell, is increased via increasing the gene product number, e.g. by increasing the expression rate, like introducing a stronger promoter, or by increasing the stability of the mRNA expressed, thus increasing the translation rate, and/or increasing the stability of the gene product, thus reducing the proteins decayed. Further, the activity or turnover of enzymes can be
- 10 influenced in such a way that a reduction or increase of the reaction rate or a modification (reduction or increase) of the affinity to the substrate results, is reached. A mutation in the catalytic centre of an polypeptide of the invention, e.g. as enzyme, can modulate the turn over rate of the enzyme, e.g. a knock out of an essential amino acid can lead to a reduced or completely knock out activity of the enzyme, or the deletion or
- 15 mutation of regulator binding sites can reduce a negative regulation like a feedback inhibition (or a substrate inhibition, if the substrate level is also increased). The specific activity of an enzyme of the present invention can be increased such that the turn over rate is increased or the binding of a co-factor is improved. Improving the stability of the encoding mRNA or the protein can also increase the activity of a gene product. The stimulation of the activity is also under the scope of the term "increased activity".
- 20

- 0090.0.2** Moreover, the regulation of the abovementioned nucleic acid sequences may be modified so that gene expression is increased. This can be achieved advantageously by means of heterologous regulatory sequences or by modifying, for example mutating, the natural regulatory sequences which are present. The
- 25 advantageous methods may also be combined with each other.

- 0091.0.2** In general, an activity of a gene product in an organism or part thereof, in particular in a plant cell, a plant, or a plant tissue or a part thereof or in a microorganism can be increased by increasing the amount of the specific encoding mRNA or the corresponding protein in said organism or part thereof. "Amount of protein or mRNA" is understood as meaning the molecule number of polypeptides or mRNA
- 30 molecules in an organism, a tissue, a cell or a cell compartment. "Increase" in the amount of a protein means the quantitative increase of the molecule number of said protein in an organism, a tissue, a cell or a cell compartment or part thereof - for example by one of the methods described herein below - in comparison to a wild type, control or reference.
- 35

0092.0.2 The increase in molecule number amounts preferably to at least 1%, preferably to more than 10%, more preferably to 30% or more, especially preferably to

50%, 70% or more, very especially preferably to 100%, most preferably to 500% or more. However, a de novo expression is also regarded as subject of the present invention.

0093.0.2 A modification, i.e. an increase or decrease, can be caused by endogenous or exogenous factors. For example, an increase in activity in an organism or a part thereof can be caused by adding a gene product or a precursor or an activator or an agonist to the media or nutrition or can be caused by introducing said subjects into an organism, transient or stable.

0094.0.2 In one embodiment the increase or decrease in metabolic activity in the plant or a part thereof, e.g. in a cell, a tissue, an organ, an organelle etc., is achieved by increasing the endogenous level of the polypeptide of the invention. Accordingly, in an embodiment of the present invention, the present invention relates to a process wherein the gene copy number of a gene encoding the polynucleotide or nucleic acid molecule of the invention is increased. Further, the endogenous level of the polypeptide of the invention can for example be increased by modifying the transcriptional or translational regulation of the polypeptide.

0095.0.2 In one embodiment the metabolic activity in the plant or part thereof can be altered by targeted or random mutagenesis of the endogenous genes of the invention. For example homologous recombination can be used to either introduce positive regulatory elements like for plants the 35S enhancer into the promoter or to remove repressor elements from regulatory regions. In addition gene conversion like methods described by Kochevenko and Wilmitzer (Plant Physiol. 2003 May;132(1):174-84) and citations therein can be used to disrupt repressor elements or to enhance to activity of positive regulatory elements. Furthermore positive elements can be randomly introduced in (plant) genomes by T-DNA or transposon mutagenesis and lines can be screened for, in which the positive elements has been integrated near to a gene of the invention, the expression of which is thereby enhanced. The activation of plant genes by random integrations of enhancer elements has been described by Hayashi et al., 1992 (Science 258:1350-1353) or Weigel et al., 2000 (Plant Physiol. 122, 1003-1013) and others cited therein.

0096.0.2 Reverse genetic strategies to identify insertions (which eventually carrying the activation elements) near in genes of interest have been described for various cases eg. Krysan et al., 1999 (Plant Cell 1999, 11, 2263-2290); Sessions et al., 2002 (Plant Cell 2002, 14, 2985-2994); Young et al., 2001, (Plant Physiol. 2001, 125, 513-518); Koprek et al., 2000 (Plant J. 2000, 24, 253-263); Jeon et al., 2000 (Plant J. 2000, 22, 561-570); Tissier et al., 1999 (Plant Cell 1999, 11, 1841-1852); Spaulmann et al., 1999 (Plant Cell 1999, 11, 1853-1866). Briefly material from all plants of a large

T-DNA or transposon mutagenized plant population is harvested and genomic DNA prepared. Then the genomic DNA is pooled following specific architectures as described for example in Krysan et al., 1999 (Plant Cell 1999, 11, 2283-2290). Pools of genomic DNAs are then screened by specific multiplex PCR reactions detecting the combination of the Insertional mutagen (eg T-DNA or Transposon) and the gene of interest. Therefore PCR reactions are run on the DNA pools with specific combinations of T-DNA or transposon border primers and gene specific primers. General rules for primer design can again be taken from Krysan et al., 1999 (Plant Cell 1999, 11, 2283-2290). Rescreening of lower levels DNA pools lead to the identification of individual plants in which the gene of interest is activated by the insertional mutagen.

0097.0.2 The enhancement of positive regulatory elements or the disruption or working of negative regulatory elements can also be achieved through common mutagenesis techniques: The production of chemically or radiation mutated populations is a common technique and known to the skilled worker. Methods for plants are described by Koomeef et al. 1982 and the citations therein and by Lighner and Caspar In "Methods in Molecular Biology" Vol 82. These techniques usually induce pointmutations that can be identified in any known gene using methods such as TILLING (Colbert et al. 2001).

0098.0.2 Accordingly, the expression level can be increased if the endogenous genes encoding a polypeptide conferring an increased expression of the polypeptide of the present invention, in particular genes comprising the nucleic acid molecule of the present invention, are modified via homologous recombination, Tilling approaches or gene conversion

0099.0.2 Regulatory sequences can be operatively linked to the coding region of an endogenous protein and control its transcription and translation or the stability or decay of the encoding mRNA or the expressed protein. In order to modify and control the expression, promoter, UTRs, splicing sites, processing signals, polyadenylation sites, terminators, enhancers, repressors, post transcriptional or posttranslational modification sites can be changed, added or amended. For example, the activation of plant genes by random integrations of enhancer elements has been described by Hayashi et al., 1992 (Science 258:1350-1353) or Weigel et al., 2000 (Plant Physiol. 122, 1003-1013) and others cited therein. For example, the expression level of the endogenous protein can be modulated by replacing the endogenous promoter with a stronger transgenic promoter or by replacing the endogenous 3'UTR with a 3'UTR, which provides more stability without amending the coding region. Further, the transcriptional regulation can be modulated by introduction of a artificial transcription

factor as described in the examples. Alternative promoters, terminators and UTRs are described below.

0100.0.2 The activation of an endogenous polypeptide having above-mentioned activity, e.g. conferring an increased tolerance to environmental stress after altering the metabolic activity can also be increased by introducing a synthetic transcription factor, which binds close to the coding region of the protein of the invention encoding gene and activates its transcription. A chimeric zinc finger protein can be construed, which comprises a specific DNA-binding domain and an activation domain as e.g. the VP16 domain of Herpes Simplex virus. The specific binding domain can bind to the regulatory region of the protein coding region. The expression of the chimeric transcription factor in a plant leads to a specific expression of the protein of the invention, see e.g. in WO01/52830, Ortiz, Proc. Natl. Acad. Sci. USA, 2002, Vol. 99, 13290 or Guan, Proc. Natl. Acad. Sci. USA, 2002, Vol. 99, 13296.

0101.0.2 In one further embodiment of the method according to the invention, plants are used in which one of the abovementioned genes, or one of the abovementioned nucleic acids, is mutated in a way that the activity of the encoded gene products is less influenced by cellular factors, or not at all, in comparison with the unmutated proteins. For example, well known regulation mechanism of enzymic activity are substrate inhibition or feed back regulation mechanisms. Ways and techniques for the introduction of substitutions, deletions and additions of one or more bases, nucleotides or amino acids of a corresponding sequence are described herein below in the corresponding paragraphs and the references listed there, e.g. in Sambrook et al., Molecular Cloning, Cold Spring Harbour, NY, 1989. The person skilled in the art will be able to identify regulation domains and binding sites of regulators by comparing the sequence of the nucleic acid molecule of the present invention or the expression product thereof with the state of the art by computer software means which comprise algorithms for the identifying of binding sites and regulation domains or by introducing into a nucleic acid molecule or in a protein systematically mutations and assaying for those mutations which will lead to an increased specific activity or an increased activity per volume, in particular per cell.

0102.0.2 It is therefore advantageously to express in a plant a nucleic acid molecule of the invention or a polypeptide of the invention derived from a evolutionary distantly related organism, as e.g. using a prokaryotic gene in a eukaryotic host, as in these cases the regulation mechanism of the host cell may not weaken the activity (cellular or specific) of the gene or its expression product.

0103.0.2 The mutation is introduced in such a way that the production of the amino acids is not adversely affected.

- 0104.0.2** Less influence on the regulation of a gene or its gene product is understood as meaning a reduced regulation of the enzymatic activity leading to an increased specific or cellular activity of the gene or its product. An increase of the enzymatic activity is understood as meaning an enzymatic activity, which is increased by at least 10%, advantageously at least 20, 30 or 40%, especially advantageously by at least 50, 60 or 70% in comparison with the starting organism.
- 0105.0.1** The invention provides that the above methods can be performed such that the stress tolerance is increased. It is also possible to obtain a decrease in stress tolerance.
- 0106.0.1** The invention is not limited to specific nucleic acids, specific polypeptides, specific cell types, specific host cells, specific conditions or specific methods etc., as such, but may vary and numerous modifications and variations therein will be apparent to those skilled in the art. It is also to be understood that the terminology used herein is for the purpose of describing specific embodiments only and is not intended to be limiting.
- 0107.0.1** The present invention also relates to isolated Stress Related Proteins (SRP) which are selected from the group comprising the proteins of Fig. 1a, 1b or 1c and/or homologs thereof. Preferably, the isolated Stress Related Proteins (SRP) of the present invention are selected from yeast or *E. coli*. Further, the present invention is related to isolated Stress Related Protein (SRP) encoding nucleic acids selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs thereof. Here, preferably, an isolated Stress Related Protein (SRP) encoding nucleic acid encodes an SRP which is selected from yeast or *E. coli*.
- 0108.0.1** The present invention provides stress related gene sequences selected from the group consisting of the the nucleic acid of Fig. 1a, 1b or 1c of yeast, preferably from *Saccharomyces cerevisiae* or *E. coli*.
- 0109.0.1** Homologs of the aforementioned sequences can be isolated advantageously from yeast, fungi, viruses, algae, bacteria, such as *Acetobacter* (subgen. *Acetobacter*) *aceti*; *Acidithiobacillus ferrooxidans*; *Acinetobacter* sp.; *Actinobacillus* sp.; *Aeromonas salmonicida*; *Agrobacterium tumefaciens*; *Aquifex aeolicus*; *Arcanobacterium pyogenes*; *Aster yellows phytoplasma*; *Bacillus* sp.; *Bifidobacterium* sp.; *Borrelia burgdorferi*; *Brevibacterium linens*; *Brucella melitensis*; *Buchnera* sp.; *Butyrivibrio fibrisolvens*; *Campylobacter jejuni*; *Caulobacter crescentus*; *Chlamydia* sp.; *Chlamydomophila* sp.; *Chlorobium limicola*; *Citrobacter rodentium*; *Clostridium* sp.; *Comamonas testosteroni*; *Corynebacterium* sp.; *Coxiella burnetii*; *Deinococcus radiodurans*; *Dichelobacter nodosus*; *Edwardsiella ictaluri*; *Enterobacter* sp.; *Erysipelothrix rhusopathiae*; *Escherichia coli*; *Flavobacterium* sp.; *Francisella*

- tularans; *Frankia* sp. Cpl1; *Fusobacterium nucleatum*; *Geobacillus stearothermophilus*; *Gluconobacter oxydans*; *Haemophilus* sp.; *Helicobacter pylori*; *Klebsiella pneumoniae*; *Lactobacillus* sp.; *Lactococcus lactis*; *Listeria* sp.; *Mannheimia haemolytica*; *Mesorhizobium loti*; *Methylophaga thalassica*; *Microcystis aeruginosa*;
- 5 *Microscilla* sp. PRE1; *Moraxella* sp. TA144; *Mycobacterium* sp.; *Mycoplasma* sp.; *Neisseria* sp.; *Nitrosomonas* sp.; *Nostoc* sp. PCC 7120; *Novosphingobium aromaticivorans*; *Oenococcus oeni*; *Pantoea citrea*; *Pasteurella multocida*; *Pediococcus pentosaceus*; *Phormidium foveolarum*; *Phytoplasma* sp.; *Plectonoma boryanum*; *Prevotella ruminicola*; *Propionibacterium* sp.; *Proteus vulgaris*;
- 10 *Pseudomonas* sp.; *Ralstonia* sp.; *Rhizobium* sp.; *Rhodococcus equi*; *Rhodothermus marinus*; *Rickettsia* sp.; *Riemerella anatipestifer*; *Ruminococcus flavefaciens*; *Salmonella* sp.; *Selenomonas ruminantium*; *Serratia citromophila*; *Shigella* sp.; *Sinorhizobium meliloti*; *Staphylococcus* sp.; *Streptococcus* sp.; *Streptomyces* sp.; *Synechococcus* sp.; *Synechocystis* sp. PCC 6803; *Thermotoga maritima*; *Treponema*
- 15 sp.; *Ureaplasma urealyticum*; *Vibrio cholerae*; *Vibrio parahaemolyticus*; *Xylella fastidiosa*; *Yersinia* sp.; *Zymomonas mobilis*, preferably *Salmonella* sp. or *Escherichia coli* or plants, preferably from yeasts such as from the genera *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Torulopsis* or *Schizosaccharomyces* or plants such as *Arabidopsis thaliana*, maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut,
- 20 cotton, borage, sunflower, linseed, pyramise, rapeseed, canola and turnip rape, manihot, pepper, sunflower, tagetes, solanaceous plant such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants such as coffee, cacao, tea, *Saltix* species, trees such as oil palm, coconut, perennial grass, such as ryegrass and fescue, and forage crops, such as alfalfa and clover and from spruce, pine or fir for
- 25 example. More preferably homologs of aforementioned sequences can be isolated from *Saccharomyces cerevisiae*, *E. coli* or plants, preferably *Brassica napus*, *Glycine max*, or *Oryza sativa*.

- 0110.0.1** The stress related proteins of the present invention are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule
- 30 encoding the protein is cloned into an expression vector, for example in to a binary vector, the expression vector is introduced into a host cell, for example the *Arabidopsis thaliana* wild type NASC N906 or any other plant cell as described in the examples see below, and the stress related protein is expressed in said host cell. Examples for binary vectors are pBIN19, pBI101, pBinAR, pGPV, pCambia, pBIB-HYG, pBecks,
- 35 pGreen or pPZP (Hajdukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 889-994 and Hellens et al, Trends in Plant Science (2000) 5, 446-451.).

- 0111.0.1** Advantageously, the nucleic acid sequences according to the invention or the gene construct together with at least one reporter gene are cloned into an expression cassette, which is introduced into the organism via a vector or directly into the genome. This reporter gene should allow easy detection via a growth, fluorescence, chemical, bioluminescence or resistance assay or via a photometric measurement. Examples of reporter genes which may be mentioned are antibiotic- or herbicide-resistance genes, hydrolase genes, fluorescence protein genes, bioluminescence genes, sugar or nucleotide metabolic genes or biosynthesis genes such as the Ura3 gene, the *Ilv2* gene, the luciferase gene, the β -galactosidase gene, the *gfp* gene, the 2-deoxyglucose-6-phosphate phosphatase gene, the β -glucuronidase gene, β -lactamase gene, the neomycin phosphotransferase gene, the hygromycin phosphotransferase gene or the BASTA (= glyphosate-resistance) gene. These genes permit easy measurement and quantification of the transcription activity and hence of the expression of the genes. In this way genome positions may be identified which exhibit differing productivity.
- 0112.0.1** In a preferred embodiment a nucleic acid construct, for example an expression cassette, comprises upstream, i.e. at the 5' end of the encoding sequence, a promoter and downstream, i.e. at the 3' end, a polyadenylation signal and optionally other regulatory elements which are operably linked to the intervening encoding sequence with the nucleic acid of Fig. 1a, 1b or 1c. By an operable linkage is meant the sequential arrangement of promoter, encoding sequence, terminator and optionally other regulatory elements in such a way that each of the regulatory elements can fulfill its function in the expression of the encoding sequence in due manner. The sequences preferred for operable linkage are targeting sequences for ensuring subcellular localization in plastids. However, targeting sequences for ensuring subcellular localization in the mitochondrion, in the endoplasmic reticulum (= ER), in the nucleus, in oil corpuscles or other compartments may also be employed as well as translation promoters such as the 5' lead sequence in tobacco mosaic virus (Gallie et al., Nucl. Acids Res. 15 (1987), 8593-8711).
- 0113.0.1** A nucleic acid construct, for example an expression cassette may, for example, contain a constitutive promoter or a tissue-specific promoter (preferably the USP or napin promoter) the gene to be expressed and the ER retention signal. For the ER retention signal the KDEL amino acid sequence (lysine, aspartic acid, glutamic acid, leucine) or the KKX amino acid sequence (lysine-lysine-X-stop, wherein X means every other known amino acid) is preferably employed.
- 0114.0.1** For expression in a prokaryotic or eukaryotic host organism, for example a microorganism such as a fungus or a plant the expression cassette is

- advantageously inserted into a vector such as by way of example a plasmid, a phage or other DNA which allows optimum expression of the genes in the host organism. Examples of suitable plasmids are: in *E. coli* pLG338, pACYC184, pBR series such as e.g. pBR322, pUC series such as pUC18 or pUC19, M13mp series, pKC30, pRep4,
- 5 pHS1, pHS2, pPI₂236, pMBL24, pLG200, pUR290, pIN-III¹³-B1, λ gt11 or pBdCl; in *Streptomyces* pIJ101, pIJ364, pIJ702 or pIJ361; in *Bacillus* pUB110, pC194 or pBD214; in *Corynebacterium* pSA77 or pAJ687; in fungi pALS1, pIL2 or pBS116; other advantageous fungal vectors are described by Romanos, M.A. et al., [(1992) „Foreign gene expression in yeast: a review“, *Yeast* 8; 423-488] and by van den Hondel,
- 10 C.A.M.J.J. et al. [(1991) „Heterologous gene expression in filamentous fungi“ as well as in *More Gene Manipulations in Fungi* [J.W. Bennet & L.L. Lasure, eds., pp. 398-428; Academic Press: San Diego] and in „Gene transfer systems and vector development for filamentous fungi“ [van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. et al., eds., pp. 1-28, Cambridge University Press: Cambridge].
- 15 Examples of advantageous yeast promoters are 2 μ M, pAG-1, YE6 δ , YEp18 or pEMBLYe28. Examples of algal or plant promoters are pLGV23, pGHec⁺, pBIN19, p2K2004, pVKH or pDH51 (see Schmidt, R. and Wilmitsch, L., 1986). The vectors identified above or derivatives of the vectors identified above are a small selection of the possible plasmids. Further plasmids are well known to those skilled in the art and may be found, for example, in the book *Cloning Vectors* (Eds. Pouwels P.H. et al. Elsevier, Amsterdam-New York-Oxford, 1985 , ISBN 0 444 804018). Suitable plant vectors are described inter alia in „*Methods in Plant Molecular Biology and Biotechnology*“ (CRC Press), Ch. 6/7, pp. 71-118. Advantageous vectors are known as shuttle vectors or binary vectors which replicate in
- 20 *E. coli* and *Agrobacterium*.

0115.0.1 By vectors is meant with the exception of plasmids all other vectors known to those skilled in the art such as by way of example phages, viruses such as SV40, CMV, baculovirus, adenovirus, transposons, IS elements, plasmids, phagemids, cosmids, linear or circular DNA. These vectors can be replicated

30 autonomously in the host organism or be chromosomally replicated, chromosomal replication being preferred.

0116.0.1 In a further embodiment of the vector the expression cassette according to the invention may also advantageously be introduced into the organisms in the form of a linear DNA and be integrated into the genome of the host organism by way of

35 heterologous or homologous recombination. This linear DNA may be composed of a linearized plasmid or only of the expression cassette as vector or the nucleic acid sequences according to the invention.

0117.0.1 In a further advantageous embodiment the nucleic acid sequence according to the invention can also be introduced into an organism on its own.

0118.0.1 If in addition to the nucleic acid sequence according to the invention further genes are to be introduced into the organism, all together with a reporter gene in a single vector or each single gene with a reporter gene in a vector in each case can be introduced into the organism, whereby the different vectors can be introduced simultaneously or successively.

0119.0.1 The vector advantageously contains at least one copy of the nucleic acid sequences according to the invention and/or the expression cassette (= gene construct) according to the invention.

0120.0.3 The invention further provides an isolated recombinant expression vector comprising a SRP nucleic acid as described above, wherein expression of the vector in a host cell results in increased tolerance to environmental stress as compared to a wild type variety of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent functions.

0121.0.3 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. As used herein with respect to a recombinant expression vector, "operatively linked" is intended to mean

- that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *In vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers, and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990) and Gruber and Crosby, in: *Methods in Plant Molecular Biology and Biotechnology*, eds. Glick and Thompson, Chapter 7, 89-108, CRC Press: Boca Raton, Florida, including the references therein. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides or peptides, encoded by nucleic acids as described herein (e.g., SRPs, mutant forms of SRPs, fusion polypeptides, etc.).
- 20 0122.0.3 The recombinant expression vectors of the invention can be designed for expression of SRPs in prokaryotic or eukaryotic cells. For example, SRP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (See Romano, M.A. et al., 1992, Foreign gene expression in yeast: a review, *Yeast* 8:423-438; van den Hondel, C.A.M.J.J. et al., 1991, Heterologous gene expression in filamentous fungi, in: *More Gene Manipulations in Fungi*, J.W. Bennet & L.L. Lasura, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J., 1991, Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. et al., eds., p. 1-28, Cambridge University Press: Cambridge), algae (Falcione et al., 1999, *Marine Biotechnology* 1(3):239-251), ciliates of the types: Holotrichia, Peritrichia, Spirotrichia, Suctorina, Tetrahymena, Paramacium, Colpidium, Glaucoma, Platyophrya, Potomacus, Pseudocostinilembus, Euplotes, Engelmanniella, and Stylonychia, especially of the genus *Stylonychia* lemnsee with vectors following a transformation method as described in PCT Application No. WO 98/01572, and multicellular plant cells (See Schmidt, R. and Willmitzer, L., 1998, High efficiency *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants, *Plant Cell Rep.* 583-588; *Plant Molecular Biology* and

Biotechnology, G. Press, Boca Raton, Florida, chapter 6/7, S.71-119 (1993); F.F. White, B. Jenas et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. Kung und R. Wu, 129-43, Academic Press: 1993; Potrykus, 1991, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42:205-225 and references cited therein) or mammalian cells. Suitable host cells are discussed further in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press: San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- 10 **0123.0.3** Expression of polypeptides in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide but also to the C-terminus or fused within suitable regions in the polypeptides. Such fusion vectors typically serve three purposes: 1) to increase expression of a recombinant polypeptide; 2) to increase the solubility of a recombinant polypeptide; and 3) to aid in the purification of a recombinant polypeptide by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin, and enterokinase.
- 15 20

- 0124.0.1** By way of example the plant expression cassette can be installed in the pRT transformation vector ((a) Toepfer et al., 1983, Methode Enzymol., 217: 68-78; (b) Toepfer et al. 1987, Nucl. Acids. Res. 15: 5690 ff.).
- 25

0125.0.1 Alternatively, a recombinant vector (= expression vector) can also be transcribed and translated *in vitro*, e.g. by using the T7 promoter and the T7 RNA polymerase.

- 0126.0.1** Expression vectors employed in prokaryotes frequently make use of inducible systems with and without fusion proteins or fusion oligopeptides, wherein these fusions can ensue in both N-terminal and C-terminal manner or in other useful domains of a protein. Such fusion vectors usually have the following purposes: i.) to increase the RNA expression rate; ii.) to increase the achievable protein synthesis rate; iii.) to increase the solubility of the protein; iv.) or to simplify purification by means of a binding sequence usable for affinity chromatography. Proteolytic cleavage points are also frequently introduced via fusion proteins, which allow cleavage of a portion of the
- 30 35

fusion protein and purification. Such recognition sequences for proteases are recognized, e.g. factor Xa, thrombin and enterokinase.

0127.0.1 Typical advantageous fusion and expression vectors are pGEX [Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1986) *Gene* 87: 31-40], pMAL
5 (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which contains glutathione S-transferase (GST), maltose binding protein or protein A.

0128.0.3 In one embodiment, the coding sequence of the SRP is cloned into a pGEX expression vector to create a vector encoding a fusion polypeptide comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X polypeptide. The
10 fusion polypeptide can be purified by affinity chromatography using glutathione-agarose resin. Recombinant PKSRP unfused to GST can be recovered by cleavage of the fusion polypeptide with thrombin.

0129.0.1 Other examples of *E. coli* expression vectors are pTrc [Amann et al., (1988) *Gene* 69:301-315] and pET vectors [Studler et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; Stratagene, Amsterdam, The Netherlands].

0130.0.3 Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid *trp-lac* fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 *gn10-lac* fusion promoter
20 mediated by a co-expressed viral RNA polymerase (T7 *gn1*). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 *gn1* gene under the transcriptional control of the *lacUV5* promoter.

0131.0.3 One strategy to maximize recombinant polypeptide expression is to express the polypeptide in a host bacteria with an impaired capacity to proteolytically
25 cleave the recombinant polypeptide (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum*
30 (Wada et al., 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

0132.0.1 Other advantageous vectors for use in yeast are pYepSac1 [Baldari, et al., (1987) *Embo J.* 6:229-234], pMFa [Kurjan and Herskowitz, (1982) *Cell* 30:933-943], pJRY68 [Schultz et al., (1987) *Gene* 54:113-123], and pYES derivatives [Invitrogen Corporation, San Diego, CA]. Vectors for use in filamentous fungi are described in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) „Gene transfer systems

and vector development for filamentous fungi", in: Applied Molecular Genetics of Fungi, J.F. Peberdy, et al., eds., pp. 1-28, Cambridge University Press: Cambridge.

0133.0.1 Alternatively, insect cell expression vectors can also be advantageously utilized, e.g. for expression in Sf 9 cells. These are e.g. the vectors of the pAc series (Smith et al. (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

0134.0.1 Furthermore, plant cells or algal cells can advantageously be used for gene expression. Examples of plant expression vectors may be found in Becker, D., et al. (1992) „New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197 or in Bevan, M.W. (1984) „Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721.

0135.0.1 Furthermore, the nucleic acid sequences may also be expressed in mammalian cells, advantageously in nonhuman mammalian cells. Examples of corresponding expression vectors are pCDM8 and pMT2PC referred to in: Seed, B. (1987) *Nature* 329:640 or Kaulman et al. (1987) *EMBO J.* 6: 187-195). At the same time promoters preferred for use are of viral origin, such as by way of example promoters of polyoma, adenovirus 2, cytomegalovirus or simian virus 40. Other prokaryotic and eukaryotic expression systems are referred to in chapters 16 and 17 of Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

0136.0.3 In a preferred embodiment of the present invention, the SRPs are expressed in plants and plant cells such as unicellular plant cells (e.g. algae) (See Felciatore et al., 1999, *Marine Biotechnology* 1(3):239-251 and references therein) and plant cells from higher plants (e.g., the spermatophytes, such as crop plants). A SRP may be "introduced" into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, and the like. One transformation method known to those of skill in the art is the dipping of a flowering plant into an *Agrobacteria* solution, wherein the *Agrobacteria* contains the SRP nucleic acid, followed by breeding of the transformed gametes.

0137.0.3 Other suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, and other laboratory manuals such as *Methods in Molecular Biology*, 1995, Vol. 44, *Agrobacterium* protocols, ed: Gartland and Davey, Humana Press, Totowa, New Jersey. As biotic and abiotic stress tolerance is a general trait wished to be inherited into a wide variety of plants like maize, wheat, rye,

oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses, and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention. Forage crops include, but are not limited to, Wheatgrass, Canarygrass, Bromegrass, Wildrye Grass, Bluegrass, Orchardgrass, Alfalfa, Salfoni, Birdsfoot Trefoli, Alsike Clover, Red Clover, and Sweet Clover.

0138.0.3 In one embodiment of the present invention, transfection of a SRP into a plant is achieved by *Agrobacterium* mediated gene transfer. *Agrobacterium* mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986, Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) *Agrobacterium tumefaciens* strain. Transformation can be performed by standard transformation and regeneration techniques (Deblacq et al., 1994, Nucl. Acids Res. 13:4777-4782; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Centrale Signatur: BT11-P ISBN 0-7823-2731-4; Glick, Bernard R.; Thompson, John E., methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989, Plant Cell Report 8:238-242; De Block et al., 1989, Plant Physiol. 91:694-701). Use of antibiotics for *Agrobacterium* and plant selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Repressed selection is normally performed using kanamycin as selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994, Plant Cell Report 13:262-265. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 867, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387, and a specific example of wheat transformation can be found in PCT Application No. WO 93/07258.

0139.0.3 According to the present invention, the introduced SRP may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the

introduced SRP may be present on an extra-chromosomal non-replicating vector and be transiently expressed or transiently active.

0140.0.3 In one embodiment, a homologous recombinant microorganism can be created wherein the SRP is integrated into a chromosome, a vector is prepared which contains at least a portion of a SRP gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the SRP gene. Preferably, the SRP gene is a yeast, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP gene, but it can be a homolog from a related plant or even from a mammalian or insect source. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRP gene is functionally disrupted (i.e., no longer encodes a functional polypeptide; also referred to as a knock-out vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SRP gene is mutated or otherwise altered but still encodes a functional polypeptide (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRP). To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasty (Cole-Streuss et al., 1998, *Nucleic Acids Research* 27(5):1323-1330 and Kmiec, 1999 *Gene therapy American Scientist*, 87(3):240-247). Homologous recombination procedures in *Physcomitrella patens* are also well known in the art and are contemplated for use herein.

0141.0.3 Whereas in the homologous recombination vector, the altered portion of the SRP gene is flanked at its 5' and 3' ends by an additional nucleic acid molecule of the SRP gene to allow for homologous recombination to occur between the exogenous SRP gene carried by the vector and an endogenous SRP gene, in a microorganism or plant. The additional flanking SRP nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See, e.g., Thomas, K.R., and Capocchi, M.R., 1987, *Cell* 51:503 for a description of homologous recombination vectors or Strepp et al., 1998, *PNAS*, 95 (8):1368-1373 for cDNA based recombination in *Physcomitrella patens*. The vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and calls in which the introduced PKSRP gene has homologously recombined with the endogenous PKSRP gene are selected using art-known techniques.

0142.0.3 In another embodiment, recombinant microorganisms can be produced that contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of a SRP gene on a vector placing it under control of the

lac operon permits expression of the SRP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

0143.0.3 Whether present in an extra-chromosomal non-replicating vector or a vector that is integrated into a chromosome, the SRP polynucleotide preferably resides in a plant expression cassette. A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells that are operatively linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* t-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gielen et al., 1984, EMBO J. 3:835) or functional equivalents thereof but also all other terminators functionally active in plants are suitable. As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operatively linked sequences like translational enhancers such as the overdrive-sequence containing the 5'-untranslated leader sequence from tobacco mosaic virus enhancing the polypeptide per RNA ratio (Gallie et al., 1987, Nucl. Acids Research 15:8683-8711). Examples of plant expression vectors include those detailed in: Becker, D. et al., 1992, New plant binary vectors with selectable markers located proximal to the left border, Plant Mol. Biol. 20: 1195-1197; and Bevan, M.W., 1984, Binary *Agrobacterium* vectors for plant transformation, Nucl. Acid. Res. 12:8711-8721; and Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds.: Kung and R. Wu, Academic Press, 1993, S. 15-38.

0144.0.1 "Transformation" is defined herein as a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. It may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed and may include, but is not limited to, viral infection, electroporation, lipofection, and particle bombardment. Such "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

0145.0.1 The terms "transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into

the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, e.g., a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

0146.0.1 A "transgenic plant", as used herein, refers to a plant which contains a foreign nucleotide sequence inserted into either its nuclear genome or organellar genome. It encompasses further the offspring generations i.e. the T1-, T2- and consecutively generations or BC1-, BC2- and consecutively generation as well as crossbreeds thereof with non-transgenic or other transgenic plants.

0147.0.1 The host organism (= transgenic organism) advantageously contains at least one copy of the nucleic acid according to the invention and/or of the nucleic acid construct according to the invention.

0148.0.2 In principle all plants can be used as host organism. Preferred transgenic plants are, for example, selected from the families Aceraceae, Anacardiaceae, Apiaceae, Asteraceae, Brassicaceae, Cactaceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Malvaceae, Nymphaeaceae, Papaveraceae, Rosaceae, Salicaceae, Solanaceae, Arecaceae, Bromeliaceae, Cyperaceae, Iridaceae, Liliaceae, Orchidaceae, Gentianaceae, Labiaceae, Magnoliaceae, Ranunculaceae, Carifolaceae, Rubiaceae, Scrophulariaceae, Caryophyllaceae, Ericaceae, Polygonaceae, Violaceae, Juncaceae or Poaceae and preferably from a plant selected from the group of the families Apiaceae, Asteraceae, Brassicaceae, Cucurbitaceae, Fabaceae, Papaveraceae, Rosaceae, Solanaceae, Liliaceae or Poaceae. Preferred are crop plants such as plants advantageously selected from the group of the genus peanut, oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin/squash, linseed, soya, pistachio, borage, maize, wheat, rye, oats, sorghum and millet, triticale, rice, barley, cassava, potato, sugarbeet, egg plant, alfalfa, and perennial grasses and forage plants, oil palm, vegetables (brassicas, root vegetables, tuber vegetables, pod vegetables, fruiting vegetables, onion vegetables, leafy vegetables and stem vegetables), buckwheat, Jerusalem artichoke, broad bean, vetches, lentil, dwarf bean, lupin, clover and Lucerne for mentioning only some of them.

0149.0.2 In one preferred embodiment, the host plant is selected from the families Aceraceae, Anacardiaceae, Apiaceae, Asteraceae, Brassicaceae, Cactaceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Malvaceae, Nymphaeaceae, Papaveraceae, Rosaceae, Salicaceae, Solanaceae, Arecaceae, Bromeliaceae,

- Cyperaceae, Iridaceae, Liliaceae, Orchidaceae, Gentianaceae, Labiaceae, Magnoliaceae, Ranunculaceae, Carifolaceae, Rubiaceae, Scrophulariaceae, Caryophyllaceae, Ericaceae, Polygonaceae, Violaceae, Juncaceae or Poaceae and preferably from a plant selected from the group of the families Apiaceae, Asteraceae,
- 5 Brassicaceae, Cucurbitaceae, Fabaceae, Papaveraceae, Rosaceae, Solanaceae, Liliaceae or Poaceae. Preferred are crop plants and in particular plants mentioned herein above as host plants such as the families and genera mentioned above for example preferred the species *Anacardium occidentale*, *Calendula officinalis*, *Carthamus tinctorius*, *Cichorium intybus*, *Cynara scolymus*, *Helianthus annuus*, *Tagetes*
- 10 *lucida*, *Tagetes erecta*, *Tagetes tenuifolia*, *Daucus carota*, *Corylus avellana*, *Corylus colurna*, *Borago officinalis*, *Brassica napus*, *Brassica rapa* ssp., *Sinapis arvensis*, *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapifolias*, *Melanostaphis communis*, *Brassica oleracea*, *Arabidopsis thaliana*, *Ananas comosus*, *Ananas ananass*, *Bromelia*
- 15 *comosa*, *Carica papaya*, *Cannabis sativa*, *Ipomoea batatas*, *Ipomoea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomoea fastigiata*, *Ipomoea tiliacea*, *Ipomoea triloba*, *Convolvulus panduratus*, *Beta vulgaris*, *Beta vulgaris* var. *altissima*, *Beta vulgaris* var. *vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva*, *Beta vulgaris* var. *esculenta*, *Cucurbita maxima*, *Cucurbita mixta*,
- 20 *Cucurbita pepo*, *Cucurbita moschata*, *Olea europaea*, *Manihot utilissima*, *Janipha manihot*, *Jatropha manihot*, *Manihot aipil*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot aesculenta*, *Ricinus communis*, *Pisum sativum*, *Pisum arvensis*, *Pisum humile*, *Medicago sativa*, *Medicago falcata*, *Medicago varia*, *Glycine max*, *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida*, *Soja*
- 25 *max*, *Cocos nucifera*, *Peltargonium grossularioides*, *Oleum coccaea*, *Laurus nobilis*, *Persea americana*, *Arachis hypogaea*, *Linum usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*, *Linum grandiflorum*, *Adenolinum grandiflorum*, *Linum lewisii*, *Linum narbonense*, *Linum perenne*, *Linum perenne* var. *lewisii*, *Linum pratense*, *Linum trigynum*, *Punica*
- 30 *granatum*, *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum*, *Gossypium thurberi*, *Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp., *Elaeis guineensis*, *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium*, *Sesamum indicum*, *Piper aduncum*, *Piper amalago*, *Piper angustifolium*, *Piper aurum*, *Piper betel*, *Piper cuboba*, *Piper longum*, *Piper nigrum*,
- 35 *Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper elongatum*, *Steffensia elongata*, *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum murinum*, *Hordeum scaberrimum*, *Hordeum distichon*, *Hordeum aegyptiacum*, *Hordeum*

- hexastichon*, *Hordeum hexastichum*, *Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum*, *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida*, *Sorghum bicolor*, *Sorghum halepense*, *Sorghum saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum caffrorum*, *Sorghum oeruum*, *Sorghum vochina*, *Sorghum drummondii*, *Sorghum dura*, *Sorghum guineense*, *Sorghum lanceolatum*, *Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum millaceum* millet, *Panicum millaceum*, *Zea mays*, *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernium*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare*, *Coffea* spp., *Coffea arabica*, *Coffea canephora*, *Coffea liberica*, *Capsicum annuum*, *Capsicum annuum* var. *glabrusculum*, *Capsicum frutescens*, *Capsicum annuum*, *Nicotiana tabacum*, *Solanum tuberosum*, *Solanum melongena*, *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium*, *Solanum lycopersicum* *Theobroma cacao* or *Camellia sinensis*.
- 0150.0.2 Anacardiaceae such as the genera *Pistacia*, *Mangifera*, *Anacardium* e.g. the species *Pistacia vera* [pistachios, *Pistazie*], *Mangifera indica* [Mango] or *Anacardium occidentale* [Cashew]; Asteraceae such as the genera *Calendula*, *Carthamus*, *Centaurea*, *Cichorium*, *Cynara*, *Helianthus*, *Lactuca*, *Luxusta*, *Tagetes*, *Valeriana* e.g. the species
- 20 *Calendula officinalis* [Marigold], *Carthamus tinctorius* [safflower], *Centaurea cyanus* [cornflower], *Cichorium intybus* [blue daisy], *Cynara scolymus* [Artichoke], *Helianthus annuus* [sunflower], *Lactuca sativa*, *Lactuca crisper*, *Lactuca esculenta*, *Lactuca scariola* L. ssp. *sativa*, *Lactuca scariola* L. var. *integrata*, *Lactuca scariola* L. var. *integrifolia*, *Lactuca sativa* subsp. *romana*, *Lactuca communis*, *Valeriana locustia* [lettuce], *Tagetes lucida*, *Tagetes erecta* or *Tagetes tenuifolia* [Marigold]; Apiaceae such as the genera *Daucus* e.g. the species *Daucus carota* [carrot]; Betulaceae such as the genera *Corylus* e.g. the species *Corylus avellana* or *Corylus cornuta* [hazelnut]; Boraginaceae such as the genera *Borago* e.g. the species *Borago officinalis* [borage]; Brassicaceae such as the genera *Brassica*, *Melanosinapis*, *Sinapis*, *Arabidopsis* e.g. the species *Brassica napus*,
- 30 *Brassica rapa* ssp. [canola, oilseed rape, turnip rape], *Sinapis arvensis* *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapioides*, *Melanosinapis communis* [mustard], *Brassica oleracea* [cabbage] or *Arabidopsis thaliana*; Bromeliaceae such as the genera *Ananas*, *Bromelia* e.g. the species *Ananas comosus*, *Ananas ananass* or *Bromelia comosa* [pineapple]; Caricaceae such as the genera *Carica* e.g. the species *Carica papaya* [papaya]; Cannabaceae such as the genera *Cannabis* e.g. the species *Cannabis*

- sative [hemp], Convolvulaceae such as the genera *Ipomoea*, *Convolvulus* e.g. the species *Ipomoea batatas*, *Ipomoea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomoea fastigata*, *Ipomoea tiliacea*, *Ipomoea triloba* or *Convolvulus panduratus* [sweet potato, Man of the Earth, wild potato], Chenopodiaceae such as the genera *Beta*, i.e. the species *Beta vulgaris*, *Beta vulgaris* var. *atissima*, *Beta vulgaris* var. *Vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva* or *Beta vulgaris* var. *esculenta* [sugar beet]; Cucurbitaceae such as the genera *Cucurbita* e.g. the species *Cucurbita maxima*, *Cucurbita mixta*, *Cucurbita pepo* or *Cucurbita moschata* [pumpkin, squash]; Elaeagnaceae such as the genera *Elaeagnus* e.g. the species *Olea europaea* [olive]; Ericaceae such as the genera *Kalmia* e.g. the species *Kalmia latifolia*, *Kalmia angustifolia*, *Kalmia microphylla*, *Kalmia polifolia*, *Kalmia occidentalis*, *Cistus chamaerhodendros* or *Kalmia lucida* [American laurel, broad-leaved laurel, calico bush, spoon wood, sheep laurel, alpine laurel, bog laurel, western bog-laurel, swamp-laurel]; Euphorbiaceae such as the genera *Manihot*, *Jaripha*, *Jatropha*, *Ricinus* e.g. the species *Manihot utilisima*, *Jaripha manihot*, *Jatropha manihot*, *Manihot aipi*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot esculenta* [manihot, arrowroot, tapioca, cassava] or *Ricinus communis* [castor bean, Castor Oil Bush, Castor Oil Plant, Palma Christi, Wonder Tree]; Fabaceae such as the genera *Pisum*, *Albizia*, *Cathormion*, *Feuillea*, *Inga*, *Pithecolobium*, *Acacia*, *Mimosa*, *Medicago*, *Glycine*, *Dolichos*, *Phaseolus*, *Soja* e.g. the species *Pisum sativum*, *Pisum arvense*, *Pisum humile* [pea], *Albizia berteriana*, *Albizia julibrissin*, *Albizia lebbek*, *Acacia berteriana*, *Acacia littoralis*, *Albizia berteriana*, *Albizia berteriana*, *Cathormion berteriana*, *Feuillea berteriana*, *Inga fragrans*, *Pithecolobium berterianum*, *Pithecolobium fragrans*, *Pithecolobium berterianum*, *Pseudalbizia berteriana*, *Acacia julibrissin*, *Acacia nenu*, *Albizia nenu*, *Feuillea julibrissin*, *Mimosa julibrissin*, *Mimosa speciosa*, *Sericantha julibrissin*, *Acacia lebbek*, *Acacia macrophylla*, *Albizia lebbek*, *Feuillea lebbek*, *Mimosa lebbek*, *Mimosa speciosa* [bastard logwood, silk tree, East Indian Walnut], *Medicago sativa*, *Medicago falcata*, *Medicago varia* [alfalfa] *Glycine max* *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida* or *Soja max* [soybean]; Geraniaceae such as the genera *Pelargonium*, *Cocos*, *Oleum* e.g. the species *Cocos nucifera*, *Pelargonium grossularioides* or *Oleum cocois* [coconut]; Gramineae such as the genera *Saccharum* e.g. the species *Saccharum officinarum*; Juglandaceae such as the genera *Juglans*, *Wallia* e.g. the species *Juglans regia*, *Juglans ailanthifolia*, *Juglans sieboldiana*, *Juglans cinerea*, *Wallia cinerea*, *Juglans bixbyi*, *Juglans californica*, *Juglans hindsii*, *Juglans intermedia*, *Juglans jamaicensis*, *Juglans major*,

- Juglans microcarpa*, *Juglans nigra* or *Wattia nigra* [walnut, black walnut, common walnut, persian walnut, white walnut, butternut, black walnut]; Lauraceae such as the genera *Persea*, *Laurus* e.g. the species *laurel* [*Laurus nobilis* (bay, laurel, bay laurel, sweet bay)], *Persea americana* [*Persea americana*, *Persea gratissima* or *Persea persea* 5 [avocado]]; Leguminosae such as the genera *Arachis* e.g. the species *Arachis hypogaea* [peanut]; Linaceae such as the genera *Linum*, *Adenclonum* e.g. the species *Linum usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*, *Linum grandiflorum*, *Adenclonum grandiflorum*, *Linum lewisii*, *Linum narbonne*, *Linum perenne*, *Linum poronae* var. *lewisii*, *Linum* 10 *pratense* or *Linum trigynum* [flax, linseed]; Lythraceae such as the genera *Punica* e.g. the species *Punica granatum* [pomegranate]; Malvaceae such as the genera *Gossypium* e.g. the species *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum* or *Gossypium thurberi* [cotton]; Musaceae such as the genera *Musa* e.g. the species *Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp. 15 [banana]; Onagraceae such as the genera *Camissonia*, *Oenothera* e.g. the species *Oenothera biennis* or *Camissonia brevipes* [primrose, evening primrose]; Palmae such as the genera *Elais* e.g. the species *Elais guineensis* [oil palm]; Papaveraceae such as the genera *Papaver* e.g. the species *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium* [poppy, oriental poppy, corn poppy, field poppy, Shirley poppies, field poppy, long-headed poppy, long-pod poppy]; Pedaliaceae such as the genera *Sesamum* e.g. the species *Sesamum indicum* [sesame]; Pipraccaceae such as the genera *Piper*, *Artanthe*, *Peperomia*. *Steffensia* e.g. the species *Piper aduncum*, *Piper amalago*, *Piper* 20 *angustifolium*, *Piper auritum*, *Piper betel*, *Piper cubeba*, *Piper longum*, *Piper nigrum*, *Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper elongatum*, *Steffensia elongata*. [Cayenne pepper, wild pepper]; Poaceae such as the genera *Hordeum*, *Secale*, *Avena*, *Sorghum*, *Andropogon*, *Holcus*, *Panicum*, *Oryza*, *Zea*, *Triticum* e.g. the species *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum murinum*, *Hordeum secalinum*, *Hordeum distichon*, *Hordeum aegyptiacum*, *Hordeum hexastichon*, *Hordeum hexastichum*, *Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum* 25 [barley, pearl barley, foxtail barley, wall barley, meadow barley], *Secale cereale* [rye], *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* [oat], *Sorghum bicolor*, *Sorghum halepense*, *Sorghum saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum cafreum*, *Sorghum cernuum*, *Sorghum dochna*, 30 *Sorghum drummondii*, *Sorghum durra*, *Sorghum guineense*, *Sorghum lanceolatum*,

- Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum millicecum* millet, *Panicum mititricum* [*Sorghum*, millet], *Oryza sativa*, *Oryza latifolia* [rice], *Zea mays* [corn, maize] *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum*
 5 *hybernium*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare* [wheat, bread wheat, common wheat], Proteaceae such as the genera *Macadamia* e.g. the species *Macadamia integrifolia* [macadamia]; Rubiaceae such as the genera *Coffea* e.g. the species *Coffea* spp., *Coffea arabica*, *Coffea canephora* or *Coffea liberica* [coffee]; Scrophulariaceae such as the genera *Verbascum* e.g. the species *Verbascum blattaria*, *Verbascum chaixii*,
 10 *Verbascum densiflorum*, *Verbascum lagurus*, *Verbascum longifolium*, *Verbascum lychnitis*, *Verbascum nigrum*, *Verbascum olympicum*, *Verbascum phlomoides*, *Verbascum phoenicum*, *Verbascum pulverulentum* or *Verbascum thapsus* [mullein, white moth mullein, nettle-leaved mullein, dense-flowered mullein, silver mullein, long-leaved mullein, white mullein, dark mullein, greek mullein, orange mullein, purple
 15 mullein, hoary mullein, great mullein]; Solanaceae such as the genera *Capsicum*, *Nicotiana*, *Solanum*. *Lycopersicon* e.g. the species *Capsicum annuum*, *Capsicum annuum* var. *globulosum*, *Capsicum frutescens* [pepper], *Capsicum annuum* [paprika], *Nicotiana tabacum*, *Nicotiana glauca*, *Nicotiana attenuata*, *Nicotiana glauca*, *Nicotiana langsdorffii*, *Nicotiana obtusifolia*, *Nicotiana quadrivalvis*, *Nicotiana*
 20 *repanda*, *Nicotiana rustica*, *Nicotiana sylvestris* [tobacco], *Solanum tuberosum* [potato], *Solanum melongena* [egg-plant] (*Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium* or *Solanum lycopersicum* [tomato]); Sterculiaceae such as the genera *Theobroma* e.g. the species *Theobroma cacao* [cacao]; Theaceae such as the genera *Camellia* e.g. the species
 25 *Camellia sinensis* [tea].

0151.0.1 The introduction of the nucleic acids according to the invention, the expression cassette or the vector into organisms, plants for example, can in principle be done by all of the methods known to those skilled in the art. The introduction of the nucleic acid sequences gives rise to recombinant or transgenic organisms.

- 30 **0152.0.1** In the case of microorganisms, those skilled in the art can find appropriate methods in the textbooks by Sambrook, J. et al. (1989) Molecular cloning: A laboratory manual, Cold Spring Harbor Laboratory Press, by F.M. Ausubel et al. (1994) Current protocols in molecular biology, John Wiley and Sons, by D.M. Glover et al., DNA Cloning Vol.1, (1995), IRL Press (ISBN 019-963476-9), by Kaiser et al. (1994)
 35 Methods In Yeast Genetics, Cold Spring Harbor Laboratory Press or Guthrie et al.

Guide to Yeast Genetics and Molecular Biology, Methods In Enzymology, 1994, Academic Press.

- 0153.0.1** The transfer of foreign genes into the genome of a plant is called transformation. In doing this the methods described for the transformation and regeneration of plants from plant tissues or plant cells are utilized for transient or stable transformation. Suitable methods are protoplast transformation by poly(ethylene glycol)-induced DNA uptake, the „biolistic“ method using the gene cannon – referred to as the particle bombardment method, electroporation, the incubation of dry embryos in DNA solution, microinjection and gene transfer mediated by *Agrobacterium*. Said methods are described by way of example in B. Jones et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225). The nucleic acids or the construct to be expressed is preferably cloned into a vector which is suitable for transforming *Agrobacterium tumefaciens*, for example pBin19 (Devan et al., Nucl. Acids Res. 12 (1984) 8711). *Agrobacterium* transformed by such a vector can then be used in known manner for the transformation of plants, in particular of crop plants such as by way of example tobacco plants, for example by bathing bruised leaves or chopped leaves in an *agrobacterial* solution and then culturing them in suitable media. The transformation of plants by means of *Agrobacterium tumefaciens* is described, for example, by Höfgen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

- 0154.0.1** *Agrobacteria* transformed by an expression vector according to the invention may likewise be used in known manner for the transformation of plants such as test plants like *Arabidopsis* or crop plants such as cereal crops, corn, oats, rye, barley, wheat, soybean, rice, cotton, sugar beet, canola, sunflower, flax, hemp, potatoes, tobacco, tomatoes, carrots, paprika, oilseed rape, tapioca, cassava, arrowroot, tagetes, alfalfa, lettuce and the various tree, nut and vine species, in particular of oil-containing crop plants such as soybean, peanut, castor oil plant, sunflower, corn, cotton, flax, oilseed rape, coconut, oil palm, safflower (*Carthamus tinctorius*) or cocoa bean, e.g. by bathing bruised leaves or chopped leaves in an *agrobacterial* solution and then culturing them in suitable media.

- 0155.0.1** The genetically modified plant cells may be regenerated by all of the methods known to those skilled in the art. Appropriate methods can be found in the publications referred to above by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

0156.0.1 Accordingly, a further aspect of the invention relates to transgenic organisms transformed by at least one nucleic acid sequence, expression cassette or vector according to the invention as well as cells, cell cultures, tissue, parts – such as, for example, leaves, roots, etc. in the case of plant organisms – or reproductive material derived from such organisms. The terms „host organism“, „host cell“, „recombinant (host) organism“ and „transgenic (host) cell“ are used here interchangeably. Of course these terms relate not only to the particular host organism or the particular target cell but also to the descendants or potential descendants of these organisms or cells. Since, due to mutation or environmental effects certain modifications may arise in successive generations, these descendants need not necessarily be identical with the parental cell but nevertheless are still encompassed by the term as used here.

0157.0.1 For the purposes of the invention „transgenic“ or „recombinant“ means with regard for example to a nucleic acid sequence, an expression cassette (= gene construct, nucleic acid construct) or a vector containing the nucleic acid sequence according to the invention or an organism transformed by the nucleic acid sequences, expression cassette or vector according to the invention all those constructions produced by genetic engineering methods in which either

- a) the nucleic acid sequence depicted in Fig. 1a, 1b or 1c or its derivatives or parts thereof or
- b) a genetic control sequence functionally linked to the nucleic acid sequence described under (a), for example a 3'- and/or 5'- genetic control sequence such as a promoter or terminator, or
- c) (a) and (b)

are not found in their natural, genetic environment or have been modified by genetic engineering methods, wherein the modification may by way of example be a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. Natural genetic environment means the natural genomic or chromosomal locus in the organism of origin or inside the host organism or presence in a genomic library. In the case of a genomic library the natural genetic environment of the nucleic acid sequence is preferably retained at least in part. The environment borders the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, particularly preferably at least 1,000 bp, most particularly preferably at least 5,000 bp. A naturally occurring expression cassette – for example the naturally occurring combination of the natural promoter of the nucleic acid sequence according to the invention with the corresponding Δ -8-desaturase, Δ -9-elongase and/or Δ -5-desaturase gene – turns into a transgenic expression cassette

when the latter is modified by unnatural, synthetic („artificial“) methods such as by way of example a mutagenation. Appropriate methods are described by way of example in US 5,565,350 or WO 00/15315.

- 5 **0158.0.1** Suitable organisms or host organisms for the nucleic acid, expression cassette or vector according to the invention are advantageously in principle all organisms, which are suitable for the expression of recombinant genes as described above. Further examples which may be mentioned are plants such as *Arabidopsis*, *Asteraceae* such as *Calendula* or crop plants such as soybean, peanut, castor oil plant, sunflower, flax, corn, cotton, flax, oilseed rape, coconut, oil palm, safflower (*Carthamus tinctorius*) or cocoa bean.

10 **0159.0.1** A further object of the invention relates to the use of a nucleic acid construct, e.g. an expression cassette, containing DNA sequences encoding polypeptides of Fig. 1a, 1b or 1c or DNA sequences hybridizing therewith for the transformation of plant cells, tissues or parts of plants.

- 15 **0160.0.1** In doing so, depending on the choice of promoter, the sequences Fig. 1a, 1b or 1c can be expressed specifically in the leaves, in the seeds, the nodules, in roots, in the stem or other parts of the plant. Those transgenic plants overproducing sequences of Fig. 1a, 1b or 1c, the reproductive material thereof, together with the plant cells, tissues or parts thereof are a further object of the present invention.

- 20 **0161.0.1** The expression cassette or the nucleic acid sequences or construct according to the invention containing sequences of Fig. 1a, 1b or 1c can, moreover, also be employed for the transformation of the organisms identified by way of example above such as bacteria, yeasts, filamentous fungi and plants.

- 25 **0162.0.1** Within the framework of the present invention, altering metabolic activity means, for example, the artificially acquired trait of increased biosynthetic performance due to functional over expression of sequences of Fig. 1a, 1b or 1c in the organisms according to the invention, advantageously in the transgenic plants according to the invention, by comparison with the nongenetically modified initial plants at least for the duration of at least one plant generation.

- 30 **0163.0.1** A constitutive expression of the exogenous sequences of the Fig. 1a, 1b or 1c is, moreover, advantageous. On the other hand, however, an inducible expression may also appear desirable.

- 35 **0164.0.1** The efficiency of the expression of the sequences of the Fig. 1a, 1b or 1c can be determined, for example, in vitro by shoot meristem propagation. In addition, an expression of the sequences of Fig. 1a, 1b or 1c modified in nature and level and its effect on the metabolic pathways performance can be tested on test plants in greenhouse trials.

- 0165.0.1** An additional object of the invention comprises transgenic organisms such as transgenic plants transformed by an expression cassette containing sequences of Fig. 1a, 1b or 1c according to the invention or DNA sequences hybridizing therewith, as well as transgenic cells, tissue, parts and reproduction material of such plants. Particular preference is given in this case to transgenic crop plants such as by way of example barley, wheat, rye, oats, corn, soybean, rice, cotton, sugar beet, oilseed rape and canola, sunflower, flax, hemp, thistle, potatoes, tobacco, tomatoes, tapioca, cassava, arrowroot, alfalfa, lettuce and the various tree, nut and vine species.
- 0166.0.1** For the purposes of the invention plants are mono- and dicotyledonous plants, mosses or algae.
- 0167.0.1** A further refinement according to the invention are transgenic plants as described above which contain a nucleic acid sequence or construct according to the invention or an expression cassette according to the invention.
- 0168.0.1** Furthermore, by derivatives is meant homologues of the sequences of Fig. 1a, 1b or 1c, for example eukaryotic homologues, truncated sequences, single-stranded DNA of the encoding and nonencoding DNA sequence or RNA of the encoding and nonencoding DNA sequence.
- 0169.0.1** In addition, by homologues of the sequences of Fig. 1a, 1b or 1c is meant derivatives such as by way of example promoter variants. These variants may be modified by one or more nucleotide exchanges, by insertion(s) and/or deletion(s) without, however, adversely affecting the functionality or efficiency of the promoters. Furthermore, the promoters can have their efficiency increased by altering their sequence or be completely replaced by more effective promoters even of foreign organisms.
- 0170.0.1** By derivatives is also advantageously meant variants whose nucleotide sequence has been altered in the region from -1 to -2000 ahead of the start codon in such a way that the gene expression and/or the protein expression is modified, preferably increased. Furthermore, by derivatives is also meant variants which have been modified at the 3' end.
- 0171.0.1** Suitable promoters in the expression cassette are in principle all promoters which can control the expression of foreign genes in organisms such as microorganisms like protozoa such as ciliates, algae such as green, brown, red or blue algae such as *Euglenia*, bacteria such as gram-positive or gram-negative bacteria, yeasts such as *Saccharomyces*, *Pichia* or *Schizosaccharomyces* or fungi such as *Mortierella*, *Thraustochytrium* or *Schizochytrium* or plants, advantageously in plants or fungi. Use is preferably made in particular of plant promoters or promoters derived from

a plant virus. Advantageous regulation sequences for the method according to the invention are found for example in promoters such as *cos*, *lac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lack*, *T7*, *T5*, *T3*, *gal*, *trc*, *ara*, *SP6*, λ -*PR* or in λ -*PL* promoters which are employed advantageously in gram-negative bacteria. Other advantageous regulation sequences are found, for example, in the gram-positive promoters *amy* and *SPO2*, in the yeast or fungal promoters *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *px28*, *ADH* or in the plant promoters *CaMV35S* [Franck et al., *Cell* 21(1980) 285-294], *SSU*, *OCS*, *lib4*, *STLS1*, *B33*, *noe* (= *Nopal*in Synthase Promoter) or in the ubiquitin or phaseolin promoter. The expression cassette may also contain a chemically inducible promoter by means of which the expression of the exogenous sequences of the odd numbers of SEQ. ID No. 1-269 in the organisms can be controlled advantageously in the plants at a particular time. Advantageous plant promoters of this type are by way of example the *PRP1* promoter [Ward et al., *Plant.Mol. Biol.*22(1993), 361-366], a promoter inducible by benzenesulfonamide (EP 388 186), a promoter inducible by tetracycline [Gatz et al., (1992) *Plant J.* 2,397-404], a promoter inducible by salicylic acid (WO 95/19443), a promoter inducible by abscisic acid (EP 335 528) and a promoter inducible by ethanol or cyclohexanone (WO93/21394). Other examples of plant promoters which can advantageously be used are the promoter of cytosolic FBPase from potato, the *ST-LSI* promoter from potato [Stockhaus et al., *EMBO J.* 8 (1989) 2445-245], the promoter of phosphoribosyl pyrophosphate amidotransferase from *Glycine max* (see also gene bank accession number U87999) or a nodine-specific promoter as described in EP 249 070. Particularly advantageous are those plant promoters which ensure expression in tissues or plant parts/organs in which fatty acid biosynthesis or the precursor stages thereof occurs, as in endosperm or in the developing embryo for example. Particularly noteworthy are advantageous promoters which ensure seed-specific expression such as by way of example the *USP* promoter or derivatives thereof, the *LEB4* promoter, the phaseolin promoter or the napin promoter. The particularly advantageous *USP* promoter cited according to the invention or its derivatives mediate very early gene expression in seed development [Baeumelein et al., *Mol Gen Genet*, 1991, 225 (3): 459-67]. Other advantageous seed-specific promoters which may be used for monocotyledonous or dicotyledonous plants are the promoters suitable for dicotyledons such as napin gene promoters, likewise cited by way of example, from oilseed rape (US 5,608,152), the oleosin promoter from *Arabidopsis* (WO 98/45461), the phaseolin promoter from *Phaseolus vulgaris* (US 5,504,200), the *Bca4* promoter from *Brassica* (WO 91/13980) or the leguminous *B4* promoter (LeB4, Baeumelein et al., *Plant J.*, 2, 2, 1992: 233 - 239) or promoters suitable for monocotyledons such as the promoters of the *lpt2* or *lpt1* gene in barley (WO 95/15389

and WO 95/23230) or the promoters of the barley hordein gene, the rice glutelin gene, the rice oryzin gene, the rice prolamins gene, the wheat gliadin gene, the white glutelin gene, the corn zein gene, the oats glutelin gene, the sorghum kafirin gene or the rye secalin gene which are described in WO98/16890.

- 5 **0172.0.1** Furthermore, particularly preferred are those promoters, which ensure the expression in tissues, or plant parts in which, for example, the biosynthesis of fatty acids, oils and lipids or the precursor stages thereof takes place. Particularly noteworthy are promoters, which ensure a seed-specific expression. Noteworthy are the promoter of the napin gene from oilseed rape (US 5,608,152), the USP promoter from *Vicia faba* (USP = unknown seed protein, Baumelein et al., Mol Gen Genet, 1991, 10 225 (3): 459-67), the promoter of the oleosin gene from *Arabidopsis* (WO98/45461), the phaseolin promoter (US 5,504,200) or the promoter of the legumin B4 gene (LeB4; Baumelein et al., 1992, Plant Journal, 2 (2): 233-9). Other promoters to be mentioned are that of the *lpt2* or *lpt1* gene from barley (WO95/15389 and WO95/23230) which 15 mediate seed-specific expression in monocotyledonous plants. Other advantageous seed specific promoters are promoters such as the promoters from rice, corn or wheat disclosed in WO 99/16890 or *Amy32b*, *Amy6-6* or *aleurain* (US 5,877,474), *Boc4* (rape, US 5,530,149), *glycinin* (soy bean, EP 571 741), *phosphoenol pyruvate carboxylase* (soy bean, JP 06/62870), *ADR12-2* (soy bean, WO 98/08982), *isocitratylase* (rape, US 20 5,688,040) or β -amylase (barley, EP 761 349).

- 0173.0.1** As described above, the expression construct (= gene construct, nucleic acid construct) may contain yet other genes, which are to be introduced into the organisms. These genes can be subject to separate regulation or be subject to the same regulation region as sequences Fig. 1a, 1b or 1c. These genes are by way of 25 example other biosynthesis genes, advantageously for fatty acid biosynthesis, vitamin biosynthesis etc. that allow increased synthesis.

- 0174.0.1** In principle all natural promoters with their regulation sequences can be used like those named above for the expression cassette according to the invention and the method according to the invention. Over and above this, synthetic promoters 30 may also advantageously be used.

- 0175.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated in order to obtain a nucleotide sequence, which usefully reads in the correct direction and is equipped with a correct reading raster. To connect the DNA fragments (= nucleic acids according to the invention) to one another adaptors or 35 linkers may be attached to the fragments.

0176.0.1 The promoter and the terminator regions can usefully be provided in the transcription direction with a linker or polylinker containing one or more restriction

points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5'-3' transcription direction the expression cassette contains the promoter, a DNA sequence which encodes of Fig. 1a, 1b or 1c gene and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

0177.0.1 Furthermore, manipulations which provide suitable restriction interfaces or which remove excess DNA or restriction interfaces can be employed. Where insertions, deletions or substitutions, such as transitions and transversions, come into consideration, in vitro mutagenesis, primer repair, restriction or ligation may be used. In suitable manipulations such as restriction, chewing back or filling of overhangs for blunt ends complementary ends of the fragments can be provided for the ligation.

0178.0.1 For an advantageous high expression the attachment of the specific ER retention signal/SEKDEL inter alia can be of importance (Schouten, A. et al., Plant Mol. Biol. 30 (1996), 781-792). In this way the average expression level is tripled or even quadrupled. Other retention signals which occur naturally in plant and animal proteins located in the ER may also be employed for the construction of the cassette. In another preferred embodiment a plastidial targeting sequence is used as described by Napier J.A. [Targeting of foreign proteins to the chloroplast, Methods Mol. Biol., 49, 1995: 369 - 376]. A preferred used vector comprising said plastidial targeting sequence is disclosed by Colin Lazarus [Guerineau F., Woolston S., Brooks L., Mullineaux P. "An expression cassette for targeting foreign proteins into chloroplast; Nucleic. Acids Res., Dec 9, 18 (23), 1998: 11380].

0179.0.1 Preferred polyadenylation signals are plant polyadenylation signals, preferably those which substantially correspond to T-DNA polyadenylation signals from *Agrobacterium tumefaciens*, in particular gene 3 of the T-DNA (octopine synthase) of the Ti plasmid pTiACH5 (Gielen et al., EMBO J.3 (1984), 835 et seq.) or corresponding functional equivalents.

0180.0.1 An expression cassette is produced by fusion of a suitable promoter with suitable sequences of Fig. 1a, 1b or 1c together with a polyadenylation signal by common recombination and cloning techniques as described, for example, in T. Maniatis, E.F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) as well as in T.J. Silhavy, M.L. Berman and L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and in Ausubel, F.M. et al., Current

Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley-Interscience (1987).

5 **0181.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adapters or linkers can be attached to the fragments for joining the DNA fragments.

10 **0182.0.1** The promoter and the terminator regions can usefully be provided in the transcription direction with a linker or polylinker containing one or more restriction points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5'-3' transcription direction the expression cassette contains the promoter, a DNA sequence which either encodes
15 gene of the odd numbers of SEQ. ID No. 1-269 and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

20 **0183.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adapters or linkers can be attached to the fragments for joining the DNA fragments.

25 **0184.0.1** The DNA sequences encoding the nucleic acid sequences used in the inventive processes such as the sequences of the Fig. 1a, 1b or 1c contain all the sequence characteristics needed to achieve correct localization of respective biosynthesis. Accordingly, no further targeting sequences are needed per se. However, such a localization may be desirable and advantageous and hence artificially modified or reinforced so that such fusion constructs are also a preferred advantageous embodiment of the invention.

30 **0185.0.1** Particularly preferred are sequences which ensure targeting in plastids. Under certain circumstances targeting into other compartments (reported in: Kemada, Crit. Rev. Plant Sci. 15, 4 (1996), 285-423) may also be desirable, e.g. into vacuoles, the mitochondrion, the endoplasmic reticulum (ER), peroxisomes, lipid structures or due to lack of corresponding operative sequences retention in the compartment of origin, the cytosol.

35 **0186.0.1** As used herein, the term "environmental stress" refers to any sub-optimal growing condition and includes, but is not limited to, sub-optimal conditions associated with salinity, drought, temperature, metal, chemical, pathogenic and

- oxidative stresses, or combinations thereof. In preferred embodiments, the environmental stress can be salinity, drought, heat, or low temperature, or combinations thereof, and in particular, can be low water content or low temperature. Wherein drought stress means any environmental stress which leads to a lack of water
- 5 in plants or reduction of water supply to plants, wherein low temperature stress means freezing of plants below + 4 °C as well as chilling of plants below 15 °C and wherein high temperature stress means for example a temperature above 35 °C. The range of stress and stress response depends on the different plants which are used for the invention, i.e. it differs for example between a plant such as wheat and a plant such as
- 10 Arabidopsis. A common response of plants to environmental stress is the loss of yield or the loss of quality. It is also to be understood that as used in the specification and in the claims, "a" or "an" can mean one or more, depending upon the context in which it is used. Thus, for example, reference to "a cell" can mean that at least one cell can be utilized.
- 15 **0187.0.1** As also used herein, the terms "nucleic acid" and "nucleic acid molecule" are intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 1000 nucleotides of
- 20 sequence upstream from the 5' end of the coding region and at least about 200 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.
- 0188.0.1** A(n) "isolated" nucleic acid molecule is one that is substantially separated
- 25 from other nucleic acid molecules, which are present in the natural source of the nucleic acid. That means other nucleic acid molecules are present in an amount less than 5% based on weight of the amount of the desired nucleic acid, preferably less than 2% by weight, more preferably less than 1% by weight, most preferably less than 0.5% by weight. Preferably, an "isolated" nucleic acid is free of some of the sequences
- 30 that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated stress related protein encoding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid
- 35 molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium

when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

0189.0.1 A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule encoding an SRP or a portion thereof which confers tolerance and/or resistance to environmental stress in plants, can be isolated using standard molecular biological techniques and the sequence information provided herein. For example, a *Arabidopsis thaliana* stress related protein encoding cDNA can be isolated from a *A. thaliana* c-DNA library using all or portion of one of the sequences of Fig. 1a, 1b or 1c. Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Fig. 1a, 1b or 1c can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence. For example, mRNA can be isolated from plant cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin et al., 1979 *Biochemistry* 18:5294-5299) and cDNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Fig. 1a, 1b or 1c. A nucleic acid molecule of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid molecule so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to a SRP encoding nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

0190.0.1 In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in sequences Fig. 1a, 1b or 1c encoding the SRP (i.e., the "coding region"), as well as 5' untranslated sequences and 3' untranslated sequences.

0191.0.1 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c, for example, a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a SRP.

0192.0.1 Portions of proteins encoded by the SRP encoding nucleic acid molecules of the invention are preferably biologically active portions described herein. As used herein, the term "biologically active portion of" a SRP is intended to include a portion, e.g., a domain/motif, of stress related protein that participates in a stress tolerance and/or resistance response in a plant. To determine whether a SRP, or a

- biologically active portion thereof, results in increased stress tolerance in a plant, a stress analysis of a plant comprising the SRP may be performed. Such analysis methods are well known to those skilled in the art, as detailed in the Examples. More specifically, nucleic acid fragments encoding biologically active portions of a SRP can be prepared by isolating a portion of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c expressing the encoded portion of the SRP or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SRP or peptide.

- 0193.0.1** Biologically active portions of a SRP are encompassed by the present invention and include peptides comprising amino acid sequences derived from the amino acid sequence of a SRP encoding gene, or the amino acid sequence of a protein homologous to a SRP, which includes fewer amino acids than a full length SRP or the full length protein which is homologous to a SRP, and exhibits at least some enzymatic activity of a SRP. Typically, biologically active portions (e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of a SRP. Moreover, other biologically active portions in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of a SRP include one or more selected domains/motifs or portions thereof having biological activity.

- 0194.0.1** The term "biological active portion" or "biological activity" means a SRP or a portion of a SRP which still has at least 10 % or 20 %, preferably 20 %, 30 %, 40 % or 50 %, especially preferably 80 %, 70 % or 80 % of the enzymatic activity of the natural or starting enzyme.

- 0195.0.2** A nucleic acid molecule encompassing a complete sequence of the nucleic acid molecules used in the process, for example the polynucleotide of the invention, or a part thereof may additionally be isolated by polymerase chain reaction, oligonucleotide primers based on this sequence or on parts thereof being used. For example, a nucleic acid molecule comprising the complete sequence or part thereof can be isolated by polymerase chain reaction using oligonucleotide primers which have been generated on the basis of this sequence. For example, mRNA can be isolated from cells (for example by means of the guanidinium thiocyanate extraction method of Chirgwin et al. (1979) *Biochemistry* 18:5294-5299) and cDNA can be generated by means of reverse transcriptase (for example Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD, or AMV reverse transcriptase, obtainable from Seikagaku America, Inc., St. Petersburg, FL).

0196.0.2 Synthetic oligonucleotide primers for the amplification, e.g. as shown in table 2, by means of polymerase chain reaction can be generated on the basis of a sequence shown herein, for example the sequence shown in Fig. 1a, 1b or 1c or the sequences derived from polypeptides as shown in Fig. 1a, 1b or 1c.

5 **0197.0.2** Moreover, it is possible to identify conserved regions from various organisms by carrying out protein sequence alignments with the polypeptide used in the process of the invention, in particular with sequences of the polypeptide of the invention, from which conserved regions, and in turn, degenerate primers can be derived. Conserved region for the polypeptide of the invention are indicated in the
10 alignment shown in the figure Fig. 1a, 1b or 1c. Conserved regions are those, which show a very little variation in the amino acid in one particular position of several homologs from different origin. The consensus sequences shown in Fig. 2 are derived from said alignments.

0198.0.2 Degenerated primers can then be utilized by PCR for the amplification
15 of fragments of novel proteins having above-mentioned activity, e.g. having an SPR activity or further functional homologs of the polypeptide of the invention from other organisms.

0199.0.2 These fragments can then be utilized as hybridization probe for isolating the complete gene sequence. As an alternative, the missing 5' and 3' sequences can
20 be isolated by means of RACE-PCR (rapid amplification of cDNA ends). A nucleic acid molecule according to the invention can be amplified using cDNA or, as an alternative, genomic DNA as template and suitable oligonucleotide primers, following standard PCR amplification techniques. The nucleic acid molecule amplified thus can be cloned into a suitable vector and characterized by means of DNA sequence analysis.
25 Oligonucleotides, which correspond to one of the nucleic acid molecules used in the process can be generated by standard synthesis methods, for example using an automatic DNA synthesizer.

0200.0.2 Nucleic acid molecules which are advantageously for the process according to the invention can be isolated based on their homology to the nucleic acid
30 molecules disclosed herein using the sequences or part thereof as hybridization probe and following standard hybridization techniques under stringent hybridization conditions. In this context, it is possible to use, for example, isolated nucleic acid molecules of at least 15, 20, 25, 30, 35, 40, 50, 60 or more nucleotides, preferably of at least 15, 20 or 25 nucleotides in length which hybridize under stringent conditions with
35 the above-described nucleic acid molecules, in particular with those which encompass a nucleotide sequence of the nucleic acid molecule used in the process of the invention or encoding a protein used in the invention or of the nucleic acid molecule of the

invention. Nucleic acid molecules with 30, 50, 100, 250 or more nucleotides may also be used.

0201.0.1 In addition to fragments of the SRP described herein, the present invention includes homologs and analogs of naturally occurring SRP and SRP encoding nucleic acids in a plant.

0202.0.1 "Homologs" are defined herein as two nucleic acids or proteins that have similar, or "homologous", nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralog, agonists and antagonists of SRP as defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in sequences with SEQ ID No. XXX (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRP as that encoded by the amino acid sequences shown in sequences with SEQ ID No. XXX. As used herein a "naturally occurring" SRP refers to a SRP amino acid sequence that occurs in nature.

0203.0.2 The term "homology" means that the respective nucleic acid molecules or encoded proteins are functionally and/or structurally equivalent. The nucleic acid molecules that are homologous to the nucleic acid molecules described above and that are derivatives of said nucleic acid molecules are, for example, variations of said nucleic acid molecules which represent modifications having the same biological function, in particular encoding proteins with the same or substantially the same biological function. They may be naturally occurring variations, such as sequences from other plant varieties or species, or mutations. These mutations may occur naturally or may be obtained by mutagenesis techniques. The allelic variations may be naturally occurring allelic variants as well as synthetically produced or genetically engineered variants. Structurally equivalents can, for example, be identified by testing the binding of said polypeptide to antibodies or computer based predictions. Structurally equivalent have the similar immunological characteristic, e.g. comprise similar epitopes.

0204.0.2 Functional equivalents derived from one of the polypeptides as shown in SEQ ID NO: YYY according to the invention by substitution, insertion or deletion have at least 30%, 35%, 40%, 45% or 50%, preferably at least 55%, 60%, 65% or 70% by preference at least 80%, especially preferably at least 85% or 90%, 91%, 92%, 93% or 94%, very especially preferably at least 95%, 97%, 98% or 99% homology with one of the polypeptides as shown in Fig. 1a, 1b or 1c according to the invention and are distinguished by essentially the same properties as the polypeptide as shown in Fig. 1a, 1b or 1c.

0205.0.2 Functional equivalents derived from the nucleic acid sequence as shown in SEQ ID NO: YYY according to the invention by substitution, insertion or deletion have at least 30%, 35%, 40%, 45% or 50%, preferably at least 55%, 60%, 65% or 70% by preference at least 80%, especially preferably at least 85% or 90%, 91%, 92%, 93% or 94%, very especially preferably at least 95%, 97%, 98% or 99% homology with one of the polypeptides as shown in Fig. 1a, 1b or 1c according to the invention and encode polypeptides having essentially the same properties as the polypeptide as shown in Fig. 1a, 1b or 1c.

0206.0.2 "Essentially the same properties" of a functional equivalent is above all understood as meaning that the functional equivalent has above mentioned activity, e.g. conferring an increase in the fine chemical amount while increasing the amount of protein, activity or function of said functional equivalent in an organism, e.g. a microorganism, a plant or plant or animal tissue, plant or animal cells or a part of the same.

0207.0.2 By "hybridizing" it is meant that such nucleic acid molecules hybridize under conventional hybridization conditions, preferably under stringent conditions such as described by, e.g., Sambrook (Molecular Cloning; A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989)) or in Current Protocols in Molecular Biology, John Wiley & Sons, N. Y. (1989), 6.3.1-6.3.6.

0208.0.2 According to the invention, DNA as well as RNA molecules of the nucleic acid of the invention can be used as probes. Further, as template for the identification of functional homologues Northern blot assays as well as Southern blot assays can be performed. The Northern blot assay advantageously provides further informations about the expressed gene product: e.g. expression pattern, occurrence of processing steps, like splicing and capping, etc. The Southern blot assay provides additional information about the chromosomal localization and organization of the gene encoding the nucleic acid molecule of the invention.

0209.0.2 A preferred, nonlimiting example of stringent hybridization conditions are hybridizations in 6 x sodium chloride/sodium citrate (= SSC) at approximately 45°C, followed by one or more wash steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C, for example at 50°C, 55°C or 60°C. The skilled worker knows that these hybridization conditions differ as a function of the type of the nucleic acid and, for example when organic solvents are present, with regard to the temperature and concentration of the buffer. The temperature under "standard hybridization conditions" differs for example as a function of the type of the nucleic acid between 42°C and 58°C, preferably between 45°C and 50°C in an aqueous buffer with a concentration of 0.1 x 0.5 x, 1 x, 2x, 3x, 4x or 5 x SSC (pH 7.2). If organic solvent(s) is/are present in the

- abovementioned buffer, for example 50% formamide, the temperature under standard conditions is approximately 40°C, 42°C or 45°C. The hybridization conditions for DNA:DNA hybrids are preferably for example 0.1 x SSC and 20°C, 25°C, 30°C, 35°C, 40°C or 45°C, preferably between 30°C and 45°C. The hybridization conditions for
- 5 DNA:RNA hybrids are preferably for example 0.1 x SSC and 30°C, 35°C, 40°C, 45°C, 50°C or 55°C, preferably between 45°C and 55°C. The abovementioned hybridization temperatures are determined for example for a nucleic acid approximately 100 bp (= base pairs) in length and a G + C content of 50% in the absence of formamide. The skilled worker knows to determine the hybridization conditions required with the aid of
- 10 textbooks, for example the ones mentioned above, or from the following textbooks: Sambrook et al., "Molecular Cloning", Cold Spring Harbor Laboratory, 1989; Hames and Higgins (Ed.) 1985, "Nucleic Acids Hybridization: A Practical Approach", IRL Press at Oxford University Press, Oxford; Brown (Ed.) 1991, "Essential Molecular Biology: A Practical Approach", IRL Press at Oxford University Press, Oxford.
- 15 **0210.0.2** A further example of one such stringent hybridization condition is hybridization at 4XSSC at 65°C, followed by a washing in 0.1XSSC at 65°C for one hour. Alternatively, an exemplary stringent hybridization condition is in 50 % formamide, 4XSSC at 42°C. Further, the conditions during the wash step can be selected from the range of conditions delimited by low-stringency conditions
- 20 (approximately 2X SSC at 50°C) and high-stringency conditions (approximately 0.2X SSC at 50°C, preferably at 65°C) (20X SSC: 0.3M sodium citrate, 3M NaCl, pH 7.0). In addition, the temperature during the wash step can be raised from low-stringency conditions at room temperature, approximately 22°C, to higher-stringency conditions at approximately 65°C. Both of the parameters salt concentration and temperature can be
- 25 varied simultaneously, or else one of the two parameters can be kept constant while only the other is varied. Denaturants, for example formamide or SDS, may also be employed during the hybridization. In the presence of 50% formamide, hybridization is preferably effected at 42°C. Relevant factors like i) length of treatment, ii) salt conditions, iii) detergent conditions, iv) competitor DNAs, v) temperature and vi) probe
- 30 selection can be combined case by case so that not all possibilities can be mentioned herein.
- 0211.0.2** Thus, in a preferred embodiment, Northern blots are prehybridized with Rothi-Hybi-Quick buffer (Roth, Karlsruhe) at 68°C for 2h. Hybridization with radioactive labelled probe is done overnight at 68°C. Subsequent washing steps are performed at
- 35 68°C with 1xSSC.
- 0212.0.2** For Southern blot assays the membrane is prehybridized with Rothi-Hybi-Quick buffer (Roth, Karlsruhe) at 68°C for 2h. The hybridization with radioactive

labelled probe is conducted over night at 68°C. Subsequently the hybridization buffer is discarded and the filter shortly washed using 2xSSC; 0,1% SDS. After discarding the washing buffer new 2xSSC; 0,1% SDS buffer is added and incubated at 68°C for 15 minutes. This washing step is performed twice followed by an additional washing step using 1xSSC; 0,1% SDS at 68°C for 10 min.

0213.0.2 Some further examples of conditions for DNA hybridization (Southern blot assays) and wash step are shown hereinbelow:

(1) Hybridization conditions can be selected, for example, from the following conditions:

- a) 4X SSC at 65°C,
- b) 6X SSC at 45°C,
- c) 6X SSC, 100 mg/ml denatured fragmented fish sperm DNA at 88°C,
- d) 6X SSC, 0.5% SDS, 100 mg/ml denatured salmon sperm DNA at 68°C,
- e) 6X SSC, 0.5% SDS, 100 mg/ml denatured fragmented salmon sperm DNA, 50% formamide at 42°C,
- f) 50% formamide, 4X SSC at 42°C,
- g) 50% (vol/vol) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer pH 6.5, 750 mM NaCl, 75 mM sodium citrate at 42°C,
- h) 2X or 4X SSC at 50°C (low-stringency condition), or
- i) 30 to 40% formamide, 2X or 4X SSC at 42°C (low-stringency condition).

(2) Wash steps can be selected, for example, from the following conditions:

- a) 0.015 M NaCl/0.0015 M sodium citrate/0.1% SDS at 50°C.
- b) 0.1X SSC at 65°C.
- c) 0.1X SSC, 0.5 % SDS at 68°C.
- d) 0.1X SSC, 0.5% SDS, 50% formamide at 42°C.
- e) 0.2X SSC, 0.1% SDS at 42°C.
- f) 2X SSC at 65°C (low-stringency condition).

0214.0.1 In an other embodiment is meant by standard conditions, for example, depending on the nucleic acid in question temperatures between 42°C and 58°C in an aqueous buffer solution having a concentration of between 0.1 and 5 x SSC (1 X SSC = 0.15 M NaCl, 15 mM sodium citrate, pH 7.2) or additionally in the presence of 50 % formamide, such as by way of example 42°C in 5 x SSC, 50 % formamide. Hybridization conditions for DNA:DNA hybrids are advantageously 0.1 x SSC and temperatures between approximately 20°C and 45°C, preferably between

approximately 30 °C and 45 °C. For DNA:RNA hybrids the hybridization conditions are advantageously 0.1 x SSC and temperatures between approximately 30°C and 55°C, preferably between approximately 45°C and 55°C. These specified temperatures for hybridization are melting temperature values calculated by way of example for a nucleic acid having a length of approximately 100 nucleotides and a G + C content of 50 % in the absence of formamide. The experimental conditions for DNA hybridization are described in relevant genetics textbooks such as by way of example Sambrook et al., „Molecular Cloning“, Cold Spring Harbor Laboratory, 1989, and may be calculated by formulae known to those skilled in the art, for example as a function of the length of the nucleic acids, the nature of the hybrids or the G + C content. Those skilled in the art may draw on the following textbooks for further information on hybridization: Ausubel et al. (eds), 1985, Current Protocols in Molecular Biology, John Wiley & Sons, New York; Hames and Higgins (eds), 1985, Nucleic Acids Hybridization: A Practical Approach, IRL Press at Oxford University Press, Oxford; Brown (ed), 1991, Essential Molecular Biology: A Practical Approach, IRL Press at Oxford University Press, Oxford.

0216.0.2 Polypeptides having above-mentioned activity, i.e. conferring the altered metabolic activity, derived from other organisms, can be encoded by other DNA sequences which hybridize to the sequences shown in Fig. 1a, 1b or 1c under relaxed hybridization conditions and which code on expression for peptides conferring an altered metabolic activity.

0216.0.2 Further, some applications have to be performed at low stringency hybridisation conditions, without any consequences for the specificity of the hybridisation. For example, a Southern blot analysis of total DNA could be probed with a nucleic acid molecule of the present invention and washed at low stringency (55°C in 2xSSPE/0,1% SDS). The hybridisation analysis could reveal a simple pattern of only genes encoding polypeptides of the present invention or used in the process of the invention, e.g. having herein-mentioned activity of increasing the fine chemical . A further example of such low-stringent hybridization conditions is 4XSSC at 50°C or hybridization with 30 to 40% formamide at 42°C. Such molecules comprise those which are fragments, analogues or derivatives of the polypeptide of the invention or used in the process of the invention and differ, for example, by way of amino acid and/or nucleotide deletion(s), insertion(s), substitution (s), addition(s) and/or recombination (s) or any other modification(s) known in the art either alone or in combination from the above-described amino acid sequences or their underlying nucleotide sequence(s). However, it is preferred to use high stringency hybridisation conditions.

0217.0.2 Hybridization should advantageously be carried out with fragments of at least 5, 10, 15, 20, 25, 30, 35 or 40 bp. advantageously at least 50, 60, 70 or 80 bp,

preferably at least 90, 100 or 110 bp. Most preferably are fragments of at least 15, 20, 25 or 30 bp. Preferably are also hybridizations with at least 100 bp or 200, very especially preferably at least 400 bp in length. In an especially preferred embodiment, the hybridization should be carried out with the entire nucleic acid sequence with conditions described above.

0218.0.2 The terms "fragment", "fragment of a sequence" or "part of a sequence" mean a truncated sequence of the original sequence referred to. The truncated sequence (nucleic acid or protein sequence) can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to or hybridizing with the nucleic acid molecule of the invention or used in the process of the invention under stringent conditions, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence.

0219.0.3 In addition to fragments and fusion polypeptides of the SRPs described herein, the present invention includes homologs and analogs of naturally occurring SRPs and SRP encoding nucleic acids in a plant. "Homologs" are defined herein as two nucleic acids or polypeptides that have similar, or substantially identical, nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralog, agonists and antagonists of SRPs as defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Fig. 1a, 1b or 1c (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRP as that encoded by the nucleotide sequences shown in Fig. 1a, 1b or 1c. As used herein a "naturally occurring" SRP refers to a SRP amino acid sequence that occurs in nature. Preferably, a naturally occurring SRP comprises an amino acid sequence selected from the group consisting of polypeptides of Fig. 1a, 1b or 1c.

0220.0.3 An agonist of the SRP can retain substantially the same, or a subset, of the biological activities of the SRP. An antagonist of the SRP can inhibit one or more of the activities of the naturally occurring form of the SRP. For example, the SRP antagonist can competitively bind to a downstream or upstream member of the cell membrane component metabolic cascade that includes the SRP, or bind to a SRP that mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

0221.0.3 Nucleic acid molecules corresponding to natural allelic variants and analogs, orthologs and paralog of a SRP cDNA can be isolated based on their identity

to the *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP nucleic acids described herein using SRP cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. In an alternative embodiment, homologs of the SRP can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the SRP for SRP agonist or antagonist activity. In one embodiment, a variegated library of SRP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SRP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion polypeptides (e.g., for phage display) containing the set of SRP sequences therein. There are a variety of methods that can be used to produce libraries of potential SRP homologs from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene is then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art. See, e.g., Narang, S.A., 1983, *Tetrahedron* 39:3; Itakura et al., 1984, *Annu. Rev. Biochem.* 53:323; Itakura et al., 1984, *Science* 198:1056; Ike et al., 1983, *Nucleic Acid Res.* 11:477.

0222.0.3 In addition, libraries of fragments of the SRP coding regions can be used to generate a variegated population of SRP fragments for screening and subsequent selection of homologs of a SRP. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a SRP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA, which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal, and internal fragments of various sizes of the SRP.

0223.0.3 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRP homologs. The most widely used techniques, which are amenable to high

through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SRP homologs (Arkin and Yourvan, 1992, PNAS 89:7811-7815; Delgrave et al., 1993, Polypeptide Engineering 6(3):327-331). In another embodiment, cell based assays can be exploited to analyze a variegated SRP library, using methods well known in the art. The present invention further provides a method of identifying a novel SRP, comprising (a) raising a specific antibody response to a SRP, or a fragment thereof, as described herein; (b) screening putative SRP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel SRP; and (c) analyzing the bound material in comparison to known SRP, to determine its novelty.

0224.0.3 As stated above, the present invention includes SRPs and homologs thereof. To determine the percent sequence identity of two amino acid sequences (e.g., one of the sequences of Fig. 1a, 1b or 1c, and a mutant form thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one polypeptide for optimal alignment with the other polypeptide or nucleic acid). The amino acid residues at corresponding amino acid positions are then compared. When a position in one sequence (e.g., one of the sequences of Fig. 1a, 1b or 1c) is occupied by the same amino acid residue as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from the polypeptide of Fig. 1a, 1b or 1c), then the molecules are identical at that position. The same type of comparison can be made between two nucleic acid sequences.

0225.0.3 The percent sequence identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent sequence identity = numbers of identical positions/total numbers of positions x 100). Preferably, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more identical to an entire amino acid sequence shown in Fig. 1a, 1b or 1c. In yet another embodiment, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more identical to an entire amino

acid sequence encoded by a nucleic acid sequence shown in Fig. 1a, 1b or 1c. In other embodiments, the SRP amino acid homologs have sequence identity over at least 15 contiguous amino acid residues, more preferably at least 25 contiguous amino acid residues, and most preferably at least 35 contiguous amino acid residues of Fig. 1a, 1b or 1c.

0226.0.3 In another preferred embodiment, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which is at least about 50-80%, preferably at least about 60-70%, more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical to a nucleotide sequence shown Fig. 1a, 1b or 1c, or to a portion comprising at least 20, 30, 40, 50, 60 consecutive nucleotides thereof. The preferable length of sequence comparison for nucleic acids is at least 75 nucleotides, more preferably at least 100 nucleotides and most preferably the entire length of the coding region.

0227.0.3 It is further preferred that the isolated nucleic acid homolog of the invention encodes a SRP, or portion thereof, that is at least 85% identical to an amino acid sequence of Fig. 1a, 1b or 1c and that functions as a modulator of an environmental stress response in a plant. In a more preferred embodiment, overexpression of the nucleic acid homolog in a plant increases the tolerance of the plant to an environmental stress.

0228.0.3 For the purposes of the invention, the percent sequence identity between two nucleic acid or polypeptide sequences is determined using the Vector NTI 8.0 (PC) software package (Informa, 7800 Wisconsin Ave., Bethesda, MD 20814). A gap opening penalty of 15 and a gap extension penalty of 6.66 are used for determining the percent identity of two nucleic acids. A gap opening penalty of 10 and a gap extension penalty of 0.1 are used for determining the percent identity of two polypeptides. All other parameters are set at the default settings. For purposes of a multiple alignment (Clustal W algorithm), the gap opening penalty is 10, and the gap extension penalty is 0.05 with blosum62 matrix. It is to be understood that for the purposes of determining sequence identity when comparing a DNA sequence to an RNA sequence, a thymidine nucleotide is equivalent to a uracil nucleotide.

0228.1.3 In another aspect, the invention provides an isolated nucleic acid comprising a polynucleotide that hybridizes to the polynucleotide of Fig. 1a, 1b or 1c under stringent conditions. More particularly, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Fig. 1a, 1b or 1c. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in

length. Preferably, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which hybridizes under highly stringent conditions to the nucleotide sequence shown in Fig. 1a, 1b or 1c, and functions as a modulator of stress tolerance in a plant. In a further preferred embodiment, overexpression of the isolated nucleic acid homolog in a plant increases a plant's tolerance to an environmental stress.

0229.0.3 As used herein with regard to hybridization for DNA to DNA blot, the term "stringent conditions" refers in one embodiment to hybridization overnight at 60°C in 10X Denhardt's solution, 6X SSC, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 62°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS and finally 0.1X SSC/0.1% SDS. As also used herein, "highly stringent conditions" refers to hybridization overnight at 65°C in 10X Denhardt's solution, 6X SSC, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 65°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS and finally 0.1X SSC/0.1% SDS. Methods for nucleic acid hybridizations are described in Meinkoth and Wahl, 1984, *Anal. Biochem.* 138:267-284; Ausubel et al. eds, 1985, *Current Protocols in Molecular Biology*, Chapter 2, Greene Publishing and Wiley-Interscience, New York; and Tijssen, 1993, *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization with Nucleic Acid Probes*, Part I, Chapter 2, Elsevier, New York. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent or highly stringent conditions to a sequence of Fig. 1a, 1b or 1c corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural polypeptide). In one embodiment, the nucleic acid encodes a naturally occurring *Saccharomyces cerevisiae*, *E. coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP.

0230.0.3 Using the above-described methods, and others known to those of skill in the art, one of ordinary skill in the art can isolate homologs of the SRPs comprising amino acid sequences shown in Fig. 1a, 1b or 1c. One subset of these homologs are allelic variants. As used herein, the term "allelic variant" refers to a nucleotide sequence containing polymorphisms that lead to changes in the amino acid sequences of a SRP and that exist within a natural population (e.g., a plant species or variety). Such natural allelic variations can typically result in 1-5% variance in a SRP nucleic acid. Allelic variants can be identified by sequencing the nucleic acid sequence of interest in a number of different plants, which can be readily carried out by using hybridization probes to identify the same SRP genetic locus in those plants. Any and

all such nucleic acid variations and resulting amino acid polymorphisms or variations in a SRP that are the result of natural allelic variation and that do not alter the functional activity of a SRP, are intended to be within the scope of the invention.

0231.0.3 An isolated nucleic acid molecule encoding a SRP having sequence identity with a polypeptide sequence of Fig. 1a, 1b or 1c can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Fig. 1a, 1b or 1c, respectively, such that one or more amino acid substitutions, additions, or deletions are introduced into the encoded polypeptide. Mutations can be introduced into one of the sequences of Fig. 1a, 1b or 1c by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

0232.0.3 Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a SRP is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a SRP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for a SRP activity described herein to identify mutants that retain SRP activity. Following mutagenesis of one of the sequences of SEQ ID NO:XXX, the encoded polypeptide can be expressed recombinantly and the activity of the polypeptide can be determined by analyzing the stress tolerance of a plant expressing the polypeptide as described herein.

0233.0.3 Additionally, optimized SRP nucleic acid can be created. As used herein, "optimized" refers to a nucleic acid that is genetically engineered to increase its expression in a given plant or animal. To provide plant optimized SRP nucleic acids, the DNA sequence of the gene can be modified to 1) comprise codons preferred by highly expressed plant genes; 2) comprise an A+T content in nucleotide base composition to that substantially found in plants; 3) form a plant initiation sequence; or 4) eliminate sequences that cause destabilization, inappropriate polyadenylation, degradation, and termination of RNA, or that form secondary structure hairpins or RNA

splice sites. Increased expression of SRP nucleic acids in plants can be achieved by utilizing the distribution frequency of codon usage in plants in general or a particular plant. Methods for optimizing nucleic acid expression in plants can be found in EPA 0359472; EPA 0385962; PCT Application No. WO 91/16432; U.S. Patent No. 5,380,831; U.S. Patent No. 5,436,391; Parlack et al., 1991, Proc. Natl. Acad. Sci. USA 88:3324-3328; and Murray et al., 1989, Nucleic Acids Res. 17:477-496.

0234.0.3 As used herein, "frequency of preferred codon usage" refers to the preference exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. To determine the frequency of usage of a particular codon in a gene, the number of occurrences of that codon in the gene is divided by the total number of occurrences of all codons specifying the same amino acid in the gene. Similarly, the frequency of preferred codon usage exhibited by a host cell can be calculated by averaging frequency of preferred codon usage in a large number of genes expressed by the host cell. It is preferable that this analysis be limited to genes that are highly expressed by the host cell. The percent deviation of the frequency of preferred codon usage for a synthetic gene from that employed by a host cell is calculated first by determining the percent deviation of the frequency of usage of a single codon from that of the host cell followed by obtaining the average deviation over all codons. As defined herein, this calculation includes unique codons (i.e., ATG and TGG). In general terms, the overall average deviation of the codon usage of an optimized gene from that of a host cell is calculated using the equation $1A = \frac{1}{Z} \sum_{n=1}^Z \frac{X_n - Y_n}{X_n} \times 100$ where X_n = frequency of usage for codon n in the host cell; Y_n = frequency of usage for codon n in the synthetic gene; n represents an individual codon that specifies an amino acid; and the total number of codons is Z . The overall deviation of the frequency of codon usage, A , for all amino acids should preferably be less than about 25%, and more preferably less than about 10%.

0235.0.3 Hence, a SRP nucleic acid can be optimized such that its distribution frequency of codon usage deviates, preferably, no more than 25% from that of highly expressed plant genes and, more preferably, no more than about 10%. In addition, consideration is given to the percentage G+C content of the degenerate third base (monocotyledons appear to favor G+C in this position, whereas dicotyledons do not). It is also recognized that the XCG (where X is A, T, C, or G) nucleotide is the least preferred codon in dicots whereas the XTA codon is avoided in both monocots and dicots. Optimized SRP nucleic acids of this invention also preferably have CG and TA doublet avoidance indices closely approximating those of the chosen host plant (i.e., *Brassica napus*, *Glycine max*, or *Oryza sativa*). More preferably these indices deviate from that of the host by no more than about 10-15%.

0236.0.3 In addition to the nucleic acid molecules encoding the SRPs described above, another aspect of the invention pertains to isolated nucleic acid molecules that are antisense thereto. Antisense polynucleotides are thought to inhibit gene expression of a target polynucleotide by specifically binding the target polynucleotide and interfering with transcription, splicing, transport, translation, and/or stability of the target polynucleotide. Methods are described in the prior art for targeting the antisense polynucleotide to the chromosomal DNA, to a primary RNA transcript, or to a processed mRNA. Preferably, the target regions include splice sites, translation initiation codons, translation termination codons, and other sequences within the open reading frame.

0237.0.3 The term "antisense," for the purposes of the invention, refers to a nucleic acid comprising a polynucleotide that is sufficiently complementary to all or a portion of a gene, primary transcript, or processed mRNA, so as to interfere with expression of the endogenous gene. "Complementary" polynucleotides are those that are capable of base pairing according to the standard Watson-Crick complementarity rules. Specifically, purines will base pair with pyrimidines to form a combination of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. It is understood that two polynucleotides may hybridize to each other even if they are not completely complementary to each other, provided that each has at least one region that is substantially complementary to the other. The term "antisense nucleic acid" includes single stranded RNA as well as double-stranded DNA expression cassettes that can be transcribed to produce an antisense RNA. "Active" antisense nucleic acids are antisense RNA molecules that are capable of selectively hybridizing with a primary transcript or mRNA encoding a polypeptide having at least 80% sequence identity with the polypeptide of Fig. 1a, 1b or 1c.

0238.0.3 The antisense nucleic acid can be complementary to an entire SRP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding a SRP. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding a SRP. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions). The antisense nucleic acid molecule can be complementary to the entire coding region of SRP mRNA, but more preferably is an oligonucleotide which is antisense to only a

portion of the coding or noncoding region of SRP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of PKSRP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. Typically, the antisense molecules of the present invention comprise an RNA having 60-100% sequence identity with at least 14 consecutive nucleotides of one of the nucleic acid of Fig. 1a, 1b or 1c. Preferably, the sequence identity will be at least 70%, more preferably at least 75%, 80%, 85%, 90%, 95%, 98% and most preferably 99%.

0239.0.3 An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylquosine, inosine, N8-isopentenyladenosine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylquosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenosine, uracil-5-oxyacetic acid (v), wybutosine, pseudouracil, quosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methyl ester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

0240.0.3 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucleic Acids. Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (Inoue et al., 1987, Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

0241.0.3 The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a SRP to thereby inhibit expression of the polypeptide, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic (including plant) promoter are preferred.

0242.0.3 As an alternative to antisense polynucleotides, ribozymes, sense polynucleotides, or double stranded RNA (dsRNA) can be used to reduce expression of a SRP polypeptide. By "ribozyme" is meant a catalytic RNA-based enzyme with ribonuclease activity which is capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which it has a complementary region. Ribozymes (e.g., hammerhead ribozymes described in Haeseleir and Gerlach, 1988, Nature 334:585-591) can be used to catalytically cleave SRP mRNA transcripts to thereby inhibit translation of SRP mRNA. A ribozyme having specificity for a SRP-encoding nucleic acid can be designed based upon the nucleotide sequence of a SRP cDNA, as disclosed herein (i.e., Fig. 1a, 1b or 1c) or on the basis of a heterologous sequence to be isolated according to methods taught in this invention. For example, a derivative of a Tetrahymena I-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SRP-encoding mRNA. See, e.g., U.S. Patent Nos. 4,987,071 and 5,116,742 to Cech et al. Alternatively, SRP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W., 1993, Science 261:1411-1418. In preferred embodiments, the ribozyme will contain a portion having at least 7, 8, 9, 10, 12, 14, 16, 18 or 20 nucleotides, and more preferably 7 or 8 nucleotides, that have 100% complementarity to a portion of the target RNA. Methods

for making ribozymes are known to those skilled in the art. See, e.g., U.S. Patent Nos. 6,025,167; 5,773,260; and 5,496,698.

0243.0.3 The term "dsRNA," as used herein, refers to RNA hybrids comprising two strands of RNA. The dsRNAs can be linear or circular in structure. In a preferred embodiment, dsRNA is specific for a polynucleotide encoding either the polypeptide of Fig. 1a, 1b or 1c or a polypeptide having at least 70% sequence identity with a polypeptide of Fig. 1a, 1b or 1c. The hybridizing RNAs may be substantially or completely complementary. By "substantially complementary," is meant that when the two hybridizing RNAs are optimally aligned using the BLAST program as described above, the hybridizing portions are at least 95% complementary. Preferably, the dsRNA will be at least 100 base pairs in length. Typically, the hybridizing RNAs will be of identical length with no over hanging 5' or 3' ends and no gaps. However, dsRNAs having 5' or 3' overhangs of up to 100 nucleotides may be used in the methods of the invention.

0244.0.3 The dsRNA may comprise ribonucleotides or ribonucleotide analogs, such as 2'-O-methyl ribosyl residues, or combinations thereof. See, e.g., U.S. Patent Nos. 4,130,341 and 4,024,222. A dsRNA polyribonucleosinic acid:polyribocytidylic acid is described in U.S. patent 4,283,393. Methods for making and using dsRNA are known in the art. One method comprises the simultaneous transcription of two complementary DNA strands, either *in vivo*, or in a single *in vitro* reaction mixture. See, e.g., U.S. Patent No. 5,795,715. In one embodiment, dsRNA can be introduced into a plant or plant cell directly by standard transformation procedures. Alternatively, dsRNA can be expressed in a plant cell by transcribing two complementary RNAs.

0245.0.3 Other methods for the inhibition of endogenous gene expression, such as triple helix formation (Moser et al., 1987, *Science* 238:645-650 and Cooney et al., 1988, *Science* 241:456-459) and coexpression (Napoli et al., 1990, *The Plant Cell* 2:279-289) are known in the art. Partial and full-length cDNAs have been used for the coexpression of endogenous plant genes. See, e.g., U.S. Patent Nos. 4,801,340, 5,034,323, 5,231,020, and 5,283,184; Van der Krol et al., 1990, *The Plant Cell* 2:291-299; Smith et al., 1990, *Mol. Gen. Genetics* 224:177-181 and Napoli et al., 1990, *The Plant Cell* 2:279-289.

0246.0.3 For sense suppression, it is believed that introduction of a sense polynucleotide blocks transcription of the corresponding target gene. The sense polynucleotide will have at least 65% sequence identity with the target plant gene or RNA. Preferably, the percent identity is at least 80%, 90%, 95% or more. The introduced sense polynucleotide need not be full length relative to the target gene or transcript. Preferably, the sense polynucleotide will have at least 65% sequence

identity with at least 100 consecutive nucleotides of one of the nucleic acids of Fig. 1a, 1b or 1c. The regions of identity can comprise introns and and/or exons and untranslated regions. The introduced sense polynucleotide may be present in the plant cell transiently, or may be stably integrated into a plant chromosome or extrachromosomal replicon.

0247.0.1 Moreover, nucleic acid molecules encoding SRP from the same or other species such as SRP analogs, orthologs and paralogs, are intended to be within the scope of the present invention. As used herein, the term "analogs" refers to two nucleic acids that have the same or similar function, but that have evolved separately in unrelated organisms. As used herein, the term "orthologs" refers to two nucleic acids from different species that have evolved from a common ancestral gene by speciation. Normally, orthologs encode proteins having the same or similar functions. As also used herein, the term "paralogs" refers to two nucleic acids that are related by duplication within a genome. Paralogs usually have different functions, but these functions may be related (Tatusov, R.L. et al. 1997 Science 278(5338):831-837). Analogs, orthologs and paralogs of a naturally occurring stress related protein can differ from the naturally occurring stress related protein by post-translational modifications, by amino acid sequence differences, or by both. Post-translational modifications include in vivo and in vitro chemical derivatization of polypeptides e.g., acetylation, carboxylation, phosphorylation or glycosylation, and such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. In particular, orthologs of the invention will generally exhibit at least 80-85%, more preferably 90%, 91%, 92%, 93%, 94%, and most preferably 95%, 96%, 97%, 98% or even 99% identity or homology with all or part of a naturally occurring stress related protein amino acid sequence and will exhibit a function similar to a stress related protein. Orthologs of the present invention are also preferably capable of participating in the stress response in plants.

0248.0.1 In addition to naturally-occurring variants of a stress related protein sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the Fig. 1a, 1b or 1c, thereby leading to changes in the amino acid sequence of the encoded stress related protein, without altering the functional ability of the stress related protein or enhancing the functional ability of the stress related protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Fig 1. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of stress related proteins without altering the activity thereof, whereas an "essential" amino acid residue is

required for stress related protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having SRP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRP activity.

- 5 **0249.0.1** Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding stress related proteins that contain changes in amino acid residues that are not essential for stress related protein activity. Such SRP differ in amino acid sequence from a sequence Fig. 1a, 1b or 1c, yet retain at least one of the stress related protein activities described herein. In one embodiment, the isolated
- 10 nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Fig. 1a, 1b or 1c. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-80% homologous to one of the sequences of the Fig. 1a, 1b or 1c, more preferably at least about 60 - 70% homologous to one of the sequences of the Fig. 1a, 1b or 1c, even more preferably at least about 70 - 80%, 80 - 90%, more preferably 90%, 91%, 92%, 93%, 94% homologous to one of the sequences of the Fig. 1a, 1b or 1c and most preferably at least about 85%, 87%, 88%, or 95% homologous to one of the sequences of the Fig. 1a, 1b or 1c. The preferred stress related protein homologs of the present invention are preferably capable of
- 20 participating in the stress tolerance response in a plant. The homology (= identity) was calculated over the entire amino acid range. The program used was PileUp (J. Mol. Evolution., 25 (1987), 351-360, Higgins et al., CABIOS, 5 1988: 151-153).

- 0250.0.1** Homologs of the sequences given in Fig. 1a, 1b or 1c are furthermore to be understood as meaning, for example, homologs, analogs, orthologs and paralog
- 25 which have at least 30% homology (= identity) at the derived amino acid level, preferably at least 50 %, 60 %, 70 % or 80 % homology, especially preferably at least 85 % homology, very especially preferably 90 % 91%, 92%, 93%, 94% homology, most preferably 95 %, 96 %, 97 %, 98 % or 99 % homology. The homology (= identity) was calculated over the entire amino acid range. The program used was PileUp (J. Mol. Evolution., 25 (1987), 351 - 360, Higgins et al., CABIOS, 5 1989: 151 - 153) or the program Gap and BestFit [Needleman and Wunsch (J. Mol. Biol. 48; 443 - 453 (1970) and Smith and Waterman respectively (Adv. Appl. Math. 2; 482 - 489 (1981))] which are part of the GCG software package [Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991)]. The above mentioned percentages of
- 30 sequence homology are calculated with the program BestFit or Gap, preferably Gap, over the total sequence length with the following parameters used: Gap Weight: 8, Length Weight: 2.
- 35

0251.0.1 Variants shall also be encompassed, in particular, functional variants which can be obtained from the sequence shown in the Fig. 1a, 1b or 1c by means of deletion, insertion or substitution of nucleotides, the enzymatic activity of the derived synthetic proteins being retained or enhanced.

- 5 **0252.0.1** An isolated nucleic acid molecule encoding a stress related protein homologous to a protein sequence of Fig. 1a, 1b or 1c can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Fig. 1a, 1b or 1c such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one
10 of the sequences of Fig. 1a, 1b or 1c by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Another route to the mutagenesis of enzymes, disclosed in the European Publication EP-A-O 909 821, is a method using the specific *Escherichia coli* strain XL1-Red to generate mutants and altered the enzyme activity.

- 15 **0253.0.1** Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

- 0254.0.1** Families of amino acid residues having similar side chains have been
20 defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g.,
25 threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a stress related protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a stress related protein coding sequence, such as by
30 saturation mutagenesis, and the resultant mutants can be screened for a stress related protein activity as described herein to identify mutants that retain stress related protein activity or show enhanced stress related protein activity. Following mutagenesis of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c, the encoded protein can be expressed recombinantly and the activity of the protein can be determined by analyzing
35 the stress tolerance of a plant expressing the protein as described in the examples below.

0255.0.1 A useful method to ascertain the level of transcription of the gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: New York). This information at least partially demonstrates the degree of transcription of the gene. Total cellular RNA can be prepared from cells, tissues or organs by several methods, all well-known in the art, such as that described in Bormann, E.R. et al., 1992 Mol. Microbiol. 8:317-326. To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed. These techniques are well known to one of ordinary skill in the art (see, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: New York).

0256.0.1 The present invention also relates to a plant expression cassette comprising a SRP coding nucleic acid selected from the group comprising sequences of SEQ IDs No. XXX and/or homologs or parts thereof operatively linked to regulatory sequences and/or targeting sequences.

0257.0.1 Further, object of the invention is an expression vector comprising a SRP encoding nucleic acid selected from the group comprising sequences of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs or parts thereof or a plant expression cassette as described above, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type host cell.

0258.0.1 The invention further provides an isolated recombinant expression vector comprising a stress related protein encoding nucleic acid as described above, wherein expression of the vector or stress related protein encoding nucleic acid, respectively in a host cell results in increased tolerance and/or resistance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to the corresponding non-transformed wild type of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Further types of vectors can be linearized nucleic acid sequences, such as transposons, which are pieces of DNA which can copy and insert themselves. There have been 2 types of transposons found: simple transposons, known as Insertion Sequences and composite transposons, which can have several genes as well as the genes that are required for transposition.

0259.0.1 Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

0260.0.1 A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells and operably linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* T-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gislen et al., 1984 EMBO J. 3:835) or functional equivalents thereof but also all other terminators functionally active in plants are suitable.

0261.0.1 As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operably linked sequences like translational enhancers such as the overdrive-sequence containing the 5'-untranslated leader sequence from tobacco mosaic virus enhancing the protein per RNA ratio (Gallie et al., 1987 Nucl. Acids Research 15:8893-8711).

0262.0.1 Plant gene expression has to be operably linked to an appropriate promoter conferring gene expression in a timely, cell or tissue specific manner. Preferred are promoters driving constitutive expression (Bentley et al., 1989 EMBO J. 8:2195-2202) like those derived from plant viruses like the 35S CaMV (Frank et al., 1980 Cell 21:285-294), the 19S CaMV (see also U.S. Patent No. 5352605 and PCT Application No. WO 8402913) or plant promoters like those from Rubisco small subunit described in U.S. Patent No. 4,962,028.

0263.0.1 Additional advantageous regulatory sequences are, for example, included in the plant promoters such as CaMV/35S [Frank et al., Cell 21 (1980) 285 - 294], PRP1 [Ward et al., Plant. Mol. Biol. 22 (1993)], SSU, OCS, lib4, usp, STLS1, B33, LEB4, nos or in the ubiquitin, napin or phaseolin promoter. Also advantageous in this connection are inducible promoters such as the promoters described in EP-A-0

- 388 186 (benzyl sulfonamide inducible), Plant J. 2, 1992: 397 - 404 (Gatz et al., Tetracyclin inducible), EP-A-0 335 528 (abscisic acid inducible) or WO 93/21334 (ethanol or cyclohexanol inducible). Additional useful plant promoters are the cytosolic FBPase promoter or ST-LSI promoter of the potato (Stockhaus et al., EMBO J. 8, 1989, 2445), the phosphorylcholine phosphatase promoter of Glycine max (gene bank accession No. U87999) or the noden specific promoter described in EP-A-0 249 676. Additional particularly advantageous promoters are seed specific promoters which can be used for monocotyledonae or dikotyledonae and are described in US 5,608,152 (napin promoter from rapeseed), WO 98/45461 (phaseolin promoter from Arobidops), US 5,504,200 (phaseolin promoter from Phaseolus vulgaris), WO 91/13980 (Bce4 promoter from Brassica) and Baumlein et al., Plant J., 2, 2, 1992: 233-239 (LEB4 promoter from leguminosa). Said promoters are useful in dikotyledonae. The following promoters are useful for example in monocotyledonae lpt-2- or lpt-1- promoter from barley (WO 95/15389 and WO 95/23230) or hordein promoter from barley. Other useful promoters are described in WO 98/16090.

15 **0264.0.1** It is possible in principle to use all natural promoters with their regulatory sequences like those mentioned above for the novel process. It is also possible and advantageous in addition to use synthetic promoters.

0265.0.1 The gene construct may also comprise further genes which are to be inserted into the organisms and which are for example involved in stress resistance. It is possible and advantageous to insert and express in host organisms regulatory genes such as genes for inducers, repressors or enzymes which intervene by their enzymatic activity in the regulation of one or more or all genes of a biosynthetic pathway. These genes can be heterologous or homologous in origin. The inserted genes may have their own promoter or else be under the control of same promoter as the sequences of the nucleic acid of Fig. 1a, 1b or 1c or their homologs.

0266.0.1 The gene construct advantageously comprises, for expression of the other genes present, additionally 3' and/or 5' terminal regulatory sequences to enhance expression, which are selected for optimal expression depending on the selected host organism and gene or genes.

30 **0267.0.1** These regulatory sequences are intended to make specific expression of the genes and protein expression possible as mentioned above. This may mean, depending on the host organism, for example that the gene is expressed or overexpressed only after induction, or that it is immediately expressed and/or overexpressed.

0268.0.1 The regulatory sequences or factors may moreover preferably have a beneficial effect on expression of the introduced genes, and thus increase it. It is

possible in this way for the regulatory elements to be enhanced advantageously at the transcription level by using strong transcription signals such as promoters and/or enhancers. However, in addition, it is also possible to enhance translation by, for example, improving the stability of the mRNA.

- 5 **0269.0.1** Other preferred sequences for use in plant gene expression cassettes are targeting-sequences necessary to direct the gene product in its appropriate cell compartment (for review see Kermode, 1996 *Crit. Rev. Plant Sci.* 15(4):285-423 and references cited therein) such as the vacuole, the nucleus, all types of plastids like amyloplasts, chloroplasts, chromoplasts, the extracellular space, mitochondria, the
- 10 endoplasmic reticulum, oil bodies, peroxisomes and other compartments of plant cells.

0270.0.1 Plant gene expression can also be facilitated via an inducible promoter (for review see Gaiz, 1997 *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 48:89-108). Chemically inducible promoters are especially suitable if gene expression is wanted to occur in a time specific manner.

- 15 **0271.0.1** Table 1 lists several examples of promoters that may be used to regulate transcription of the stress related protein nucleic acid coding sequences.

0272.0.1 Tab. 1: Examples of Tissue-specific and Stress inducible promoters in plants

Expression	Reference
Cor78- Cold, drought, salt, ABA, wounding-inducible	Ishitani, <i>et al.</i> , <i>Plant Cell</i> 9:1935-1949 (1997). Yamaguchi-Shinozaki and Shinozaki, <i>Plant Cell</i> 8:251-264 (1994).
Rci2A - Cold, dehydration-inducible	Capel <i>et al.</i> , <i>Plant Physiol</i> 115:568-576 (1997)
Rd22 - Drought, salt	Yamaguchi-Shinozaki and Shinozaki, <i>Mol Gen Genet</i> 238:17-25 (1993).
Cor15A - Cold, dehydration, ABA	Baker <i>et al.</i> , <i>Plant Mol. Biol.</i> 24:701-713 (1994).
GH3- Auxin inducible	Liu <i>et al.</i> , <i>Plant Cell</i> 6:645-657 (1994)
ARSK1-Root, salt inducible	Hwang and Goodman, <i>Plant J</i> 8:37-43 (1995).
PtxA - Root, salt inducible	GenBank accession X67427

SbHRGP3 - Root specific	Ahn <i>et al.</i> , Plant Cell 8:1477-1490 (1998).
KST1 - Guard cell specific	Plesch <i>et al.</i> , Plant Journal. 28(4):455-64, (2001)
KAT1 - Guard cell specific	Plesch <i>et al.</i> , Gene 249:83-89 (2000) Nakamura <i>et al.</i> , Plant Physiol. 109:371-374 (1995)
salicylic acid inducible	PCT Application No. WO 95/19443
tetracycline inducible	Gatz <i>et al.</i> , Plant J. 2:397-404 (1992)
Ethanol Inducible	PCT Application No. WO 93/21334
pathogen inducible PRF1	Ward <i>et al.</i> , 1993 Plant. Mol. Biol. 22:361-366
heat inducible hsp80	U.S. Patent No. 5187287
cold inducible alpha-amylase	PCT Application No. WO 95/12814
Wound-inducible pinII	European Patent No. 375091
RD29A - salt-inducible	Yamaguchi-Shinozaki <i>et al.</i> (1993) Mol. Gen. Genet. 238:331-340
plastid-specific viral RNA-polymerase	PCT Application No. WO 95/16783 and. WO 97/06250

0273.0.1 Other promoters, e.g. superpromotor (Ni *et al.*, Plant Journal 7, 1995: 661-676), Ubiquitin promotor (Callis *et al.*, J. Biol. Chem., 1990, 265: 12486-12493; US 5,510,474; US 6,020,190; Kawalleck *et al.*, Plant. Molecular Biology, 1993, 21: 873-884) or 34S promotor (GenBank Accession numbers M59930 and X10673) were similar useful for the present invention and are known to a person skilled in the art.

0274.0.3 Developmental stage-preferred promoters are preferentially expressed at certain stages of development. Tissue and organ preferred promoters include those that are preferentially expressed in certain tissues or organs, such as leaves, roots, seeds, or xylem. Examples of tissue preferred and organ preferred promoters include, but are not limited to fruit-preferred, ovule-preferred, male tissue-preferred, seed-

preferred, integument-preferred, tuber-preferred, stalk-preferred, pericarp-preferred, and leaf-preferred, stigma-preferred, pollen-preferred, anther-preferred, a petal-preferred, sepal-preferred, pedicel-preferred, silique-preferred, stem-preferred, root-preferred promoters, and the like. Seed preferred promoters are preferentially expressed during seed development and/or germination. For example, seed preferred promoters can be embryo-preferred, endosperm preferred, and seed coat-preferred. See Thompson et al., 1989, *BioEssays* 10:108. Examples of seed preferred promoters include, but are not limited to, cellulose synthase (*celA*), *Cim1*, gamma-zein, globulin-1, maize 19 kD zein (*zZ19B1*), and the like.

10 **0275.0.3** Other promoters useful in the expression cassettes of the invention include, but are not limited to, the major chlorophyll a/b binding protein promoter, histone promoters, the *Ap3* promoter, the β -conglycin promoter, the napin promoter, the soybean lectin promoter, the maize 15kD zein promoter, the 22kD zein promoter, the 27kD zein promoter, the g-zein promoter, the waxy, shrunken 1, shrunken 2 and
15 bronze promoters, the *Zm13* promoter (U.S. Patent No. 5,086,169), the maize polygalacturonase promoters (PG) (U.S. Patent Nos. 5,412,085 and 5,546,546), and the SGB8 promoter (U.S. Patent No. 5,470,359), as well as synthetic or other natural promoters.

0276.0.3 Additional flexibility in controlling heterologous gene expression in plants
20 may be obtained by using DNA binding domains and response elements from heterologous sources (*i.e.*, DNA binding domains from non-plant sources). An example of such a heterologous DNA binding domain is the LexA DNA binding domain (Brent and Ptashne, 1989, *Cell* 43:729-736).

0277.0.3 The invention further provides a recombinant expression vector
25 comprising a SRP DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to a SRP mRNA. Regulatory sequences operatively linked to a nucleic acid molecule cloned in the antisense orientation can be
30 chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types. For instance, viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific, or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus wherein antisense nucleic acids
35 are produced under the control of a high efficiency regulatory region. The activity of the regulatory region can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense

genes, see Weintraub, H. et al., 1986, Antisense RNA as a molecular tool for genetic analysis, Reviews - Trends in Genetics, Vol. 1(1), and Mol et al., 1990, FEBS Letters 268:427-430.

0279.0.3 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a SRP can be expressed in bacterial cells such as *C. glutamicum*, yeast, *E. coli*, insect cells, fungal cells, or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi, or other microorganisms like *C. glutamicum*. Other suitable host cells are known to those skilled in the art.

0280.0.3 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) a SRP. Accordingly, the invention further provides methods for producing SRPs using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a SRP has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRP) in a suitable medium until SRP is produced. In another embodiment, the method further comprises isolating SRPs from the medium or the host cell.

0281.0.3 Another aspect of the invention pertains to isolated SRFs, and biologically active portions thereof. An "isolated" or "purified" polypeptide or biologically active portion thereof is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRP in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of a SRP having less than about 30% (by dry weight) of non-SRP material (also referred to herein as a "contaminating polypeptide"), more preferably less than about 20% of non-SRP material, still more preferably less than about 10% of non-SRP material, and most preferably less than about 5% non-PKSRP material.

0282.0.3 When the SRP or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRP in which the polypeptide is separated from chemical precursors or other chemicals that are involved in the synthesis of the polypeptide. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of a SRP having less than about 30% (by dry weight) of chemical precursors or non-SRP chemicals, more preferably less than about 20% chemical precursors or non-SRP chemicals, still more preferably less than about 10% chemical precursors or non-SRP chemicals, and most preferably less than about 5% chemical precursors or non-SRP chemicals. In preferred embodiments, isolated polypeptides, or biologically active portions thereof, lack contaminating polypeptides from the same organism from which the SRP is derived. Typically, such polypeptides are produced by recombinant expression of, for example, a *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP in plants other than *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*, or microorganism such as *C. glutamicum*, ciliates, algae or fungi.

0283.0.3 The nucleic acid molecules, polypeptides, polypeptide homologs, fusion polypeptides, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* and related organisms; mapping of genomes of organisms related to *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*; identification and localization of *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* sequences of interest; evolutionary studies; determination of SRP regions required for function; modulation of a SRP activity; modulation of the metabolism of one or more cell functions; modulation of the transmembrane transport of one or more compounds; modulation of stress resistance; and modulation of expression of SRP nucleic acids.

0284.0.3 The SRP nucleic acid molecules of the invention are also useful for evolutionary and polypeptide structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are

conserved and which are not, which may aid in determining those regions of the polypeptide that are essential for the functioning of the enzyme. This type of determination is of value for polypeptide engineering studies and may give an indication of what the polypeptide can tolerate in terms of mutagenesis without losing function.

0285.0.3 Manipulation of the SRP nucleic acid molecules of the invention may result in the production of SRPs having functional differences from the wild-type SRPs. These polypeptides may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

0286.0.3 There are a number of mechanisms by which the alteration of a SRP of the invention may directly affect stress response and/or stress tolerance. In the case of plants expressing SRPs, increased transport can lead to improved salt and/or solute partitioning within the plant tissue and organs. By either increasing the number or the activity of transporter molecules which export ionic molecules from the cell, it may be possible to effect the salt tolerance of the cell.

0287.0.3 The effect of the genetic modification in plants, *C. glutamicum*, fungi, algae, or ciliates on stress tolerance can be assessed by growing the modified microorganism or plant under less than suitable conditions and then analyzing the growth characteristics and/or metabolism of the plant. Such analysis techniques are well known to one skilled in the art, and include dry weight, wet weight, polypeptide synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 469-714, VCH: Weinheim; Belter, P.A. et al., 1988, Bioprocesses: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S., 1992, Recovery processes for biological materials, John Wiley and Sons; Shewitz, J.A. and Henry, J.D., 1988, Biochemical separations, in: Ullmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J., 1989, Separation and purification techniques in biotechnology, Moyer Publications).

0288.0.3 For example, yeast expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into *Saccharomyces cerevisiae* using standard protocols. The resulting transgenic cells can then be assayed for fall or alteration of their tolerance to drought, salt, and temperature stress. Similarly, plant expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into an appropriate

plant cell such as *Arabidopsis*, soy, rape, maize, wheat, *Medicago truncatula*, etc., using standard protocols. The resulting transgenic cells and/or plants derived therefrom can then be assayed for fail or alteration of their tolerance to drought, salt, temperature stress, and lodging.

- 5 **0289.0.3** The engineering of one or more SRP genes of the invention may also result in SRPs having altered activities which indirectly impact the stress response and/or stress tolerance of algae, plants, ciliates, or fungi, or other microorganisms like *C. glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of products (e.g., hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes. For example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T., 1999, Curr. Opin. Chem. Biol. 3(2):226-235). While these products are typically excreted, cells can be genetically altered to transport more products than is typical for a wild-type cell. By optimizing the activity of one or more PKSRPs of the invention which are involved in the export of specific molecules, such as salt molecules, it may be possible to improve the stress tolerance of the cell.

- 10 **0290.0.3** Additionally, the sequences disclosed herein, or fragments thereof, can be used to generate knockout mutations in the genomes of various organisms, such as bacteria, mammalian cells, yeast cells, and plant cells (Girke, T., 1998, The Plant Journal 15:39-48). The resultant knockout cells can then be evaluated for their ability or capacity to tolerate various stress conditions, their response to various stress conditions, and the effect on the phenotype and/or genotype of the mutation. For other methods of gene inactivation, see U.S. Patent No. 6,004,804 "Non-Chimeric Mutational Vectors" and Puttaraju et al., 1999, Spliceosome-mediated RNA trans-splicing as a tool for gene therapy, Nature Biotechnology 17:246-252.

- 25 **0291.0.3** The aforementioned mutagenesis strategies for SRPs resulting in increased stress resistance are not meant to be limiting; variations on these strategies will be readily apparent to one skilled in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and polypeptide molecules of the invention may be utilized to generate algae, ciliates, plants, fungi, or other microorganisms like *C. glutamicum* expressing mutated PKSRP nucleic acid and polypeptide molecules such that the stress tolerance is improved.

- 30 **0292.0.3** The present invention also provides antibodies that specifically bind to a SRP, or a portion thereof, as encoded by a nucleic acid described herein. Antibodies can be made by many well-known methods (See, e.g. Harlow and Lane, "Antibodies: A Laboratory Manual," Cold Spring Harbor Laboratory, Cold Spring Harbor, New York,

(1988)). Briefly, purified antigen can be injected into an animal in an amount and in intervals sufficient to elicit an immune response. Antibodies can either be purified directly, or spleen cells can be obtained from the animal. The cells can then fused with an immortal cell line and screened for antibody secretion. The antibodies can be used to screen nucleic acid clone libraries for cells secreting the antigen. Those positive clones can then be sequenced. See, for example, Kelly et al., 1992, *BioTechnology* 10:163-167; Debbington et al., 1992, *BioTechnology* 10:169-175.

0293.0.3 The phrases "selectively binds" and "specifically binds" with the polypeptide refer to a binding reaction that is determinative of the presence of the polypeptide in a heterogeneous population of polypeptides and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bound to a particular polypeptide do not bind in a significant amount to other polypeptides present in the sample. Selective binding of an antibody under such conditions may require an antibody that is selected for its specificity for a particular polypeptide. A variety of immunoassay formats may be used to select antibodies that selectively bind with a particular polypeptide. For example, solid-phase ELISA immunoassays are routinely used to select antibodies selectively immunoreactive with a polypeptide. See Harlow and Lane, "Antibodies, A Laboratory Manual," Cold Spring Harbor Publications, New York, (1988), for a description of immunoassay formats and conditions that could be used to determine selective binding.

0294.0.3 In some instances, it is desirable to prepare monoclonal antibodies from various hosts. A description of techniques for preparing such monoclonal antibodies may be found in Stiles et al., eds., "Basic and Clinical Immunology," (Langr Medical Publications, Los Altos, Calif., Fourth Edition) and references cited therein, and in Harlow and Lane, "Antibodies, A Laboratory Manual," Cold Spring Harbor Publications, New York, (1988).

0295.0.1 Gene expression in plants is regulated by the interaction of protein transcription factors with specific nucleotide sequences within the regulatory region of a gene. A common type of transcription factor contains zinc finger (ZF) motifs. Each ZF module is approximately 30 amino acids long folded around a zinc ion. The DNA recognition domain of a ZF protein is a α -helical structure that inserts into the major groove of the DNA double helix. The module contains three amino acids that bind to the DNA with each amino acid contacting a single base pair in the target DNA sequence. ZF motifs are arranged in a modular repeating fashion to form a set of fingers that recognize a contiguous DNA sequence. For example, a three-fingered ZF motif will recognize 9 bp of DNA. Hundreds of proteins have been shown to contain ZF motifs with between 2 and 37 ZF modules in each protein (Isalan M, et al., 1998 *Biochemistry*

37(35):12026-33; Moore M, et al., 2001 Proc. Natl. Acad. Sci. USA 98(4):1432-1436 and 1437-1441; US patents US 6007988 and US 6013453).

5 **0296.0.1** The regulatory region of a plant gene contains many short DNA sequences (cis-acting elements) that serve as recognition domains for transcription factors, including ZF proteins. Similar recognition domains in different genes allow the coordinate expression of several genes encoding enzymes in a metabolic pathway by common transcription factors. Variation in the recognition domains among members of a gene family facilitates differences in gene expression within the same gene family, for example, among tissues and stages of development and in response to environmental conditions.

10 **0297.0.1** Typical ZF proteins contain not only a DNA recognition domain but also a functional domain that enables the ZF protein to activate or repress transcription of a specific gene. Experimentally, an activation domain has been used to activate transcription of the target gene (US patent 5789538 and patent application WO9519431), but it is also possible to link a transcription repressor domain to the ZF and thereby inhibit transcription (patent applications WO00/47754 and WO2001002019). It has been reported that an enzymatic function such as nucleic acid cleavage can be linked to the ZF (patent application WO00/20622).

15 **0298.0.1** The invention provides a method that allows one skilled in the art to isolate the regulatory region of one or more stress related protein encoding genes from the genome of a plant cell and to design zinc finger transcription factors linked to a functional domain that will interact with the regulatory region of the gene. The interaction of the zinc finger protein with the plant gene can be designed in such a manner as to alter expression of the gene and preferably thereby alter metabolic activity to confer increased (or decreased) tolerance of abiotic stress such as drought.

20 The invention provides a method of producing a transgenic plant with a transgene encoding this designed transcription factor, or alternatively a natural transcription factor, that modifies transcription of the Stress-Related Protein, particularly stress related protein gene to provide increased tolerance of environmental stress, which is preferably achieved by altering metabolic activity. Such a regulation of plant genes by artificial polydactyl zinc fingers has been demonstrated by Ordiz et al. (Regulation of transgene Expression in plants with polydactyl zinc finger transcription factors, Ordiz et al., PNAS, 99 (20) 13290-13295, 2002) or Guan et al. (Heritable endogenous gene regulation in plants with designed polydactyl zinc finger transcription factors, PNAS, Vol. 99 (20), 13296-13301 (2002)).

25 **0299.0.1** In particular, the invention provides a method of producing a transgenic plant with a stress related protein coding nucleic acid, wherein expression of the

- nucleic acid(s) in the plant results in increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant comprising: (a) transforming a plant cell with an expression vector comprising a stress related protein encoding nucleic acid, and (b) generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a wild type plant. For such plant transformation, binary vectors such as pBINAR can be used (Höfgen and Willmitzer, 1990 Plant Science 66:221-230). Moreover suitable binary vectors are for example pBIN19, pBIN101, pGPTV or pPZP (Hajdukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 989-994).
- 10 **0300.0.1** Construction of the binary vectors can be performed by ligation of the cDNA into the T-DNA. 5' to the cDNA a plant promoter activates transcription of the cDNA. A polyadenylation sequence is located 3' to the cDNA. Tissue-specific expression can be achieved by using a tissue specific promoter as listed above. Also, any other promoter element can be used. For constitutive expression within the whole
- 15 plant, the CaMV 35S promoter can be used. The expressed protein can be targeted to a cellular compartment using a signal peptide, for example for plastids, mitochondria or endoplasmic reticulum (Kermode, 1998 Crit. Rev. Plant Sci. 4(15):285-423). The signal peptide is cloned 5' in frame to the cDNA to achieve subcellular localization of the fusion protein. Additionally, promoters that are responsive to abiotic stresses can be
- 20 used with, such as the Arabidopsis promoter RD29A. One skilled in the art will recognize that the promoter used should be operatively linked to the nucleic acid such that the promoter causes transcription of the nucleic acid which results in the synthesis of a mRNA which encodes a polypeptide.
- 0301.0.1** Alternate methods of transformation include the direct transfer of DNA into
- 25 developing flowers via electroporation or Agrobacterium mediated gene transfer. Agrobacterium mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986 Mol. Gen. Genet. 204:383-396) or LBA4404 (Ooms et al., Plasmid, 1982, 7: 15-29; Hoekema et al., Nature, 1983, 303: 179-180) Agrobacterium tumefaciens strain. Transformation can be performed by standard
- 30 transformation and regeneration techniques (Deblaere et al., 1994 Nucl. Acids. Res. 13:4777-4788; Gelvin and Schilperoort, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, B R and Thompson, J E, Methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993. - 360 S., ISBN 0-8493-
- 35 5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989 Plant Cell Reports 8:238-242; De Block et al., 1989 Plant Physiol. 91:694-701). Use of antibiotics for Agrobacterium and plant

selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994 Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 687, U.S. Patent No. 5,378,543 or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake or via the silicon carbide fiber technique (see, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387 and a specific example of wheat transformation can be found in PCT Application No. WO 93/07266.

0302.0.1 The stress related protein encoding nucleic acid molecules of the invention have a variety of uses. Most importantly, the nucleic acid and amino acid sequences of the present invention can be used to transform plant cells or plants, thereby inducing tolerance to stresses such as drought, high salinity and cold. The present invention therefore provides a transgenic plant transformed by a stress related protein encoding nucleic acid (coding or antisense), wherein expression of the nucleic acid sequence in the plant results in increased tolerance to environmental stress as compared to a wild type plant. The increased stress tolerance is apparent as an increase in the yield or quality of the plant. The transgenic plant can be a monocot or a dicot or a gymnosperm plant. The invention further provides that the transgenic plant can be selected from maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, borago, sunflower, linseed, primrose, rapeseed, canola and turnip rape, manihot, pepper, sunflower, tagetes, solanaceous plant such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants such as coffee, cacao, tea, *Salix* species, trees such as oil palm, coconut, perennial grass, such as ryegrass and fescue, and forage crops, such as alfalfa and clover and *Arabidopsis thaliana*.

0303.0.1 In particular, the present invention describes using the expression of stress related proteins to engineer drought-tolerant, salt-tolerant and/or cold-tolerant plants. This strategy has herein been demonstrated for *Arabidopsis thaliana*, Ryegrass, Alfalfa, Rapeseed/Canola, Soybean, Corn and Wheat but its application is not restricted to these plants. Accordingly, the invention provides a transgenic plant containing a stress related protein encoding gene selected from the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences, wherein the

environmental stress is drought, increased salt or decreased or increased temperature but its application is not restricted to these adverse environments. Protection against other adverse conditions such as heat, air pollution, heavy metals and chemical toxicants, for example, may be obtained. In preferred embodiments, the environmental stress is drought.

0304.0.1 The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the expression of a stress related protein encoding gene in the plant. The invention provides that this method can be performed such that the stress tolerance is increased. This can for example be done by the use of transcription factors. In particular, the present invention provides methods of producing a transgenic plant having an increased tolerance to environmental stress as compared to a wild type plant due to increased expression of a stress related protein in the plant.

0306.0.1 Growing the modified plants under stress conditions and then screening and analyzing the growth characteristics and/or metabolic activity assess the effect of the genetic modification in plants on stress tolerance and/or resistance. Such analysis techniques are well known to one skilled in the art. They include next to screening (Römpp Lexikon Biotechnologie, Stuttgart/New York: Georg Thieme Verlag 1992, "screening" p. 701) dry weight, wet weight, protein synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 489-714, VCH: Weinheim; Belter, F.A. et al., 1988 Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S., 1992 Recovery processes for biological materials, John Wiley and Sons; Shastitz, J.A. and Henry, J.D., 1989 Biochemical separations, In: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications).

0306.0.1 The engineering of one or more stress related protein encoding genes of the invention may also result in stress related proteins having altered activities which indirectly impact the stress response and/or stress tolerance of plants. For example, the normal biochemical processes of metabolism result in the production of a variety of products (e.g., hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes (for example, peroxynitrite is known to react with tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T., 1999 Curr. Opin. Chem. Biol. 3(2):226-235). By

optimizing the activity of one or more stress related proteins (enzymes) of the invention, it may be possible to improve the stress tolerance of the cell.

0307.0.1 Throughout this application, various publications are referenced. The disclosures of all of these publications and those references cited within those publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

0308.0.1 It should also be understood that the foregoing relates to preferred embodiments of the present invention and that numerous changes and variations may be made therein without departing from the scope of the invention. The invention is further illustrated by the following examples, which are not to be construed in any way as limiting. On the contrary, it is to be clearly understood that various other embodiments, modifications and equivalents thereof, which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or the scope of the claims.

0309.0.1 The invention also pertains to the use of SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences for preparing a plant cell with increased environmental stress tolerance, which is preferably achieved by altering metabolic activity. The said sequences can also be used for preparing a plant with increased environmental stress tolerance.

0310.0.1 Object of the invention is further the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group of sequences of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants with increased tolerance to environmental stress or as markers for detection of stress in plants or plant cells.

0311.0.1 Example 1

0312.0.1 Engineering stress-tolerant Arabidopsis plants by over-expressing stress related protein genes.

0313.0.1 Gene cloning and transformation of Arabidopsis thaliana

0314.0.1 Amplification

0315.0.1 The standard protocol of Pfu DNA polymerase or a PfuTaq DNA polymerase mix (Herculase) was used for the amplification procedure. Amplified ORF fragments were analysed by gel electrophoresis. Each primer consists of a universal 5' end and ORF specific 3' end whereby the universal sequences differ for the forward and reverse primers (forward primer sequence contains an EcoRI for yeast or SmaI for E.coli and the reverse primer sequence a SmaI for yeast or SacI for E.coli restriction site) allowing generally a unidirectional cloning success.

- 0316.0.1** Amplification using the protocol of Pfu or Herculae DNA polymerase (Stratagene). Conditions: 1x PCR buffer, 0.2 mM dNTP, 100 ng genomic DNA *Saccharomyces cerevisiae* (S288C) or 60 ng genomic DNA *Escherichia coli* K-12 (MG1655), 25 pmol forward primer, 25 pmol reverse primer, 2.5 u Pfu or Herculae DNA polymerase. 1st cycle for 3' for yeast or 2' for E.coli at 94 °C, followed by 25 cycles for 30'' at 94 °C, 30'' 55°C for yeast or 60°C for E.coli and 5-6' 72 °C, followed by 1 cycle for 610' at 72 °C, final for 4 °C at ∞.

0317.0.1 Table 2: Forward and reverse primer sequences used for ORF amplification

Gene	Forward Seq
YGL283W	GGAATTCAGCTGACCACCATGGATGGAGCCAAATTTGAAATAC
YGR004W	GGAATTCAGCTGACCACCATGAGCGAAATAAATAATGAAATCTAG
YGH014W	GGAATTCAGCTGACCACCATGCGATTTCCATTGCTTGTCTC
YGL239C	GGAATTCAGCTGACCACCATGAAATTTTGAAGCAAAAGCACC
YBL060W	GGAATTCAGCTGACCACCATGTGCGCCAGTTTAAACGAGGTA
YGL163W	GGAATTCAGCTGACCACCATGGTCGTAAATTAACGGGGTCAAAAT
YDL202W	GGAATTCAGCTGACCACCATGTTGCGAGCTAAGGTTTATGCGCT
YAL040C	GGAATTCAGCTGACCACCATGAAAGCTCCACAGACCATGCT
YDR101C	GGAATTCAGCTGACCACCATGGCTCTAGCTATCTCCAGCGA
YDR106W	GGAATTCAGCTGACCACCATGGTTTCTTATGACACTATATG
YAL064W	GGAATTCAGCTGACCACCATGCGATATACTGCAACTTTTGGG
YDR134C	GGAATTCAGCTGACCACCATGCAATTTCTACCGTGCTTCT
YFL051W	GGAATTCAGCTGACCACCATGCAATTAACCGAGTACGATTACCTGT
YFL052V	GGAATTCAGCTGACCACCATGCGCCGCGATAGCAAGCGT
YFL042C	GGAATTCAGCTGACCACCATGTCGGATGTAGATACTGGGAA
YBR025C	GGAATTCAGCTGACCACCATGCTCCAAAGAAAGTACGAGT
YER174C	GGAATTCAGCTGACCACCATGACTGTGTTGAAATAAAAGGCG
YBR1051W	GGAATTCAGCTGACCACCATGACATCTTTTCTGTTTATTTTC
YER175C	GGAATTCAGCTGACCACCATGTCTACCTTTTCTGCTTCTGATT
YDR521W	GGAATTCAGCTGACCACCATGAAAGGTTCAAAATCGACCTTG
YER167W	GGAATTCAGCTGACCACCATGCGAAGAATAGTCACCAACAT
YER123W	GGAATTCAGCTGACCACCATGTCCCAACGATCTTCACAACAC
YDR115C	GGAATTCAGCTGACCACCATGGCCGATGAGGAACGTTTAAAG
YEL052W	GGAATTCAGCTGACCACCATGCTGCTTTGAAGCCCAATGCT
YDH536W	GGAATTCAGCTGACCACCATGAGGATTTTAAATTTATGAAATTTCA
YDR513W	GGAATTCAGCTGACCACCATGCGAGACCAATTTTCTGCTGACT
YEL045C	GGAATTCAGCTGACCACCATGAAATGTCACGCGAAACGGAC
YEL041W	GGAATTCAGCTGACCACCATGAAACTGATAGATTACTGATTAAAC
YDL238C	GGAATTCAGCTGACCACCATGACAAAAAGTATTATTATTGATAA
YBR282W	GGAATTCAGCTGACCACCATGAAAGGCTCAGCCATTTCTCAAT
YBR258C	GGAATTCAGCTGACCACCATGGCGTATAATCAAGAGATAGTAA
YCL001W-A	GGAATTCAGCTGACCACCATGACCTTTTACAATTTATGAATTAATA

YBR274W	GGAATTCAGCTGACCAACCATGAGTCTCTCGCAGGTGTCAAC
YHP090C	GGAATTCAGCTGACCAACCATGGATCCAAGTTTAGTTTAGAGGC
YGR121C	GGAATTCAGCTGACCAACCATGAGAGTGGAACTACAGGGC
YGR127W	GGAATTCAGCTGACCAACCATGTGCATTTTAATGGCCACAAGG
YGR150C	GGAATTCAGCTGACCAACCATGTACATGGCCAGATGTGGCC
YKL037W	GGAATTCAGCTGACCAACCATGCAGACAATGGCGGGGGAG
YKL051W	GGAATTCAGCTGACCAACCATGATCAATTTAAAAGTCCAGGTAAAC
YKL120W	GGAATTCAGCTGACCAACCATGTCTCTGACAACCTTAAACAAG
YKL017C	GGAATTCAGCTGACCAACCATGTCCGACAGCACAGAAAGCTAAG
YKL017C	GGAATTCAGCTGACCAACCATGAACAAGAAATGGGTTCTAAGTT
YKL049C	GGAATTCAGCTGACCAACCATGGAAAGTGAAGTACCTGCACCA
YKL132C	GGAATTCAGCTGACCAACCATGGATGATATAAGCGGAAGGCCAA
YGR126W	GGAATTCAGCTGACCAACCATGGCTGTCCCATCTGTACTGT
YKL070W	GGAATTCAGCTGACCAACCATGTACATTCCTAAACATTTGAGTC
YKL058W	GGAATTCAGCTGACCAACCATGGCAGTACCCGGGTATTACGA
YHR190C	GGAATTCAGCTGACCAACCATGACTAAAAGTATATATATTATCATCG
YIL070C	GGAATTCAGCTGACCAACCATGTTCTTAAGAAGCGTTAACCGTG
YHR195W	GGAATTCAGCTGACCAACCATGACTCGTCCCGCATTTGGTTC
YHR022W	GGAATTCAGCTGACCAACCATGAATCTAAGATTTGAATTCAGAAA
YJL089W	GGAATTCAGCTGACCAACCATGGCCAAAGAGGAATATGGGAG
YJL172W	GGAATTCAGCTGACCAACCATGATCGCCTTACCAATGAGAAAG
YHR112W	GGAATTCAGCTGACCAACCATGTTCCAGATACAACCTGAGAAGTA
YHR175W	GGAATTCAGCTGACCAACCATGGATGATAAGAAAACATGGAGTAC
YGR121W	GGAATTCAGCTGACCAACCATGATCTTAAGTTCTGCTATTGAA
YJL024C	GGAATTCAGCTGACCAACCATGATTCATCCAGTTCTGATATGATG
YGR180C	GGAATTCAGCTGACCAACCATGGAAGCACATAACCAATTTTGAA
YJL175W	GGAATTCAGCTGACCAACCATGTACAGATAGCACAGAAATGA
YJL001W	GGAATTCAGCTGACCAACCATGGAATGGAATTCAGTGAAGTCA
YJL208C	GGAATTCAGCTGACCAACCATGTGCAGTAGGATACTCTGTGCG
YJL152W	GGAATTCAGCTGACCAACCATGCCGCAATTAGCCGCGGAAAG
YJL131C	GGAATTCAGCTGACCAACCATGTTAAAAGTTCCTTTGAGTGATGT
YJL151C	GGAATTCAGCTGACCAACCATGTGACAGAGACCATATTAAATGACC
YLR441C	GGAATTCAGCTGACCAACCATGGCTGTGCGAAGGAATAAGAGA
YLR415C	GGAATTCAGCTGACCAACCATGTATCTCAGTCCCGCAGCTTATG
YLR212C	GGAATTCAGCTGACCAACCATGGGTGAGAGAAATATTACTTTGCG
YLR028C	GGAATTCAGCTGACCAACCATGGGTGCGCTACAAAATATTGGAAG
YLL041C	GGAATTCAGCTGACCAACCATGTGAAAGCTGCTATTGAGAAGCA
YLR105C	GGAATTCAGCTGACCAACCATGTCTAAAGGGAGGGTCAATCAG
YJL136W	GGAATTCAGCTGACCAACCATGTGATCAAGAAATATTGTGCGCA
YLR215C	GGAATTCAGCTGACCAACCATGTCTCACAAGAAATATACAACCTT
YLR321C	GGAATTCAGCTGACCAACCATGTGCGACCAAAACAGCTTATT
YMR280C	GGAATTCAGCTGACCAACCATGGGTAAAGAAAACAGCTAAAGGTG
YNL120C	GGAATTCAGCTGACCAACCATGATAAAAGTCGATCTCCGATG
YLR407W	GGAATTCAGCTGACCAACCATGACTGTTCTACTTCCAGAGACC
YMR197C	GGAATTCAGCTGACCAACCATGAGTTCCTTAAATATCATACGA
YMR100W	GGAATTCAGCTGACCAACCATGAGAGACTTAAATCATCGATCAT

YMR210W	GGAAATCCAGCTGACCAACCATGCGTCTAAAGAAATGTACCTAA
YMR318C	GGAAATCCAGCTGACCAACCATGTCTTATCGTGAGAAATTTGAAAG
YMR069W	GGAAATCCAGCTGACCAACCATGCGTCTCTCGGTATATAGTGAGA
YNL076W	GGAAATCCAGCTGACCAACCATGTGCGGGAGGCAITTTGATGT
YNL024C	GGAAATCCAGCTGACCAACCATGAGAGTATATTTGQTGGGTTTG
YNL125C	GGAAATCCAGCTGACCAACCATGTCAACGCACTCAACGAGCTAC
YNL026C	GGAAATCCAGCTGACCAACCATGTGCTAATAAGAGGACGATATAA
YMR115W	GGAAATCCAGCTGACCAACCATGCTTTTACAGGAATGCGTTTATC
YNL244C	GGAAATCCAGCTGACCAACCATGTGCAATTGAGAAATGTGAAATGATT
YNL034C	GGAAATCCAGCTGACCAACCATGACCGTCTGTTATCGCAGTCTT
YNR018W	GGAAATCCAGCTGACCAACCATGAAGATTTTAAACCAAGACGAAAT
YNL277W	GGAAATCCAGCTGACCAACCATGTGCGATACITTTAAATCGAAAAAC
YOL118C	GGAAATCCAGCTGACCAACCATGTCTTTTGAAGAGAAAAAAGTCAAAAC
YNL128W	GGAAATCCAGCTGACCAACCATGAGCTGTGACGAAGAAGATTTC
YOR020C	GGAAATCCAGCTGACCAACCATGTCCACCTTTTGAAGTCTGCT
YOL116W	GGAAATCCAGCTGACCAACCATGCGAAGTAACGACACATAGGA
YOR005W	GGAAATCCAGCTGACCAACCATGATAAAAAAGTATTTGGGACGGAAG
YPL267W	GGAAATCCAGCTGACCAACCATGATATCCCAICAAAAAGAGAAAG
YPL229W	GGAAATCCAGCTGACCAACCATGATGCCCTACAAACACCCCTC
YPL038W	GGAAATCCAGCTGACCAACCATGAACTGCGCGCAAGACATGAAT
YPRC47W	GGAAATCCAGCTGACCAACCATGAGGTAACITTCATTTCTCA
YPL011C	GGAAATCCAGCTGACCAACCATGACTACAAATAATGATTTCTATTTTG
YPR143C	GGAAATCCAGCTGACCAACCATGTCTGGTTATTTTTCAGGGTTTTC
YOL102W	GGAAATCCAGCTGACCAACCATGCTGAAATGAAAGATTCGACAG
YOR018C	GGAAATCCAGCTGACCAACCATGCGCGTTTTCATTTTGATTGCGA
YPL079W	GGAAATCCAGCTGACCAACCATGGGTAAATGATGTCCATATAAC
YOR280W	GGAAATCCAGCTGACCAACCATGTCAATTCAGGCTTTTGTCTTTTG
YOH360C	GGAAATCCAGCTGACCAACCATGTCCACCTTTTCTGATTGGA
YDL090W	GGAAATCCAGCTGACCAACCATGCGAGGTCAATTCACACAGGTC
YDL005C	GGAAATCCAGCTGACCAACCATGTGATACAAATAGCCAGTTT
YPL210C	GGAAATCCAGCTGACCAACCATGAAAGAAAGCAAAAAATGGCTAAA
YMR118C	GGAAATCCAGCTGACCAACCATGAAAGCAACCAITTCAAAGAGTAAC
YPR052C	GGAAATCCAGCTGACCAACCATGGTCAACCCCAAGAGAACCTAA
YLR224W	GGAAATCCAGCTGACCAACCATGAATCAGAGCGATAGAGCGTTG
YLR275W	GGAAATCCAGCTGACCAACCATGTGATGTTGATCTTAACCAATT
YMR154C	GGAAATCCAGCTGACCAACCATGAATGATTGGCATGAATTCATATG
YDR205W	GGAAATCCAGCTGACCAACCATGATAGAGGCAAGCTGCTGTTT
YPR037C	GGAAATCCAGCTGACCAACCATGAAACAGATAGTCAAAAGAGGCG
YNR008W	GGAAATCCAGCTGACCAACCATGGGCACTGTTCGAAAGAAAT
YOR084W	GGAAATCCAGCTGACCAACCATGGAACAGAACAGGTTCAAGAAAG
YGR054W	GGAAATCCAGCTGACCAACCATGTCTCATCTGATTTTTCGTGAAAC
YGL106W	GGAAATCCAGCTGACCAACCATGTGAGCCACCAAGAGCCATAAA
YAL067C	GGAAATCCAGCTGACCAACCATGTATTCATTTGTTAAAGAGATTATTG
YIL023C	GGAAATCCAGCTGACCAACCATGAAGGCGTTCGACCATTTTGCTC
YBR064V	GGAAATCCAGCTGACCAACCATGGATATGGTATCACCAGTCTTGA
b0019	TTGCTCTTCATGAAACATCTGCGATCGAATCTTTAG

b2148	TTGCTCTTCCATGAGTGGGTAAATAAGAAAAAG
b2796	TTGCTCTTCCATGGAAACGACTCAAACCGAGCAC
b2882	TTGCTCTTCCATGTTTCATTTGCTCTTATGCCAGC
b0124	TTGCTCTTCCATGGCAATTAAACAATACAGGCTCG
b5116	TTGCTCTTCCATGAGTACTTCAGATAGCATTGTATC
b1830	TTGCTCTTCCATGAACATGTTTTTATAGGCTTACC
b1453	TTGCTCTTCCATGTTTCATGGCAACTTATATGACTTTT
b2864	TTGCTCTTCCATGATCAGGAGTCACACCATGA
b2799	TTGCTCTTCCATGATGGCTAACAGAAATGATTCTGA
b3327	TTGCTCTTCCATGAATTATCGCTATCGCGCCA
b0970	TTGCTCTTCCATGCATCGTATTGTTACTTCTCAG
YER003C	GGAATTCAGCTGACCACCATGTCCAAAGCTGTTAGGTTA
YCL027W	GGAATTCAGCTGACCACCATGGTAGCAACAATATGCAGACGA
YBR112C	GGAATTCAGCTGACCACCATGAATCGGGCGGTGAACAAAC
YNL079C	GGAATTCAGCTGACCACCATGCACAAAATCACAAAACCTAAG
YFR042W	GGAATTCAGCTGACCACCATGGCAGGTATCAAGTTGACGCAT
YCR137C	GGAATTCAGCTGACCACCATGTGTGAATCATCAATAAGACTGA
YK1103C	GGAATTCAGCTGACCACCATGGAGGAACAACCTGAAATATCG
YNL090W	GGAATTCAGCTGACCACCATGCTGAAAAGGCCGTTTGAAGAGG
YGR181C	GGAATTCAGCTGACCACCATGATCGCTACCTCCAGAGCCG
YDH071C	GGAATTCAGCTGACCACCATGGCTCCTCAAGTATGACCGC

Gene	Reverse Seq
YGL283W	GATCCCCGGGAATTGCCATGTTACACATCATTGCAAGCTGATTGT
YGR004W	GATCCCCGGGAATTGCCATGTTATAGAGAAGGAGACATTGAACAT
YCR014W	GATCCCCGGGAATTGCCATGTCAAACCTTCGTTCCAAACCGAGG
YGL289C	GATCCCCGGGAATTGCCATGCTCAATTGCAGGGAATTATGGAATAAA
YBL060W	GATCCCCGGGAATTGCCATGTTAGAAGTGAACAGAACCCATGGC
YGL166W	GATCCCCGGGAATTGCCATGTTATTGTGAATGTGAGTTATGCGAAG
YDL202W	GATCCCCGGGAATTGCCATGTTACTTTGATCCCTTCGATCTGCA
YAL046C	GATCCCCGGGAATTGCCATGTGATGATGCGGAGCCCTTC
YDR101C	GATCCCCGGGAATTGCCATGTGATGATGATGCGGAGCCCTTC
YDH088W	GATCCCCGGGAATTGCCATGTGATGATGATGCGGAGCCCTTC
YAL084W	GATCCCCGGGAATTGCCATGTGATGATGATGCGGAGCCCTTC
YDR134C	GATCCCCGGGAATTGCCATGTTACACAAATAAGCGGCGAGCAC
YFL031W	GATCCCCGGGAATTGCCATGTGCAACAGCAGGCCCAACCGGT
YFL052W	GATCCCCGGGAATTGCCATGTTAAGGAAGCGCATCTACATCTTCT
YFL042C	GATCCCCGGGAATTGCCATGTGCAACCATACCTTTGATGCAACTG
YBR025C	GATCCCCGGGAATTGCCATGTGCAATTTCTTACGAGCAGGCTCT
YER174C	GATCCCCGGGAATTGCCATGTTACTGTAGAGCATGTTGGAATATT
YBR051W	GATCCCCGGGAATTGCCATGTTATATATGGCATGCTTCGCATGT
YER175C	GATCCCCGGGAATTGCCATGTGACACCCCTTTTGCCAAAGTTGTAA

YDR521W	GATCCCCGGGAATTGCCATGTTACTCACCATTAAACATCTTTCCG
YER167W	GATCCCCGGGAATTGCCATGTTAGTTGCTATTATCAAAATAAAAGAG
YER123W	GATCCCCGGGAATTGCCATGTCAAAAAAAAAAGGAAAAAGAGAAAAG
YDR415C	GATCCCCGGGAATTGCCATGTCAACATTTTTCIAAATTCACCTTAGCAC
YEL052W	GATCCCCGGGAATTGCCATGTTAGTATGTAGGCTTAGTACCCTAA
YDR336W	GATCCCCGGGAATTGCCATGTCAACCTCAAAATTTGCTTTATCTG
YDR513W	GATCCCCGGGAATTGCCATGCTATTCAAATACCGGCTTCAATATTT
YEL045C	GATCCCCGGGAATTGCCATGTCTAGGAAAGGAGGTGGTTCAGAA
YEL041W	GATCCCCGGGAATTGCCATGTTAGATTCGAAATGAGCCTGACGA
YDL238C	GATCCCCGGGAATTGCCATGCTAAATCTGCTAGACTTGTCTGGC
YBR282W	GATCCCCGGGAATTGCCATGTTATCCACGCTCCTTATAAGATAAG
YBR258C	GATCCCCGGGAATTGCCATGTTACGTACTTCCATTGCTCTCTGT
YCL001W-A	GATCCCCGGGAATTGCCATGTCAAGTTCATCAAAATTTGAAATTTCTAACCA
YBR274W	GATCCCCGGGAATTGCCATGTCTGGAATTAGGATAATATCC
YHR090C	GATCCCCGGGAATTGCCATGTCAAGTTCAGTTTCTTTTCTTTGAGTTGT
YGR121C	GATCCCCGGGAATTGCCATGTTACCTATTGGCAGGATCTTCTTGA
YGR127W	GATCCCCGGGAATTGCCATGTTACAATTTGAATTTAAACCTTTTTC
YGR150C	GATCCCCGGGAATTGCCATGCTACATGTAAAGTTCTGTGTCCTCC
YKL037W	GATCCCCGGGAATTGCCATGTTATATACTCAATCCAAACAGGGAA
YKL051W	GATCCCCGGGAATTGCCATGTCAAGCACTACTTGAATAGATTCTG
YKL120W	GATCCCCGGGAATTGCCATGTCTTAATTTAGCCCTAAACCTCTCGAC
YKL011C	GATCCCCGGGAATTGCCATGTAGTATTTGTTGTAAGTGTCTGTC
YKL017C	GATCCCCGGGAATTGCCATGTTACAATAATCTGTAATGTTGGGG
YKL048C	GATCCCCGGGAATTGCCATGTCAATAAATCTGCTCCCTGATTCTT
YKL132C	GATCCCCGGGAATTGCCATGCTATACTGGCAAGTACAGTGTGTG
YGR126W	GATCCCCGGGAATTGCCATGTTAATCGAAATTCATGAAAAACCC
YKL070W	GATCCCCGGGAATTGCCATGTCAAGAACGCTCCACTTTACTTCG
YKL058W	GATCCCCGGGAATTGCCATGTTACTCGCTCTTTTGAATTCATC
YHR130C	GATCCCCGGGAATTGCCATGCTAATTCCTGATCCCAAGTAACGA
YIL070C	GATCCCCGGGAATTGCCATGTTAGTGAAAAAATCTCTTCATCTTTTC
YHR105W	GATCCCCGGGAATTGCCATGTTAGTATCTAAATGGTTGAGAGTATG
YHR022W	GATCCCCGGGAATTGCCATGCTACTCGCCCTCAGCAGAG
YJL089W	GATCCCCGGGAATTGCCATGTAGAAAGGTCGAGTTCAAAATATTCT
YJL172W	GATCCCCGGGAATTGCCATGTTAAGCGTATTCGTTAATTAACGA
YHR113W	GATCCCCGGGAATTGCCATGTAGACAACAATTCACATTCATAG
YHR175W	CATCCCCGGGAATTGCCATGTTAATGCGAGCGAGGAGACTG
YGR212W	GATCCCCGGGAATTGCCATGCTAGTATAAATTAAGTAACTCTTCATAT
YJL024C	GATCCCCGGGAATTGCCATGTTATGCCCCGTTGCCATTTGTC
YGR180C	GATCCCCGGGAATTGCCATGTTAGAAGTCATCATCAAGTAAATTC
YJL179W	GATCCCCGGGAATTGCCATGTTAATCTTCATCAATGCTTTAGATT
YJL061W	GATCCCCGGGAATTGCCATGTTATAGTTGTTTCATATTCATCAGGT
YJL208C	GATCCCCGGGAATTGCCATGTCAATTCCTTTTTCGAGGAGGT
YJL152W	GATCCCCGGGAATTGCCATGTCAAGCAGACATGCGACTGCG
YJL173C	GATCCCCGGGAATTGCCATGTTACATTTCAATTCATTTTTCCTGTA
YJL151C	GATCCCCGGGAATTGCCATGCTAAGTACGCGCGGAGAGAGC
YLR441C	GATCCCCGGGAATTGCCATGTTACAGACTTTCAAGACTTCGTCT

YLR415C	GATCCCCGGGAATTGCCATGCTACTTCCAAACAAGTGGTCCAGA
YLR212C	GATCCCCGGGAATTGCCATGTTATACTAATTTATGATCACCGTCGG
YLR209C	GATCCCCGGGAATTGCCATGTTATTTCTGTATCTCCACAAGGAC
YLL041C	GATCCCCGGGAATTGCCATGCTAGGCAAAATGCCAAAGATTTCCTA
YLR105C	GATCCCCGGGAATTGCCATGCTAGTCTCTATTTCTTCCGGGAAC
YIL136W	GATCCCCGGGAATTGCCATGCTAGTCCCTTTTCGAGCTCCACAA
YLR215C	GATCCCCGGGAATTGCCATGCTAAGTTTCATTCTCAGTATCACTG
YLR321C	GATCCCCGGGAATTGCCATGCTACATTCTCATTTGTGGTTTCTAAG
YMR260C	GATCCCCGGGAATTGCCATGTTAATCATAAATAGTTTCATAGTGTGT
YNL129C	GATCCCCGGGAATTGCCATGCTCACTTCCTATGCAAAATGCTTAATA
YLR407W	GATCCCCGGGAATTGCCATGCTCAGTCATGGCATGCCCTTGGA
YMR197C	GATCCCCGGGAATTGCCATGCTAAAATGAAGACAGCCACAATCTG
YMR100W	GATCCCCGGGAATTGCCATGCTATTGATTGTTGTTCCACGGACT
YMR210W	GATCCCCGGGAATTGCCATGTTATGAAGTCCATGGTAAATCTGT
YMR318C	GATCCCCGGGAATTGCCATGTTACATGAGGTCATGTTCACTGTTAG
YMR069W	GATCCCCGGGAATTGCCATGTTATTTTACTTAATTTTCATCCATTAG
YNL076W	GATCCCCGGGAATTGCCATGTTATGTATCAACAATTAAATTCAGT
YNL024C	GATCCCCGGGAATTGCCATGTTAATCTCTTCAAAACAGACAGCAA
YNL125C	GATCCCCGGGAATTGCCATGCTATTTTCACTTTGGGTGTTGCC
YNL029C	GATCCCCGGGAATTGCCATGTTAAGTCTCTTGTCCCAATTTCTC
YMR115W	GATCCCCGGGAATTGCCATGTTAGTTTCTCAAGTGACTATTGTAA
YNL244C	GATCCCCGGGAATTGCCATGTTACGAATCAGTCCBATGGAGCT
YNL534C	GATCCCCGGGAATTGCCATGTTAAGCTGGAAGAGCGAATGTCTT
YHR018W	GATCCCCGGGAATTGCCATGTTATTTCAAAGTCTTGAACAATTTTCT
YNL277W	GATCCCCGGGAATTGCCATGTTAGTCTTCATGCTTATACAGAAAC
YOL118C	GATCCCCGGGAATTGCCATGCTCACTTCAAAGTCTCTGGAATATGA
YOL123W	GATCCCCGGGAATTGCCATGTTAATGCTCTCTTCCAAAGTTTGAAG
YOR020C	GATCCCCGGGAATTGCCATGCTATGAGCGATCCCGTITTTGTAA
YOL116W	GATCCCCGGGAATTGCCATGTTAATTAATTGAATTTAATTTTCTGTT
YOR305W	GATCCCCGGGAATTGCCATGCTCACCGACTCATTTTGTAAAGCTTG
YPL287W	GATCCCCGGGAATTGCCATGTTACTCATCTTCATACACGTGGAAG
YPL229W	GATCCCCGGGAATTGCCATGCTAACAATTTCTATTATCTATATATC
YPL038W	GATCCCCGGGAATTGCCATGCTAACTGCTTTTTCGTGTTGAGTA
YPR047W	GATCCCCGGGAATTGCCATGCTATTTTGCCCTTATATCAATTTT
YPL011C	GATCCCCGGGAATTGCCATGTTAGCGTITTTTGTGCTTTCTTC
YPR146C	GATCCCCGGGAATTGCCATGCTAAATTTCCAAACGATTAGAACTTT
YOL103W	GATCCCCGGGAATTGCCATGCTAAGACTTGAAATTAATTAATTCGGG
YOR018C	GATCCCCGGGAATTGCCATGCTCACTGTATCTCGCTGTCAACAAT
YPL079W	GATCCCCGGGAATTGCCATGCTATTGTAATTCCTTATCATGTTTCA
YOR260W	GATCCCCGGGAATTGCCATGTTAATTAAGCTCGAAATGGCTATTGA
YOR390C	GATCCCCGGGAATTGCCATGCTACTGTGGAAGAGGCTCTTCTAGG
YDL060W	GATCCCCGGGAATTGCCATGTTACATACCATTCCAAGGTAAACGAA
YDL005C	GATCCCCGGGAATTGCCATGCTATATATTGAAGCCGCTGAGGCTC
YPL210C	GATCCCCGGGAATTGCCATGCTACTTACGTACTGAAATAGTCTCTT
YMR118C	GATCCCCGGGAATTGCCATGTTACTGAGCCAGTAAATACGTTCTCT
YPR052C	GATCCCCGGGAATTGCCATGCTAAGCCAAAGTGCGTTATATAAC

YLR224W	GATCCCCGGGAATTGCCATGTCACTTCGAAGATAAGGGGTATTG
YLR275W	GATCCCCGGGAATTGCCATGTACTCAACAGGGGTTTTAAACACA
YMR164C	GATCCCCGGGAATTGCCATGTATTITGGTATCACATCATCGGAG
YDH205W	GATCCCCGGGAATTGCCATGTCAATTGTATAGGCTGTAGCGG
YPR037C	GATCCCCGGGAATTGCCATGTAGAACTGAATTAITTCACATTGTCT
YNR008W	GATCCCCGGGAATTGCCATGTACATTGGGAAGCGCATCTGAGA
YOR084W	GATCCCCGGGAATTGCCATGTACAGTTTTGTAGTCGTTTTAAC
YGR054W	GATCCCCGGGAATTGCCATGTATTATTCATCCTTCCAAACCACATT
YGL108W	GATCCCCGGGAATTGCCATGTCAATTGTCTCAAACATCTTGGATG
YAL067C	GATCCCCGGGAATTGCCATGTATTTTTCATCAGATACTGATAGGT
YIL023C	GATCCCCGGGAATTGCCATGTCAATGCTCATCCATCAGCGCCA
YBR064W	GATCCCCGGGAATTGCCATGTCTAAAATATGGAGGAAGTGGTTAA
b0019	TTGCTCTTCGTTAACTGATGGACGCAACGAAACG
b2148	TTGCTCTTCGTTATTCTTACCGCGGTATTTCAGTG
b2796	TTGCTCTTCGTTAGCTGAACAGAGATAGAAGATT
L2082	TTGCTCTTCGTTACATCCACATAATTGCTGCC
b0124	TTGCTCTTCGTTACTTCACATCATCGCGCAGCG
b3116	TTGCTCTTCGTTAAACAGTTTGTATACCATGTTACG
b1890	TTGCTCTTCGTTACTTGACGGGAGCGGGTTGT
b1453	TTGCTCTTCGTTAACTCGCCGTTTCAGGCTTAAA
b2564	TTGCTCTTCGTTAATTGCCAGGCGATCGGCTG
b2799	TTGCTCTTCGTTACGAGCGGATGCGTAAAGCT
b3927	TTGCTCTTCGTTAATTAACTGATTAAGTTGAAGA
b0970	TTGCTCTTCGTTAATCGCGGCGTAGCGAAGCCC
YER068C	GATCCCCGGGAATTGCCATGTCTAATTGGTTCACAAAGGCTCTA
YGL027W	GATCCCCGGGAATTGCCATGTCACTCGTATTTCTGGAGACAGTC
YBR112C	GATCCCCGGGAATTGCCATGTATGTCGTCGTAGTTTTCATCTCT
YNL079C	GATCCCCGGGAATTGCCATGTCTCAAGTTTTCCAGAGATGCAGC
YFR042W	GATCCCCGGGAATTGCCATGTCAATTTGTTAATAGTTTTTGTATGCT
YER187C	GATCCCCGGGAATTGCCATGTATTTCTTGGGTATAACTGTCACTC
YKL103C	GATCCCCGGGAATTGCCATGTCTCAAACTCGCGGAATTCATCGTA
YNL050W	GATCCCCGGGAATTGCCATGTATATAAAATATGCAACAGTTAGCCC
YGR161C	GATCCCCGGGAATTGCCATGTCTATTTCAATGAACAGTTTGAATTC
YDR071C	GATCCCCGGGAATTGCCATGTCTAGTTGTGCTATTTCTTCTTAATTA

0318.0.1 Vector preparation

0319.0.1 The preferred binary vector 1bxbigResgen for yeast and 1bxbSuperCoLic for E.coli, which is based on the modified pPZP binary vector backbone (comprising the kanamycin-gene for bacterial selection; Hajukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 989-994) carried the selection marker bar-gene (De Block et al., 1987, EMBO J. 6, 2513-2518) driven by the mas1' promoter (Velten et al., 1984, EMBO J. 3, 2723-2730; Mengiste, Amedeo and Paszkowski, 1997, Plant J., 12, 945-948) on its T-DNA. In addition the T-DNA contained the strong double 35S(Kay et al., 1987, Science 236,

- 1299-1302) for yeast or Super promoter (Nf et al., 1995, Plant Journal 7, 861-876) for E.coli in front of a cloning cassette followed by the nos-terminator (Dapicker A, Stachel S, Dhaese P, Zambryski P, Goodman HM. Nopaline synthase: transcript mapping and DNA sequence. Journal of Molecular & Applied Genetics. 1(6):561-73, 1982.). The cloning cassette consists of the following sequence:
- 0320.0.1** Yeast: 5'-GGAATTCAGCTGACCACCATGGCAATCCCGGGGATC-3' or
- 0321.0.1** E.coli: 5'-TTG CTC TTC CAT GGC AAT GAT TAA TTA ACG AAG AGC AA-3', respectively.
- 0322.0.1** Other selection marker systems, like the AHAS marker or other promoters, e.g. superpromotor (see above), 35S promotor (see above), Ubiquitin promotor (Callis et al., J. Biol. Chem., 1990, 265: 12488-12493; US 5,510,474; US 6,020,190; Kuwalleck et al., Plant. Molecular Biology, 1993, 21: 673-684) or 34S promotor (GenBank Accession numbers M59930 and X16673) were similar useful for the instant invention and are known to a person skilled in the art. The vector was linearised with EcoRI and SmaI for yeast or SmaI and SacI for E.coli using the standard protocol provided by the supplier (MBI Fermentas, Germany) and purified using Qiagen columns (Qiagen, Hilden, Germany).
- 0323.0.1** **Ligation and transformation**
- 0324.0.1** Present ORF fragments (~ 100 ng) were digested by EcoRI and SmaI for yeast and SmaI and SacI for E.coli using the standard protocol provided by the supplier (MBI Fermentas, Germany), purified using Qiagen columns (Qiagen, Hilden, Germany) and were ligated into the cloning cassette of the binary vector systems (~ 30 ng) using standard procedures (Maniatis et al.).
- 0325.0.1** In the case of internal EcoRI, SmaI and SacI restriction sites a blunt end cloning procedure was applied. The undigested ORF fragments were directly purified and ligated into the cloning cassette of the binary vector. In this case the EcoRI site was refilled by Klenow reaction and the SacI site blunted Pfu DNA polymerase.
- 0326.0.1** Ligation products were transformed into E.coli (DH5alpha) using a standard heat shock protocol (Maniatis et al.). Transformed colonies were grown on LB media and selected by respective antibiotics (Km) for 16h at 37 °C. Positive clones were identified by control PCR reactions using a combination of a vector specific and the respective ORF specific primers.
- 0327.0.1** **Plasmid preparation**
- 0328.0.1** Plasmid DNA was prepared from positive clones using standard protocols (Qiagen Hilden, Germany).

0329.0.1 Transformation of *Agrobacterium*

0330.0.1 Plasmids were transformed into *Agrobacterium tumefaciens* (GV3101pMP90; Koncz and Schell, 1986, Mol. Gen. Genet. 204: 383-396) using heat shock or electroporation protocols. Transformed colonies were grown on YEP media and selected by respective antibiotics (Rif/Gent/Km) for 2d at 28 °C. These *Agrobacterium* cultures were used for the plant transformation.

0331.0.1 *Arabidopsis thaliana* was grown and transformed according to standard conditions Bechtold 1993 (Bechtold, N., Ellis, J., Pelletier, G. 1993, In planta *Agrobacterium* mediated gene transfer by infiltration of *Arabidopsis thaliana* plants C.R. Acad.Sci.Paris. 316:1194-1199); Bent et al. 1994 (Bent, A., Kunkel, B.N., Dahlbeck, D., Brown, K.L., Schmidt, R., Giraudat, J., Leung, J., and Staskawicz, B.J. 1994; PPCS2 of *Arabidopsis thaliana*: A leucine-rich repeat class of plant disease resistant genes; Science 265: 1856-1860).

0332.0.1 Transgenic *A. thaliana* plants were grown individually in pots containing a 4:1 (v/v) mixture of soil and quartz sand in a York growth chamber. Standard growth conditions were: photoperiod of 16 h light and 8 h dark, 20 °C, 60% relative humidity, and a photon flux density of 150 μ E. To induce germination, sown seeds were kept at 4 °C, in the dark, for 3 days. Plants were watered daily until they were approximately 3 weeks old at which time drought was imposed by withholding water. Parallely, the relative humidity was reduced in 10% increments every second day to 20%. After approximately 12 days of withholding water, most plants showed visual symptoms of injury, such as wilting and leaf browning, whereas tolerant plants were identified as being visually turgid and healthy green in color. Plants were scored for symptoms of drought injury in comparison to neighbouring plants for 3 days in succession.

0333.0.1 Three successive experiments were conducted. In the first experiment, 10 independent T2 lines were sown for each gene being tested. The percentage of plants not showing visual symptoms of injury was determined. In the second experiment, the lines that had been scored as tolerant in the first experiment were put through a confirmation screen according to the same experimental procedures. In this experiment, plants of each tolerant line were grown and treated as before. In the third experiment, at least 7 replicates of the most tolerant line were grown and treated as before. The average and maximum number of days of drought survival after wild-type control had visually died were determined. Additionally measurements of chlorophyll fluorescence were made in stressed and non-stressed plants using a Mini-PAM (Heinz Walz GmbH, Effeltrich, Germany).

0334.0.1 In the first experiment, after 12 days of drought, the control, non-transgenic *Arabidopsis thaliana* and most transgenic lines expressing other transgenes

in the test showed extreme visual symptoms of stress including necrosis and cell death. Several plants expressing the genes retained viability as shown by their turgid appearance and maintenance of green color.

- 0335.0.1** The second experiment compared a smaller number of independent transgenic lines for each gene but a greater number of progeny within each independent transformation event. This experiment confirmed the previous results. Those lines containing the specific SRP encoding yeast genes survived longer than the controls. In some cases the transgenic line survived more than 3 days after the controls had died.
- 0336.0.1** According to the results of the first and second experiments some major lines containing the specific SRP encoding yeast genes were identified, which showed the best results with regard to the average days of survival after wild type and/or the hit percentage.
- 0337.0.1** In a third experiment these major lines were tested with multiple replicates (4-80 plants per line). The average number of days the plants of the major line survived longer than wild-type was measured. I.e., the number '1' means that, on average, the plants overexpressing this ORF, on average survived 1 day longer than wild-type. The value for WT in this column is '0'. The results are summarised in table 3.
- 0338.0.1** Table 3: Drought tolerance of transgenic *Arabidopsis thaliana* expressing the various SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using several plants from one transgenic line (experiment 3). Drought tolerance is measured for the indicated number of transgenic plants (Plants tested) as the average number of days (Average days of survival after WT) that the transgenic plants survived after the control (untransformed wild type). The hit percentage indicates the fraction of the tested plants of the major line that was actually resistant, i.e. the number '50' indicates that half of the tested plants were resistant (survived longer than WT). For WT, this column has the value '0'.

Sequ. ID No.	Gene	Plants tested	Average days of survival after WT
1	YGL263W	12	1,17
3	YGR004W	11	1,36
5	YGR014W	11	0,82
7	YGL239C	13	2,4
9	YBL060W	14	1,6
11	YGL166W	14	1,07
13	YDL202W	15	0,47

15	YAL046C	14	1,9
17	YDR101C	14	3,57
19	YDR108W	14	0,5
21	YAL064W	33	2,29
23	YDR134C	13	0,8
25	YFL031W	13	1,3
27	YFL052W	14	1,1
29	YFL042C	11	1,3
31	YBR025C	11	1,4
33	YER174C	22	1,05
35	YBR051W	10	1,2
37	YER175C	11	1,7
39	YDR521W	14	0,5
41	YER167W	35	0,66
43	YER123W	11	2,2
45	YDR415C	7	2,71
47	YEL052W	4	1,5
49	YDR536W	14	1,5
51	YDR313W	7	3,14
53	YEL045C	14	1,64
55	YEL041W	13	1,77
57	YDL238C	35	1,2
59	YBR282W	14	1,79
61	YBR259C	9	3,4
63	YCL001W-A	36	1,78
65	YER274W	14	2
67	YHR090C	8	4,5
69	YGR121C	40	1,6
71	YGR127W	8	1,4
73	YGR150C	12	2,6
75	YKL037W	14	0,79
77	YKL051W	16	2,4
79	YKL120W	14	0,64
81	YKL011C	12	1,9
83	YKL017C	10	1,8
85	YKL049C	80	1,92
87	YKL132C	33	1,82
89	YGR126W	8	2,3
91	YKL070W	14	2,1
93	YKL058W	9	1,44
95	YHF130C	9	1,8
97	YIL070C	13	0,66

99	YHR195W	14	1,9
101	YIR022W	14	1,07
103	YJR089W	14	0,88
105	YJL172W	11	0,82
107	YHR113W	15	2
109	YHR175W	9	0,78
111	YGR212W	13	1,48
113	YJL024C	13	0,60
115	YGR180c	14	2,9
117	YJL179W	18	1,3
119	YJL001W	14	1,6
121	YJL208C	12	1,4
123	YJL152W	13	1,3
125	YJL131C	14	0,8
127	YJL151C	14	1,9
129	YLR441C	10	2
131	YLR415C	14	1,6
133	YLR212C	13	0,64
135	YLR029C	14	1,58
137	YLL041C	13	0,92
139	YLR106C	14	0,86
141	YIL196W	6	2,25
143	YLR215C	13	1,77
145	YLR321C	14	1,29
147	YMR260C	11	2,08
149	YNL120C	7	2
151	YLR407W	12	1,17
153	YMR197C	14	0,87
155	YMR100W	12	1,25
157	YMR210W	10	1,1
159	YMR318C	13	0,85
161	YMR069W	8	1,25
163	YNL076W	13	1,31
165	YNL024C	13	1,08
167	YNL125C	4	1,75
169	YNL029C	13	1,92
171	YMR115W	12	0,75
173	YNL244C	11	1,55
175	YNL334C	14	1,6
177	YNR018W	14	1,29
179	YNL277W	14	1,14
181	YOL118C	14	1,71

183	YOL123W	14	0,71
185	YOR020C	12	1,83
187	YOL116W	13	1,08
189	YOR305w	15	1,2
191	YPL267W	6	2,5
193	YPL229w	5	2
195	YPL038W	10	1,3
197	YPR047W	11	1
199	YPL011C	12	0,75
201	YPR148C	10	1,1
203	YOL103W	12	0,75
205	YOR016C	14	0,79
207	YPL079W	15	1,33
209	YOR260W	7	1,29
211	YOR360C	15	1,53
213	YDL060W	15	0,67
215	YDL005C	15	1
217	YPL210C	15	1,13
219	YMR118C	14	1,14
221	YPR052C	14	1,07
223	YLR224W	10	2,1
225	YLR275W	9	2,44
227	YMR154C	15	1,27
229	YDR205w	12	1,08
231	YPR037C	12	2,17
233	YNR006W	14	2,29
235	YOR084W	10	2,2
237	YGR054W	14	1,5
239	YGL106W	13	3,46
241	YAL057C	13	1,62
243	YIL023c	15	1,73
245	YBR064W	15	1,13
247	b0020	13	0,78
249	b2143	15	3,13
251	b2796	15	2,33
253	b2082	14	2,43
255	b0124	15	2,87
257	b3118	15	1,07
259	b1830	15	2,07
261	b1453	14	2,29
263	b2664	13	1,85
265	b2799	15	1,87

267	b3327	15	1,47
269	b0970	15	1,33
271	YER003C	5	1
273	YGL027W	9	0,58
275	YBR112C	10	0,5
277	YNL079C	9	0,67
279	YFR042W	9	0,78
281	YER137C	3	0
283	YKL105C	9	1
285	YNL090W	6	0,83
287	YGR161C	7	0,86
289	YDR071C	9	0,78

0339.0.1 In a further experiment, for individual major lines, other lines containing the same gene construct, but resulting from a different transformation event were tested. In these lines, the specific SRP encoding yeast genes is incorporated at a different site in the plant genom. The results are summarised in table 4 in accordance to table 3. The results demonstrate the dependence of the stress tolerance and/or resistance in plants on the expression of the SRP, rather than the insertion event.

0340.0.1 Table 4: Drought tolerance of transgenic *Arabidopsis thaliana* expressing selected SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using one plant from several independent transgenic lines each (experiment 3). Drought tolerance is measured for the indicated number of transgenic plants (Plants tested) as the average number of days (Average days of survival after WT) that the transgenic plants survived after the control (untransformed wild type). The hit percentage indicates the fraction of the tested plants of the major line that was actually resistant, i.e. the number '50' indicates that half of the tested plants were resistant (survived longer than WT). For WT, this column has the value '0'.

Sequ. ID No.	Gene	Number other lines tested	Average days of survival after WT
1	YGL263W	7	1,43
3	YGR004W	8	1
5	YGN014W	9	0,75
7	YGL239C	5	1
9	YBL060W	8	2
11	YGL166W	8	0,63
13	YDL202W	8	0,25

15	YAL046C	7	1,3
17	YDR101C	9	1,1
19	YDR108W	9	0,22
21	YAL064W	8	3
28	YDR134C	6	2,2
25	YFL031W	9	2,3
27	YFL052W	5	1,4
31	YBR025C	5	1,2
33	YER174C	9	0,5
35	YBR051W	6	1,3
37	YER175C	4	1,4
39	YDR521W	3	0,7
43	YER123W	6	0,3
45	YDR415C	7	1,4
47	YEL052W	3	1,33
49	YDR536W	8	1,25
51	YDR513W	4	1,5
53	YEL045C	5	1,2
55	YEL041W	8	0,88
57	YDL288C	8	0,17
59	YBR282W	8	2,2
61	YBR258C	7	1,7
83	YGL001W-A	7	0,57
65	YBR273W	9	0,78
67	YHR090C	6	2,7
69	YGR121C	9	0,8
71	YGR127W	6	2,5
73	YGR130C	5	3
75	YKL037W	8	0,78
77	YKL051W	5	1,8
79	YKL120W	8	0,83
81	YKL011C	5	1,4
83	YKL017C	5	0,6
85	YKL019C	8	1,4
87	YKL132C	7	0,7
89	YGR126W	6	1,3
91	YKL070W	6	2
93	YKL058W	8	0,88
95	YHR130C	9	2,1
97	YIL070C	7	0,71
99	YHR195W	9	2,1
101	YHR022W	9	1,22
103	YJL069W	7	0,8
105	YJL172W	4	1
107	YHR113W	7	1,6
109	YHR175W	3	1

111	YGR212W	8	0,88
113	YJL024C	6	1,33
115	YGR180C	8	2,7
117	YJL179W	8	1,8
119	YJL001W	9	0,7
121	YJL208C	6	1,7
123	YJL152W	8	0,3
125	YJL131C	6	1
127	YJL151C	8	1,6
129	YLR441C	7	2,6
131	YLR115C	9	0,3
133	YLR212C	7	2,14
135	YLR029C	8	0,25
137	YLL041C	7	0,86
139	YLR105C	7	0,20
141	YIL136W	9	1,75
143	YLR215C	8	1,25
145	YLR321C	7	0,86
147	YMR260C	8	0,80
149	YNL120C	9	1,56
151	YLR407W	5	0,4
153	YMR187C	9	1,22
155	YMR100W	8	0,88
157	YMR210W	8	0,88
159	YMR818C	8	0,68
161	YMR069W	9	0,44
163	YNL078W	4	1,75
165	YNL024C	8	1,70
167	YNL125C	7	2,14
169	YNL029C	9	1,89
171	YMR116W	8	1,44
173	YNL244C	8	0,25
175	YNL331C	8	1,38
177	YNR018W	9	1,22
179	YNL277W	8	1
181	YOL118C	9	0,89
183	YOL128W	8	0,86
185	YOR020C	9	0,44
187	YOL116W	9	1,67
189	YOR305W	7	0,28
191	YPL267W	4	0,75
193	YPL229W	5	1,6
195	YPL038W	5	0,4
197	YPR047W	2	1
199	YPL011C	6	0,5
201	YPH148C	9	0,33

203	YOL103W	9	0,33
205	YOF1016C	9	0,56
211	YOR360C	8	0,39
213	YDL060W	8	0,5
215	YDL005C	9	0,44
217	YPL210C	8	1,5
219	YMR119C	10	1,1
221	YPR052C	7	0,96
223	YLR224W	9	1,22
225	YLR275W	8	1,75
227	YMR151C	9	1,11
229	YDR205w	4	1
231	YPH037C	5	3,4
233	YMR008W	8	0,75
235	YOR084W	6	0,5
239	YGL103W	7	2,14
241	YAL067C	6	1,83
243	YIL023c	1	3
245	YBR084W	7	0,71
247	b0020	4	1,5
249	b2145	10	0,1
251	b9796	11	0,72
253	b2082	9	1,22
255	b0124	9	3,3
257	b9116	8	1
259	b1830	7	1,71
261	b1453	6	1,13
263	b2664	9	1
267	b3327	10	0,8
269	b0970	8	1,5
271	YER003C	12	2,08
273	YCL027W	14	2,14
275	YBR112C	11	3,3
277	YNL079C	13	2,69
279	YFR042W	7	2,3
281	YER137C	13	2,2
283	YKL103C	10	2,8
285	YNL090W	12	4,33
287	YGR161C	12	2,7
289	YDR071C	11	3

0341.0.1 Chlorophyll fluorescence measurements of photosynthetic yield confirmed that severe drought stress completely inhibited photosynthesis in the control

plants, but the transgenic major lines maintained photosynthetic function longer (Table 5).

- 0342.0.1** Table 5: Drought tolerance of transgenic *Arabidopsis thaliana* expressing the various SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using several plants from one transgenic line (experiment 3). Drought tolerance is reported as photosynthetic yield measured by chlorophyll fluorescence measured at three different time point during the drought stress experiment, and compared to the untransformed wild type control. For each transgenic line, the average of 5 replicate plants is indicated, the wild type value is the average of 20-25 plants measured in the same experiment.

Sequ. ID No.	Gene	Photosynthetic yield 5 days after final watering	wild type	Photosynthetic yield 10 days after final watering	wild type	Photosynthetic yield 14 days after final watering	wild type
1	YGL263W	751	766	765	654	254	106
3	YGR004W	759	766	755	654	216	106
5	YGR014W	759	766	752	654		
7	YGL239C	762	757	786	610		
9	YBL080W	743	757	782	610	108	16
11	YGL166W	752	736	747	709		
13	YDL202W	740	766	508	548		
15	YAL046C	768	730	758	549	216	20
19	YDH108W	756	736	739	709	0	20
23	YDR134C	757	760	765	549	273	20
25	YFL031w	763	766	766	549	784	20
27	YFL062W	757	757	753	610		
29	YFL042C	743	757	780	610		
31	YBR025C	763	760	762	549	631	20
35	YBR051W	741	760	695	549	466	20
37	YER175C	749	757	627	610	140	16
43	YER123W	767	757	780	610	147	16
47	YEL052W	750	736	773	710	177	20
49	YDR536W	758	736	772	709	293	20
51	YDR513W	782	794	860	413	411	54
53	YEL045C	755	736	553	709	147	20
55	YEL041W	758	736	769	709	129	20

59	YBR282W	759	760	724	549	221	20
61	YBR258C	759	757	772	610	144	16
65	YBR274W	749	736	789	709	148	20
67	YHR090C	749	760	765	549	620	20
71	YGR127W	740	549	576	20		
73	YGR150C	771	760	742	549	618	20
75	YKL037W	761	736	760	709	134	20
77	YKL051W	733	760	740	549	153	20
79	YKL120W	759	736	518	709		
81	YKL011C	760	760	694	549	434	20
83	YKL017C	744	549	734	549	751	20
89	YGR128W	784	780	750	549	159	20
91	YKL070W	774	760	734	549	244	20
93	YKL058W	752	766	765	654	495	20
95	YHR130C	772	760	756	519	147	20
97	YIL070C	768	766	755	654		
99	YHR195W	783	757	693	610	141	16
101	YIR022W	761	736	771	709		
105	YJL172W	766	766	758	654	298	20
107	YHR113W	749	760	754	549	142	20
109	YHR175W	768	766	759	654	485	106
111	YGR212W	777	736	748	654		
113	YJL024C	762	766	759	654	738	106
115	YGR180C	763	757	776	610		
117	YJL178W	744	760	306	549	310	20
119	YJL001W	748	757	519	610	135	16
121	YJL209C	685	549	48	20		
123	YJL152W	754	757	728	610		
125	YJL131C	750	757	758	610		
127	YJL151C	755	760	764	549	152	20
129	YLR441C	745	760	762	549	277	20
131	YLR415C	789	757	503	610	144	16
133	YLR212C	740	736	759	709	103	20
135	YLR029C	746	736	790	700	292	20
139	YLR105C	761	736	764	709		
141	YIL138W	749	736	779	710	422	20
143	YLR215C	762	736	774	709	151	20
145	YLR321C	749	736	767	709	145	20
147	YMR260C	774	766	783	654	691	106
149	YML120C	764	766	740	654	298	20
151	YLR407W	774	766	640	654	138	106
153	YMR197C	761	736	723	709	65	20
155	YMR100W	770	766	596	654	171	20
157	YMR210W	753	766	755	654	738	20
159	YMR318C	761	736	780	709	135	20
161	YMR069W	756	766	750	654	519	20

163	YNL076W	765	766	757	654	244	20
165	YNL024C	767	768	761	654	273	20
167	YNL125C	761	766	750	654	203	20
169	YNL029C	764	766	758	654		
171	YMR115W	755	736	739	709		
173	YNL244C	774	766	686	654	94	20
175	YNL334C	761	736	756	709		
177	YMR018W	766	736	749	709		
181	YOL118C	727	736	756	709	280	20
183	YOL123W	747	736			140	20
185	YOR020C	764	766	748	654	207	20
187	YOL116W	774	766	735	654	135	20
189	YOR305W	773	769	565	245		
191	YPL267W	757	767	756	548		
193	YPL229W	761	769	752	245		
197	YPR047W	761	769	597	245		
199	YPL011C	766	769	582	245		
201	YPL148C	771	769	401	245		
203	YOL103W	769	769	237	245		
205	YOR018C	770	769	523	245		
211	YOR360C	771	769	851	245		
215	YDL008C	762	769	702	245		
217	YPL210C	794	769	735	245		
219	YMR119C	777	766	469	272		
221	YPR062C	772	768	283	272		
223	YLN224W	797	765	434	272		
225	YLR275W	741	768	760	272		
227	YMR154C	790	768	734	272		
229	YDR205W	787	768	241	272		
231	YPR037C	759	768	740	272		
233	YMR008W	746	768	762	272		
235	YOR064W	758	768	765	272		
237	YOR054W	766	768	140	272		
239	YGL106W	760	768	477	272		
241	YAL037C	759	766	681	272		
243	YIL023C	769		814			
245	YBR064W	745	750	770	576	117	31
249	b2148	736	768	740	272		
251	b2796	761	768	319	272		
253	b2082	755	768	706	272		
255	b0124	755	768	571	272		
257	b3116	765	768	600	272		
259	b1830	757	768	772	272		
261	b1458	750	768	648	272		
263	b2604	764	768	521	272		
265	b2799	768	768	615	272		

267	b3827	766	768	799	272		
269	b0970	764	768	560	272		
271	YER008C	768	760	769	549	729	20
273	YCL027W	749	760	770	549	145	20
275	YBR112C	760	760	780	549	731	20
277	YNL079C	763	766	762	654	216	20
279	YFR042W	789	760	739	549	232	20
281	YER137C	760	760	728	549	458	20
283	YKL103C	747	760	763	549	791	20
285	YNL090W	757	760	783	549	403	20
287	YGR161C	742	760	753	549	225	20
289	YDR071C	737	757	793	610	707	10

0343.0.4 Metabolic analysis of transgenic plants

The described metabolic changes in transgenic plants were identified using the following experimental procedure:

5 0344.0.4 a) Growth and treatment of plants

- 0345.0.4 Plants were grown in climate chambers under standard conditions on pot soil for three weeks (see above). Eight days prior to harvest, water was withheld for part of the plants (8-day treatment). Four days prior to harvest, water was withheld for another group of plants (4-day treatment). The plants of "control treatment" were normally watered throughout the growth period. Plants due to be analysed in the same analytical sequence were grown side-by-side to avoid environmental influences.
- 10 0346.0.4

b) Sampling and storage of samples

- 0347.0.4 Sampling took place in the climate chamber. Green parts were cut with a pair of scissors, quickly weighed, and immediately put into a liquid nitrogen pre-cooled extraction thimble. Racks with extraction thimbles were stored at -80°C until extraction.
- 15 0348.0.4

c) Freeze-drying

Plants were not allowed to thaw or reach temperatures > -40°C until either the first contact with solvents or the removal of water by freeze-drying.

- 0349.0.4 The sample rack with extraction thimbles was put into the pre-cooled (-40°C) freeze-dryer. The starting temperature for the main drying phase was -35°C, pressure was 0.120 mbar. For the drying process, parameters were changed according to a pressure and temperature program. The final temperature (after 12 hours) was +30°C, pressure was 0.001 - 0.004 mbar. After shutting down the vacuum pump and cooling machine, the system was aired with dried air or Argon.
- 20 0350.0.4

d) Extraction

25

- 0351.0.4** Extraction thimbles with plant material were transferred to 5 mL extraction cells on the ASE (Accelerated Solvent Extractor ASE 200 with Solvent Controller and AutoASE-Software (DIONEX)) immediately after freeze-drying.
- 0352.0.4** Polar substances were extracted with approximately 10 mL
- 5 **Methanol/Water (80/20, v/v)** at $T = 70\text{ }^{\circ}\text{C}$ und $p = 140\text{ bar}$, 5 min heating phase, 1 min static Extraction. Lipid substances were extracted with approximately 10 mL **Methanol/Dichloromethan (40/60, v/v)** at $T = 70\text{ }^{\circ}\text{C}$ und $p = 140\text{ bar}$, 5 min heating phase, 1 min static Extraction. Both extracts were collected in one extraction vial (Centrifuge tubes, 50 mL with screw-on lid and Septum for ASE (DIONEX)).
- 10 **0353.0.4** The following internal standards were added to the extracts: LC-Standards L-Methionine-d3, Boc-Ala-Gly-Gly-Gly-OH, L-Tryptophan-d5, Arginine- $^{13}\text{C}_6$ - $^{15}\text{N}_3$, CoEnzyme Q1,2,4 and ribitol, L-glycine-2,2-d2, L-alanine-2,3,3-d4, alpha-methyl-glucopyranoside, nonadecanoic acid methyl ester, undecanoic acid methyl ester, tridecanoic acid, pentadecanoic acid, nonacosanoic acid. To the resulting
- 15 mixture, 8 mL water were added. The solid residues of plant and extraction thimble were discarded.
- 0354.0.4** The extract was centrifuged at 1400 g for 5-10 minutes to speed-up phase-separation. For GC and LC analysis, 1 mL each was taken from the colourless methanol/water upper (polar) phase. The remaining upper phase was discarded. Of the
- 20 dark-green, organic bottom phase 0.5 mL was taken for GC and LC analysis, respectively. All sample aliquots were evaporated using a IR-Dancer Infrared vacuum evaporator (Hottich), using a temperature maximum of 40°C and a maximum pressure of 10 mbar.
- 0355.0.4** e) **LC/MS- and LC/MS/MS-Analysis**
- 25 HPLC mobile phase was added to the lipid and polar residues, respectively (volume adjusted to the weighted sample) and an HPLC analysis using gradient elution was performed.
- 0356.0.4** f) **Derivatisation of the lipid phase for GC/MS-Analysis**
- 0357.0.4** For transesterification, a mixture of 140 μL chloroform, 38 μL HCl (37% HCl in water), 320 μL methanol and 20 μL toluol was added to the residue. The sample
- 30 container was carefully closed and reaction was carried out at 100°C for 2 hours. Subsequently, the solution was evaporated and the pellet was dried completely.
- 0358.0.4** The methoximation of carbonyl groups was achieved by a reaction with 100 μL methoxyamine-hydrochloride (5 mg/mL in Pyridine) for 1.5 hours at 60°C , in a
- 35 closed vial. 20 μL of a mixture of linear, odd-numbered fatty acids was added to provide a time standard. Finally, derivatisation with 100 μL N-Methyl-N-(trimethylsilyl)-

2,2,2-trifluoroacetamide (MSTFA) took place in a closed vial for 30 minutes at 60°C. The final volume for GC injection was 220 µl.

0359.0.4 g) Derivatisation of the polar phase for GC/MS-Analysis

0360.0.4 The methoximation of carbonyl groups was achieved by a reaction with 50 µl methoxyamine-hydrochloride (5 mg/ml in Pyridine) for 1.5 hours at 60°C, in a closed vial. 10 µl of a mixture of linear, odd-numbered fatty acids was added to provide a time standard. Finally, derivatisation with 50 µl N-methyl-N-(trimethylsilyl)-2,2,2-trifluoroacetamide (MSTFA) took place in a closed vial for 30 minutes at 60°C. The final volume for GC injection was 110 µl.

10 0361.0.4 h) Analysis of different plant samples

0362.0.4 Samples were measured in sequences of 20. Each sequence contained 5 wild type and 5 transgenic plants grown under control conditions, as well as 5 wild type and 5 transgenic plants from either the 4 day or 8 day drought treatment.

0363.0.4 The peak height or peak area of each analyte (metabolite) was divided through the peak area of the respective internal standards. Data was normalised using the individual sample fresh weight. The resulting values were divided by the mean values found for wild type plants grown under control conditions and analysed in the same sequence, resulting in the so-called X-folds or ratios (see table 7 - 14), which represent values independent of the analytical sequence. These ratios indicate the behavior of the metabolite concentration of the target plants in comparison to the concentration in the wild type control plants.

0364.0.4 In table 6 the results of the metabolite screening for the plants transformed in genes YCL027W, YBR112C, YNL079C, YER137C, YKL109C, YNL090W, YGR161C, YDR071C are shown.

25 0365.0.4 Tables 6: Details on screening of metabolic activity.

metabolite	wild type			YDR071C		
	control	4 days	8 days	control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,26	1,18		
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
2-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			

beta-epo-E' carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis, 10-cis-hexadecadienoic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienoic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-tetrasenoic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
perotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42	0,98		
gamma-linolenic acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,87	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,04	2,69			
glycerate	1,00	1,87	2,04			
glycerinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,20	1,66			
iso-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			
lutetia	1,00	1,26	1,33			
malate	1,00	2,91	3,46			
mannose	1,00	16,40	17,80			
tricarballic acid	1,00	1,29	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			

methylglutathiotransferase	1,00	1,25	1,30			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,16	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
rutinoid	1,00	17,04	74,75			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,99	1,13			
shikimate	1,00	1,11	1,07			
sthepine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,06	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophan	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubiquinone	1,00	1,03	1,30			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,88	1,18			
zearanzoline	1,00	1,27	1,34			

	wild type			YER137C		
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54	2,15		5,67
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydroxyphenylalanine (edopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
L-oxoprolin	1,00	1,66	1,81	1,65		1,73
alanine	1,00	0,64	0,84	1,82		0,94
Alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-naphthol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydromglucose	1,00	1,02	1,18		1,26	0,83
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			
beta-apo-0' carotinal	1,00	1,21	1,22			
beta-carotene	1,00	1,26	1,26			
beta-sitosterol	1,00	1,39	1,51	0,88	1,17	1,36
beta-tocopherol	1,00	0,54	0,60	2,70		5,03
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid	1,00	1,01	1,04			

(c18:2 me)						
hexadecatrienoic acid (c16:3 mc)	1,00	1,19	1,29			
margaric acid (c17:0 mc)	1,00	1,19	1,28			
delta-15-Cis-tetraposenoic acid (c24:1 mc)	1,00	1,16	1,34			
compesterol	1,00	1,32	1,66		1,10	1,29
cerotic acid (c26:0)	1,00	0,74	1,00	3,24	1,78	
choline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
g-aminobutyric acid	1,00	1,18	1,32	4,44		10,51
gamma-tocopherol	1,00	0,54	0,60	2,78		5,83
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,89			
glycerate	1,00	1,87	2,04	1,17	2,32	
glycerinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41	1,12	1,67	2,06
glycine	1,00	0,26	0,26			
homoserine	1,00	0,61	0,80			
inositol	1,00	4,18	6,32			
isoleucine	1,00	1,28	1,69			
l-alpha-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,82			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02	2,01	1,74	2,03
linoleic acid (c18:2 (c0, c12))	1,00	1,19	1,38			
lutidine	1,00	1,28	1,33			
malate	1,00	2,91	3,46	1,67	5,70	6,01
mannose	1,00	16,40	17,60			
triacnonanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			

putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,73			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,88	1,13			
sialinate	1,00	1,11	1,07		1,40	1,50
sinepine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,63	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,63	1,94			
valine	1,00	0,98	1,18			
zeaxanthine	1,00	1,27	1,34			

metabolite	wild type			YBR112C		
	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54	0,63		
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydro-5-phenylalanine (=dopa)	1,00	1,39	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,58	1,81			
alanine	1,00	0,81	0,64			
alpha linolenic acid (c18:3 (n-3, c12, c15))	1,00	1,24	1,40	1,12		1,42
alpha-tocopherol	1,00	1,05	1,14			
aminocaproic acid	1,00	1,73	1,65	3,90	12,95	
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,98			
beta-apo-3' carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,28	1,05		
beta-sitosterol	1,00	1,39	1,51	1,19		
beta-tocopherol	1,00	0,54	0,60	0,70		
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-16-cis-tetradecadienic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,66	1,42		
cerotic acid (c28:0)	1,00	0,74	1,00			

citrullino	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,80			
eicosanoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47	1,20		
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,51	0,80	0,70		
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,93	1,17			
glutamic acid	1,00	2,01	2,89			
glycerate	1,00	1,57	2,04			
glyceraldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,88	2,41			
glycine	1,00	0,25	0,28			
homoserine	1,00	0,61	0,68			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,29	1,65			
iso-maltose	1,00	2,83	3,02			
isopentenyl pyrophosphate	1,00	1,40	2,62			
leucine	1,00	1,34	1,74			
linoleic acid (c18:2 (c9, c12))	1,00	0,91	1,02			
lutino	1,00	1,19	1,38			
lysine	1,00	1,28	1,33	1,17		
malate	1,00	2,31	3,46			
mannose	1,00	18,10	17,80			
tricarballic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,04	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38	1,11		
phenylalanine	1,00	0,82	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			

cinnapic acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,99	3,49			
sucrose	1,00	1,49	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,58	2,01			
ubiquinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,98	1,18			
zeaxanthine	1,00	1,27	1,34			

	wild type			YGR161C		
	Control	4 days	8 days	Control	4 days	8 days
acetylcholine	1,00	0,50	0,54			
2,3-dimethyl-5-phytylquinol	1,00	1,11	1,28			
2-hydroxy-palmitic acid	1,00	1,83	3,37			
3,4-dihydroxyphenylalanine (=dopa)	1,00					
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,86			
beta-spi-8' carotinal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,80			
palmitic acid	1,00	1,07	1,26			
delta-7-cis,10-cis-hexadecadienic acid (c18:2 me)	1,00	1,01	1,04	1,14		
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,20			
margaric acid (c17:0 me)	1,00	1,19	1,28	1,22		
delta-15-cis-tetraoecenic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
carotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,80			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			

fructose	1,00	14,10	19,73			
formate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42	1,15		
γ-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glycinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,28			
homoserine	1,00	0,81	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,60	2,62			
leucine	1,00	1,34	1,71			
lignoceric acid (c24:0)	1,00	0,81	1,03			
linoleic acid (c18:2 (c9, c12))	1,00	1,10	1,38			
lutidine	1,00	1,28	1,33			
malate	1,00	2,91	3,46			
mannose	1,00	16,40	17,80			
threononolonic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,48			
methylgalactopyranoside	1,00	1,25	1,36	1,18		
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,82	1,10			
phosphate	1,00	2,16	2,73			
putrescine	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,73			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapinic acid	1,00	2,74	3,44			
sorbic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,88	3,49			
sucrose	1,00	1,42	1,70			

threonine	1,00	1,26	1,68			
tryptophan	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubiquinolone	1,00	1,02	1,20			
uridin-glucose	1,00	1,58	1,64			
valine	1,00	0,96	1,18			
zeaxanthine	1,00	1,27	1,34			

YKL103C						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylglycyl	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,84	0,84			
alpha thionioic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,80			
beta-apo-8'-xanthenal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-cholesterol	1,00	1,30	1,51			
beta-tocopherol	1,00	0,54	0,80			
palmitic acid	1,00	1,07	1,25			
delta-7-cis-10-cis-hexadecadienoic acid (c16:2 me)	1,00	1,01	1,04	1,18	1,16	1,30
hexadecatrienoic acid (c19:3 me)	1,00	1,19	1,29			
mergaoic acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-linoleic acid (c24:1 mc)	1,00	1,15	1,14			
campesterol	1,00	1,32	1,65			
corolic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
farulic acid	1,00	1,37	1,47			
fructose	1,00	11,10	19,70			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,80			
glucuronic acid	1,00	2,24	3,08			

glucose	1,00	14,97	20,73		
glutamine	1,00	0,98	1,17		
glutamic acid	1,00	2,01	2,69		
glycerate	1,00	1,87	2,04		
glycerinaldehyde	1,00	1,11	1,12		
glycerol	1,00	1,22	1,29		
glycerol-3-phosphate	1,00	1,86	2,41		
glycine	1,00	0,28	0,28		
homoserine	1,00	0,61	0,69		
inositol	1,00	4,19	6,32		
isoleucine	1,00	1,28	1,68		
iso-maltose	1,00	2,83	3,02		
isopentenyl pyrophosphate	1,00	1,80	2,62		
leucine	1,00	1,34	1,74		
lignoceric acid (c24:0)	1,00	0,91	1,02		
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38		
lutein	1,00	1,26	1,33		
malate	1,00	2,91	3,46		
mannose	1,00	16,40	17,80		
threosonic acid	1,00	1,26	1,23		
methionine	1,00	1,13	1,12		
methylgalantofuranoside	1,00	1,24	1,49		
methylgalactopyranoside	1,00	1,25	1,38		
ornithine				1,70	1,52
palmitic acid (c16:0)	1,00	1,16	1,38		
phenylethanol	1,00	0,82	1,10		
phosphate	1,00	2,15	2,73		
proline	1,00	1,28	1,77		
putrescine	1,00		0,39		
pyruvate	1,00	1,30	1,21		
raffinose	1,00	17,04	24,78		
ribonic acid	1,00	2,22	3,43		
serine	1,00	0,98	1,13		
shikimate	1,00	1,11	1,07		
shikinic acid	1,00	2,74	3,44		
stearic acid (c18:0)	1,00	1,16	1,35		
succinate	1,00	2,98	3,49		
sucrose	1,00	1,42	1,70		
threonine	1,00	1,28	1,68		
tryptophan	1,00	1,13	1,69		
tyrosine	1,00	1,58	2,01		
ubichinone	1,00	1,02	1,20		
udp-glucose	1,00	1,53	1,94		
valine	1,00	0,98	1,18		

zeaxanthin	1,00	1,27	1,34			
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YCL027W						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,64			
2-hydroxy-palmitic acid	1,00	1,17	1,25			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,98	1,81			
alanine	1,00	0,81	0,64			
alpha-linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,10			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,98			
beta-apo-8'-carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,26	1,28			
beta-sitosterol	1,00	1,38	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-de,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,28			
margaric acid (c17:0 me)	1,00	1,19	1,28			
ulole-15-cis-tetradecenoic acid (c14:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
crotonic acid (c2:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthin	1,00	1,00	0,80			
cholesterol acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47	0,79	0,74	0,90
fructose	1,00	14,10	19,78			
lumarate	1,00	5,18	9,33			
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,87	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,89			
glycerate	1,00	1,87	2,04			
glycerinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			

glycerol-3-phosphate	1,00	1,95	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,43	3,02			
isopentany pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c6, c12))	1,00	1,19	1,38			
luteine	1,00	1,26	1,83			
malate	1,00	2,91	3,46			
mannose	1,00	18,40	17,89			
triacentric acid	1,00	1,26	1,43			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,38			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
shapins acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,85			
succinate	1,00	2,98	3,46			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophan	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,98	1,19			
zeaxanthine	1,00	1,27	1,34			

YNL679C						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dioctyl-5-phytylquinal	1,00	0,50	0,54	0,59		
2-hydroxy-palmitic acid	1,00	1,11	1,26			

3,4-dihydroxyphenylalanine (adopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00		1			
5-oxoproline	1,00	1,86	1,81			
alanine	1,00	0,64	0,64			
alpha-linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40		1,53	1,58
alpha-tocopherol	1,00	1,05	1,74		2,64	3,08
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,86			
beta-apo-8' carotenol	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26		1,26	1,20
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,64	0,60	0,73		0,56
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10 cis-hexadecadienic acid (c18:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,10	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28	1,22	1,53	1,36
delta-15-cis-tetradecenoic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,85		1,79	1,62
cectic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cyclopiazanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumaric acid	1,00	5,12	0,33			
galactose	1,00	1,29	1,42			
gamma-butyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,88	1,17			
glutamic acid	1,00	2,01	2,60			
glycerate	1,00	1,87	2,04			
gamma-glutamic acid	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,26	0,26			
homoserine	1,00	3,61	0,69			
inositol	1,00	4,19	6,32		4,73	6,12
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,63	3,02		4,42	4,93

isopentenyl pyrophosphate	1,00	1,30	2,62			
leucine	1,00	1,34	1,74		1,51	2,19
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (n-6, c12))	1,00	1,19	1,36			
lutidine	1,00	1,26	1,33			
malate	1,00	2,81	3,46	1,49		5,72
maltose	1,00	16,40	17,80			
tri- α -hydroxybutyric acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalacturonide	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,86			
ornithine						
palmitic acid (c16:0)	1,00	1,18	1,58			
phenylalanine	1,00	0,02	1,10			
phosphate	1,00	2,45	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,28	1,13			
shikimate	1,00	1,11	1,07			
sialic acid	1,00	2,74	3,44		3,89	2,79
sialic acid (c18:0)	1,00	1,18	1,95			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,29	1,86			
tryptophan	1,00	1,13	1,80		2,68	2,68
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20		0,88	1,02
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,93	1,18			
zeaxanthin	1,00	1,27	1,34			

metabolite	wild type			YNL090W		
	Control	2 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,64			
2-hydroxy-palmitic acid	1,00	1,11	1,25	1,15	1,25	
3,4-dihydroxyphenylalanine (dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (n-3, c12, c15))	1,00	1,24	1,40			

alpha-tocopherol	1,00	1,05	1,14	1,30		5,28
aminoadipic acid	1,00	1,73	1,66			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33		0,85	
aspartic acid	1,00	2,72	2,86			
beta-apo-8' carotene	1,90	1,21	1,22			
beta-carotene	1,00	1,26	1,28	1,15		1,31
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,80			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,29			
delta-16-cis-tetradecadienic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,85			
cerotic acid (c26:0)	1,00	0,74	1,00	2,88	3,93	
citrulline	1,00	0,61	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosanoic acid (20:1)	1,00	0,81	0,61			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumaric acid	1,00	3,19	8,33	0,78		
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			1,69
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,39			
glycerol	1,00	1,87	2,04			
glycerinaldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,81	0,69			
inositol	1,00	4,19	6,32	1,46		3,70
isoleucine	1,00	1,28	1,68		3,54	4,86
iso-maltose	1,00	2,63	3,02	3,59	20,72	14,65
isopentenyl pyrophosphate	1,00	1,80	2,62	1,79		
isocitric acid	1,00	1,84	1,74			
linoleic acid (c18:2 (n-7))	1,00	0,91	1,02			
linoleic acid (c18:2 (n-6, c12))	1,00	1,18	1,38			

luteine	1,00	1,26	1,33			
malate	1,00	2,91	3,46	2,12		14,40
mannose	1,00	16,40	17,80			
triactonox acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (C18:0)	1,00	1,16	1,36			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	9,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapic acid	1,00	2,74	3,44			
stearic acid (C18:0)	1,00	1,18	1,35			
sucinic acid	1,00	2,98	3,49			
sucrose	1,00	1,12	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,80			
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20			
ulfo-glucose	1,00	1,33	1,91			
valine	1,00	0,99	1,16	1,13	1,55	1,80
zeaxanthine	1,00	1,27	1,34			

0366.0.1 Example 2

0367.0.1 Engineering stress-tolerant *Arabidopsis* plants by over-expressing stress related protein encoding genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa* using stress-inducible and tissue-specific promoters.

- 0368.0.1 Transgenic *Arabidopsis* plants were created as in example 1 to express the stress related protein encoding transgenes under the control of either a tissue-specific or stress-inducible promoter. Constitutive expression of a transgene may cause deleterious side effects. Stress inducible expression was achieved using promoters selected from those listed above in Table 1.

0369.0.1 T2 generation plants were produced and treated with drought stress in two experiments. For the first drought experiment, the plants were deprived of water until the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed and the plants were grown to maturity. Seed yield was determined as seeds per plant. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth and produced more seeds than non-transgenic control plants. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.

0370.0.1 An alternative method to impose water stress on the transgenic plants was by treatment with water containing an osmolyte such as polyethylene glycol (PEG) at specific water potential. Since PEG may be toxic, the plants were given only a short term exposure and then normal watering was resumed. As above, seed yields were measured from the mature plants. The response was measured during the stress period by physical measurements, such as stomatal aperture or osmotic potential, or biochemical measurements, such as accumulation of proline. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.

0371.0.1 The transgenic plants with a constitutive promoter controlling transcription of the transgene were compared to those plants with a drought-inducible promoter in the absence of stress. The results indicated that the metabolite and gene expression changes did not occur when plants with the stress-inducible promoter were grown in the absence of stress. These plants also had higher seed yields than those with the constitutive promoter.

0372.0.1 Example 3

0373.0.1 Over-expression of stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa* provides tolerance of multiple abiotic stresses.

0374.0.1 Plants that exhibit tolerance of one abiotic stress often exhibit tolerance of another environmental stress or an oxygen free radical generating herbicide. This phenomenon of cross-tolerance is not understood at a mechanistic level (McKersie and Leshem, 1994). Nonetheless, it is reasonable to expect that plants exhibiting enhanced drought tolerance due to the expression of a transgene might also exhibit tolerance of low temperatures, freezing, salt, air pollutants such as ozone, and other abiotic

- stresses. In support of this hypothesis, the expression of several genes are up or down-regulated by multiple abiotic stress factors including cold, salt, osmoticum, ABA, etc (e.g. Hong et al. (1992) Developmental and organ-specific expression of an ABA- and stress-induced protein in barley. *Plant Mol Biol* 18: 663-674; Jagendorf and Takabe (2001) Inducers of glycinebetaine synthesis in barley. *Plant Physiol* 127: 1827-1835; Mizoguchi et al. (1996) A gene encoding a mitogen-activated protein kinase is induced simultaneously with genes for a mitogen-activated protein kinase and an S6 ribosomal protein kinase by touch, cold, and water stress in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A* 93: 765-769; Zhu (2001) Cell signaling under salt, water and cold stresses. *Curr Opin Plant Biol* 4: 401-406).

- 0375.0.1** To determine salt tolerance, seeds of *Arabidopsis thaliana* were sterilized (100% bleach, 0.1% TritonX for five minutes two times and rinsed five times with ddH₂O). Seeds were plated on non-selection media (1/2 MS, 0.8% phytagar, 0.5g/L MES, 1% sucrose, 2 µg/ml benamyl). Seeds are allowed to germinate for approximately ten days. At the 4-5 leaf stage, transgenic plants were potted into 5.5cm diameter pots and allowed to grow (22 °C, continuous light) for approximately seven days, watering as needed. To begin the assay, two liters of 100 mM NaCl and 1/8 MS was added to the tray under the pots. To the tray containing the control plants, three liters of 1/8 MS was added. The concentrations of NaCl supplementation were increased stepwise by 50 mM every 4 days up to 200 mM. After the salt treatment with 200 mM, fresh and dry weights of the plants as well as seed yields were determined.

- 0376.0.1** To determine cold tolerance, seeds of the transgenic and cold lines were germinated and grown for approximately 10 days to the 4-5 leaf stage as above. The plants were then transferred to cold temperatures (5 °C) and grown through the flowering and seed set stages of development. Photosynthesis was measured using chlorophyll fluorescence as an indicator of photosynthetic fitness and integrity of the photosystems. Seed yield and plant dry weight were measured as an indicator of plant biomass production.

- 0377.0.1** Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0378.0.1 Example 4

- 0379.0.1** Engineering stress-tolerant alfalfa plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

- 0380.0.1** A regenerating clone of alfalfa (*Medicago sativa*) was transformed using the method of (McKersie et al., 1999 *Plant Physiol* 119: 830-847). Regeneration and transformation of alfalfa is genotype dependent and therefore a regenerating plant is

required. Methods to obtain regenerating plants have been described. For example, these can be selected from the cultivar Rangelander (Agriculture Canada) or any other commercial alfalfa variety as described by Brown DCW and A Atanassov (1985, Plant Cell Tissue Organ Culture 4: 111-112). Alternatively, the RA3 variety (University of Wisconsin) has been selected for use in tissue culture (Walker et al., 1978 Am J Bot 65:654-659).

0381.0.1 Petiole explants were cocultivated with an overnight culture of *Agrobacterium tumefaciens* C58C1 pMP90 (McKersie et al., 1999 Plant Physiol 119: 839-847) or LBA4404 containing a binary vector. Many different binary vector systems have been described for plant transformation (e.g. An, G. in *Agrobacterium Protocols, Methods in Molecular Biology* vol 44, pp 47-62, Garland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (Nucleic Acid Research, 1984, 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the Ti plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes – a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 5767366 and 6225105). Similarly, various promoters can be used to regulate the trait gene that provides constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16873) was used to provide constitutive expression of the trait gene.

0382.0.1 The explants were cocultivated for 3 d in the dark on SH induction medium containing 288 mg/ L Pro, 53 mg/ L thioproline, 4.35 g/ L K₂SO₄, and 100 µm acetosyringone. The explants were washed in half-strength Murashige-Skoog medium (Murashige and Skoog, 1962) and plated on the same SH induction medium without acetosyringone but with a suitable selection agent and suitable antibiotic to inhibit *Agrobacterium* growth. After several weeks, somatic embryos were transferred to B0i2Y development medium containing no growth regulators, no antibiotics, and 50 g/ L sucrose. Somatic embryos were subsequently germinated on half-strength Murashige-Skoog medium. Flooded seedlings were transplanted into pots and grown in a greenhouse.

0383.0.1 The T0 transgenic plants were propagated by node cuttings and rooted in Turface growth medium. The plants were defoliated and grown to a height of about 10 cm (approximately 2 weeks after defoliation). The plants were then subjected to drought stress in two experiments.

- 0384.0.1** For the first drought experiment, the seedlings received no water for a period up to 3 weeks at which time the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed. At one week after resuming watering, the fresh and dry weights of the shoots was determined. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth whereas susceptible plants had died or suffered significant injury resulting in less dry matter. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.
- 0385.0.1** An alternative method to impose water stress on the transgenic plants was by treatment with a solution at specific water potential, containing an osmolyte such as polyethylene glycol (PEG). The PEG treatment was given to either detached leaves (e.g. Djilianov et al., 1997 Plant Science 129: 147-158) or to the roots (Wakabayashi et al., 1997 Plant Physiol 113: 967-973). Since PEG may be toxic, the plants were given only a short term exposure. The response was measured as physical measurements such as stomatal aperture or osmotic potential, or biochemical measurements such as accumulation of proline. Tolerant plants maintained their stomatal aperture and showed only slight changes in osmotic potential, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential. In addition the changes in proteins and other metabolites were less in the tolerant transgenic plants than in the non-transgenic control plants.
- 0386.0.1** Tolerance of salinity and cold were measured using methods as described in example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.
- 0387.0.1 Example 5**
- 0388.0.1 Engineering stress-tolerant ryegrass plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa***
- 0389.0.1** Seeds of several different ryegrass varieties may be used as explant sources for transformation, including the commercial variety Gunna available from Svalof Weibull seed company or the variety Affinity. Seeds were surface-sterilized sequentially with 1% Tween-20 for 1 minute, 100 % bleach for 60 minutes, 3 rinses with 5 minutes each with de-ionized and distilled H₂O, and then germinated for 3-4 days on moist, sterile filter paper in the dark. Seedlings were further sterilized for 1 minute with 1% Tween-20, 5 minutes with 75% bleach, and rinsed 3 times with ddH₂O, 5 min each.

0390.0.1 Surface-sterilized seeds were placed on the callus induction medium containing Murashige and Skoog basal salts and vitamins, 20 g/l sucrose, 150 mg/l asparagine, 500 mg/l casein hydrolysate, 3 g/l Phytagel, 10 mg/l BAP, and 5 mg/l dicamba. Plates were incubated in the dark at 25°C for 4 weeks for seed germination and embryogenic callus induction.

0391.0.1 After 4 weeks on the callus induction medium, the shoots and roots of the seedlings were trimmed away, the callus was transferred to fresh media, maintained in culture for another 4 weeks, and then transferred to MSO medium in light for 2 weeks. Several pieces of callus (11-17 weeks old) were either strained through a 10 mesh sieve and put onto callus induction medium, or cultured in 100 ml of liquid ryegrass callus induction media (same medium as for callus induction with agar) in a 250 ml flask. The flask was wrapped in foil and shaken at 175 rpm in the dark at 23°C for 1 week. Sieving the liquid culture with a 40-mesh sieve collected the cells. The fraction collected on the sieve was plated and cultured on solid ryegrass callus induction medium for 1 week in the dark at 25°C. The callus was then transferred to and cultured on MS medium containing 1% sucrose for 2 weeks.

0392.0.1 Transformation can be accomplished with either Agrobacterium or particle bombardment methods. An expression vector is created containing a constitutive plant promoter and the cDNA of the gene in a pUC vector. The plasmid DNA was prepared from E. coli cells using with Qiagen kit according to manufacturer's instruction. Approximately 2 g of embryogenic callus was spread in the center of a sterile filter paper in a Petri dish. An aliquot of liquid MSO with 10 g/l sucrose was added to the filter paper. Gold particles (1.0 µm in size) were coated with plasmid DNA according to method of Sanford et al., 1993 and delivered to the embryogenic callus with the following parameters: 500 µg particles and 2 µg DNA per shot, 1300 psi and a target distance of 8.5 cm from stopping plate to plate of callus and 1 shot per plate of callus.

0393.0.1 After the bombardment, calli were transferred back to the fresh callus development medium and maintained in the dark at room temperature for a 1-week period. The callus was then transferred to growth conditions in the light at 25°C to initiate embryo differentiation with the appropriate selection agent, e.g. 250 nM Aresenal, 5 mg/l PPT or 50 mg/L kanamycin. Shoots resistant to the selection agent appeared and once rooted were transferred to soil.

0394.0.1 Samples of the primary transgenic plants (T0) are analyzed by PCR to confirm the presence of T-DNA. These results are confirmed by Southern hybridization in which DNA is electrophoresed on a 1% agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit

(Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

0395.0.1 Transgenic T0 ryegrass plants were propagated vegetatively by excising tillers. The transplanted tillers were maintained in the greenhouse for 2 months until well established. The shoots were defoliated and allowed to grow for 2 weeks.

0396.0.1 The first drought experiment was conducted in a manner similar to that described in example 3. The seedlings received no water for a period up to 3 weeks at which time the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed. At one week after resuming watering, the lengths of leaf blades, and the fresh and dry weights of the shoots was determined. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth whereas susceptible plants had died or suffered significant injury resulting in shorter leaves and less dry matter. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.

0397.0.1 A second experiment imposing drought stress on the transgenic plants was by treatment with a solution of PEG as described in the previous example. Tolerance of salinity and cold were measured using methods as described in example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0398.0.1 Example 6

0398.0.1 Engineering stress-tolerant soybean plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

0400.0.1 Soybean was transformed according to the following modification of the method described in the Texas A&M patent US 5,164,310. Several commercial soybean varieties are amenable to transformation by this method. The cultivar Jack (available from the Illinois Seed Foundation) is a commonly used for transformation. Seeds were sterilized by immersion in 70% (v/v) ethanol for 8 min and in 25 % commercial bleach (NaOCl) supplemented with 0.1% (v/v) Tween for 20 min, followed by rinsing 4 times with sterile double distilled water. Seven-day seedlings were propagated by removing the radicle, hypocotyl and one cotyledon from each seedling. Then, the epicotyl with one cotyledon was transferred to fresh germination media in petri dishes and incubated at 25 °C under a 16-hr photoperiod (approx. 100 µE-m⁻²s⁻¹) for three weeks. Axillary nodes (approx. 4 mm in length) were cut from 3 – 4 week-old plants. Axillary nodes were excised and incubated in *Agrobacterium* LBA4404 culture.

- 0401.0.1** Many different binary vector systems have been described for plant transformation (e.g. An, G. In *Agrobacterium Protocols. Methods in Molecular Biology* vol 44, pp 17-82, Gartland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (Nucleic Acid Research. 1984. 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the T1 plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes -- a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 57673666 and 6225105). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16673) was used to provide constitutive expression of the trait gene.
- 0402.0.1** After the co-cultivation treatment, the explants were washed and transferred to selection media supplemented with 500 mg/L timentin. Shoots were excised and placed on a shoot elongation medium. Shoots longer than 1 cm were placed on rooting medium for two to four weeks prior to transplanting to soil.
- 0403.0.1** The primary transgenic plants (T0) were analyzed by PCR to confirm the presence of T-DNA. These results were confirmed by Southern hybridization in which DNA is electrophoresed on a 1 % agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.
- 0404.0.1** Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.
- 0405.0.1** Tolerance of drought, salinity and cold were measured using methods as described in example3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.
- 0406.0.1** **Example 7**
- 0407.0.1** Engineering stress-tolerant Rapeseed/Canola plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

- 0408.0.1** Cotyledonary petioles and hypocotyls of 5-6 day-old young seedlings were used as explants for tissue culture and transformed according to Babic et al.(1998, Plant Cell Rep 17: 183-186). The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can be used.
- 0409.0.1** *Agrobacterium tumefaciens* LBA4404 containing a binary vector was used for canola transformation. Many different binary vector systems have been described for plant transformation (e.g. An, G. in *Agrobacterium Protocols*, Methods in Molecular Biology vol 44, pp 47-62, Garland KMA and MR Davey eds, Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (Nucleic Acid Research, 1984, 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the Ti plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes – a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 5787388 and 6225105). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M58930 and X16673) was used to provide constitutive expression of the trait gene.
- 0410.0.1** Canola seeds were surface-sterilized in 70% ethanol for 2 min., and then in 30% Chlorox with a drop of Tween-20 for 10 min, followed by three rinses with sterilized distilled water. Seeds were then germinated in vitro 5 days on half strength MS medium without hormones, 1% sucrose, 0.7% Phytagar at 23°C, 16 hr. light. The cotyledon petiole explants with the cotyledon attached were excised from the in vitro seedlings, and inoculated with *Agrobacterium* by dipping the cut end of the petiole explant into the bacterial suspension. The explants were then cultured for 2 days on MSBAP-3 medium containing 3 mg/l BAP, 3 % sucrose, 0.7 % Phytagar at 23 °C, 16 hr light. After two days of co-cultivation with *Agrobacterium*, the petiole explants were transferred to MSBAP-3 medium containing 3 mg/l BAP, cefotaxime, carbenicillin, or timentin (300 mg/l) for 7 days, and then cultured on MSBAP-3 medium with cefotaxime, carbenicillin, or timentin and selection agent until shoot regeneration. When the shoots were 5 – 10 mm in length, they were cut and transferred to shoot elongation medium (MSBAP-0.5, containing 0.5 mg/l BAP). Shoots of about 2 cm in length were transferred to the rooting medium (MS0) for root induction.

- 0411.0.1 Samples of the primary transgenic plants (T0) were analyzed by PCR to confirm the presence of T-DNA. These results were confirmed by Southern hybridization in which DNA is electrophoresed on a 1 % agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.
- 0412.0.1 The transgenic plants were then evaluated for their improved stress tolerance according to the method described in Example 3. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.
- 0413.0.1 Tolerance of drought, salinity and cold were measured using methods as described in the previous example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.
- 0414.0.1 Example 8
- 0415.0.1 Engineering stress-tolerant corn plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*
- 0416.0.1 Transformation of maize (*Zea mays* L.) is performed with a modification of the method described by Ishida et al. (1996, Nature Biotech 14:745-50). Transformation is genotype-dependent in corn and only specific genotypes are amenable to transformation and regeneration. The inbred line A188 (University of Minnesota) or hybrids with A188 as a parent are good sources of donor material for transformation (Fromm et al. 1990 Biotech 8:833-839), but other genotypes can be used successfully as well. Ears are harvested from corn plants at approximately 11 days after pollination (DAP) when the length of immature embryos is about 1 to 1.2 mm. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors and transgenic plants are recovered through organogenesis.
- The super binary vector system of Japan Tobacco is described in WO patents WO94/00977 and WO95/06722. Vectors were constructed as described. Various selection marker genes can be used including the maize gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patent 6025541). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M56930 and X16673) was used to provide constitutive expression of the trait gene.

0417.0.1 Excised embryos are grown on callus induction medium, then maize regeneration medium, containing imidazolinone as a selection agent. The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to maize rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the imidazolinone herbicides and which are PCR positive for the transgenes.

0418.0.1 The T1 transgenic plants were then evaluated for their improved stress tolerance according to the method described in Example 3. The T1 generation of single locus insertions of the T-DNA will segregate for the transgene in a 3:1 ratio. Those progeny containing one or two copies of the transgene are tolerant of the imidazolinone herbicide, and exhibit greater tolerance of drought stress than those progeny lacking the transgenes. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels. Homozygous T2 plants exhibited similar phenotypes. Hybrid plants (F1 progeny) of homozygous transgenic plants and non-transgenic plants also exhibited increased environmental stress tolerance.

0419.0.1 Tolerance of salinity and cold were measured using methods as described in the previous example 3. Plants that had tolerance to drought, salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0420.0.1 Example 9

0421.0.1 Engineering stress-tolerant wheat plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*

0422.0.1 Transformation of wheat is performed with the method described by Ishida et al. (1998 Nature Biotech. 14745-50). The cultivar Bobwhite (available from CYMMIT, Mexico) is commonly used in transformation. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors, and transgenic plants are recovered through organogenesis. The super binary vector system of Japan Tobacco is described in WO patents WO94/00977 and WO95/06722. Vectors were constructed as described. Various selection marker genes can be used including the maize gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patent 6025541). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of

gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16673) was used to provide constitutive expression of the trait gene.

- 0423.0.1 After incubation with *Agrobacterium*, the embryos are grown on callus induction medium, then regeneration medium, containing imidazolinone as a selection agent. The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the imidazolinone herbicides and which are PCR positive for the transgenes.

- 0424.0.1 The T1 transgenic plants were then evaluated for their improved stress tolerance according to the method described in the previous example 3. The T1 generation of single locus insertions of the T-DNA will segregate for the transgene in a 3:1 ratio. Those progeny containing one or two copies of the transgene are tolerant of the imidazolinone herbicide, and exhibit greater tolerance of drought stress than those progeny lacking the transgenes. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels. Homozygous T2 plants exhibited similar phenotypes. Tolerance of salinity and cold were measured using methods as described in the previous examples. Plants that had tolerance to drought, salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0425.0.3 Example 14

- 25 0426.0.3 Identification of Identical and Heterologous Genes

- 0427.0.3 Gene sequences can be used to identify identical or heterologous genes from cDNA or genomic libraries. Identical genes (e. g. full-length cDNA clones) can be isolated via nucleic acid hybridization using for example cDNA libraries. Depending on the abundance of the gene of interest, 100,000 up to 1,000,000 recombinant bacteriophages are plated and transferred to nylon membranes. After denaturation with alkali, DNA is immobilized on the membrane by e. g. UV cross linking. Hybridization is carried out at high stringency conditions. In aqueous solution, hybridization and washing is performed at an ionic strength of 1 M NaCl and a temperature of 68°C. Hybridization probes are generated by e.g. radioactive (³²P) nick transcription labeling (High Prime, Roche, Mannheim, Germany). Signals are detected by autoradiography.

0428.0.3 Partially identical or heterologous genes that are related but not identical can be identified in a manner analogous to the above-described procedure using low

stringency hybridization and washing conditions. For aqueous hybridization, the ionic strength is normally kept at 1 M NaCl while the temperature is progressively lowered from 68 to 42°C.

- 0429.0.3** isolation of gene sequences with homology (or sequence identity/similarity) only in a distinct domain of (for example 10-20 amino acids) can be carried out by using synthetic radio labeled oligonucleotide probes. Radiolabeled oligonucleotides are prepared by phosphorylation of the 5-prime end of two complementary oligonucleotides with T4 polynucleotide kinase. The complementary oligonucleotides are annealed and ligated to form concatemers. The double stranded concatemers are then radiolabeled by, for example, nick transcription. Hybridization is normally performed at low stringency conditions using high oligonucleotide concentrations.

- Oligonucleotide hybridization solution:
6 x SSC
0.01 M sodium phosphate
1 mM EDTA (pH 8)
0.5 % SDS
100 µg/ml denatured salmon sperm DNA
0.1 % nonfat dried milk

- 0430.0.3** During hybridization, temperature is lowered stepwise to 5-10°C below the estimated oligonucleotide T_m or down to room temperature followed by washing steps and autoradiography. Washing is performed with low stringency such as 3 washing steps using 4 x SSC. Further details are described by Sambrook, J. et al., 1989, "Molecular Cloning: A Laboratory Manual," Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al., 1994, "Current Protocols in Molecular Biology," John Wiley & Sons.

0431.0.3 Example 15

- 0432.0.3 Identification of Identical Genes by Screening Expression Libraries with Antibodies**

- 0433.0.3** c-DNA clones can be used to produce recombinant polypeptide for example in *E. coli* (e.g. Qiagen QIAexpress pQE system). Recombinant polypeptides are then normally affinity purified via Ni-NTA affinity chromatography (Qiagen). Recombinant polypeptides are then used to produce specific antibodies for example by using standard techniques for rabbit immunization. Antibodies are affinity purified using a Ni-NTA column saturated with the recombinant antigen as described by Gu et al., 1994, BioTechniques 17:257-262. The antibody can then be used to screen expression cDNA libraries to identify identical or heterologous genes via an immunological screening (Sambrook, J. et al., 1989, "Molecular Cloning: A Laboratory

Manual," Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al., 1994, "Current Protocols in Molecular Biology", John Wiley & Sons).

0434.0.3 Example 16

0435.0.3 In vivo Mutagenesis

- 5 **0436.0.3** In vivo mutagenesis of microorganisms can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D., 1996, DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those skilled in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M., 1994, Strategies 7: 32-34. Transfer of mutated DNA molecules into plants is preferably done after selection and testing in microorganisms. Transgenic plants are generated according to various examples within the exemplification of this document.

0437.0.3 Example 17

0438.0.3 Identification and Analysis of YNL090W Homologs

- 0439.0.3** Transgenic Arabidopsis plants overexpressing YNL 090W (ORF 3165) lived 4.33 days longer than the wild type control under drought conditions. The protein sequence of YNL090W was used to identify related gene sequences of expressed sequence tags (ESTs) proprietary libraries constructed from *Oryza sativa* cv. Nippon-Barré (a japonica rice), *Brassica napus* cv. "AC Excel" "Quantum" and "Cresor" (canola), and *Glycine max* cv. Resnick (soybean) by Blast analysis (Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990 J Mol Biol 215:403-10).

- 0440.0.3** The plant cDNA sequences were translated into a predicated amino acid sequences, and relationship among the amino acids sequences was determined by sequence alignment using the clustal W algorithm in Vector NTI Version 7 (Figure 2). They have 75% similarity overall. In general, proteins having conserved domains referred to as I (GXXXGKT), II (DXXG), III (VGTK), IV (EXSS), and E (FXXYXXQ), are classified as small GTPases. All five domains in the proteins in Figure 1 are more conserved than in other known small GTPases, particularly Domain I (KXVXXGDXXXGKT), Domain E (FXXYXXQ), Domain II (WDTAGQE) and Domain III (VGTKXDL). In addition, polybasic amino acids in C terminus are shown in the Figure 2, as well as a C-terminal CAAL domain (wherein A is an aliphatic amino acid), which is the signature sequence for post translational modification by the enzyme geranylgeranyltransferase I. Another important Nho-specific feature was shown in

most proteins in Figure 1 is the highly conserved amino acids between Domain II and Domain III.

CLAIMS

1. A transformed plant cell with altered metabolic activity compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.
2. The transformed plant cell of claim 1, wherein metabolic activity is altered concerning one or more metabolites selected from the group consisting of 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4-dihydroxyphenyl-alanine (= dopa), 3-hydroxy-palmitic acid, 5-oxoproline, alanine, alpha linolenic acid (c18:3 (c9, c12, c15)), alpha-tocopherol, aminoadipic acid, anhydroglucose, arginine, aspartic acid, beta-apo-8' carotenal, beta-carotene, beta-sitosterol, beta-tocopherol, (delta-7-cis,10-cis)-hexadecadienic acid, hexadecatrienic acid, margoric acid, delta-15-cis-tetracosenic acid, ferulic acid, campesterol, cerotic acid (c26:0), citrullino, cryptoxanthine, eicosenoic acid (20:1), fructose, fumarate, galactose, gamma-aminobutyric acid, gamma-tocopherol, gluconic acid, glucose, glutamic acid, glutamine, glycerate, glyceraldehyde, glycerol, glycerol-3-phosphate, glycine, homoserine, inositol, isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignocoric acid (c24:0), linoleic acid (c18:2 (c8, c12)), luteina, lycopene, malate, mannose, methionine, methylgalactofuranoside, methylgalactopyranoside, methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate, proline, putrescine, pyruvat, raffinose, ribonic acid, serine, shikimate, sinapins acid, stearic acid (c18:0), succinate, sucrose, threonine, triacontanoic acid, tryptophane, tyrosine, ubiquinone, udp-glucose, valine, zeaxanthine.
3. The transgenic plant cell of claim 1 or 2, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid selected from the group consisting of:
- a) nucleic acid molecule encoding one of the polypeptides shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
 - b) nucleic acid molecule comprising one of the nucleic acid molecules shown in Fig. 1a, 1b or 1c;
 - c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;

- d) nucleic acid molecule which encodes a polypeptide which has at least 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;
- 5 c) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 10 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- 15 h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring an altered metabolic activity in an organism or a part thereof.
- 20 or comprising a sequence which is complementary thereto.
4. The transgenic plant cell of claim 3, wherein the environmental stress is selected from the group consisting of salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof.
5. The transgenic plant cell of any of claims 1 – 4 derived from a monocotyledonous plant.
- 30 6. The transgenic plant cell of any of claims 1 – 5 derived from a dicotyledonous plant.
7. The transgenic plant cell of any of claims 1 – 6, wherein the plant is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, flax, borage, safflower,
- 35 linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco,

eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass, forage crops and *Arabidopsis thaliana*.

8. The transgenic plant cell of any of claims 1 - 4, derived from a gymnosperm plant.
- 5 9. The transgenic plant cell of any of claims 1 - 4 or 6, wherein the plant is selected from the group of spruce, pine and fir.
10. A transgenic plant generated from a plant cell according to any of claims 1 - 7 and which is a monocot or dicot plant.
11. A transgenic plant of claim 10, which is selected from the group consisting of
10 maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, popper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, tump rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass, forage crops and *Arabidopsis thaliana*.
- 15 12. A transgenic plant generated from a plant cell according to any of claims 1 - 4, 8 or 9 and which is a gymnosperm plant.
13. A transgenic plant of claim 12, which is selected from the group consisting of spruce, pine and fir.
14. A seed produced by a transgenic plant of any of claims 10 - 13, wherein the
20 seed is genetically homozygous for a transgene conferring altered metabolic activity resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.
15. An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
25 a) nucleic acid molecule encoding of the polypeptide shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
b) nucleic acid molecule comprising of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;
30 c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;
d) nucleic acid molecule which encodes a polypeptide which has at least
35 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;

- e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- 5 f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 10 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- 15 i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring altered
- 20 metabolic activity in an organism or a part thereof;

whereby the nucleic acid molecule distinguishes over the sequence as shown in Fig. 1a, 1b or 1c by one or more nucleotides.

16. An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
- 25 a) nucleic acid molecule encoding of the polypeptide shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
- b) nucleic acid molecule comprising of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;
- 30 c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;
- d) nucleic acid molecule which encodes a polypeptide which has at least
- 35 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;

- e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- 5 f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 10 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- 15 i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring altered metabolic activity in an organism or a part thereof.
- 20 17. A nucleic acid construct which confers the expression of the nucleic acid molecule of claim 15 or 16, comprising one or more regulatory elements, whereby expression of the SRP coding nucleic acid in a host cell results altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
- 25 18. A vector comprising the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 17, whereby expression of the SRP coding nucleic acid in a host cell results altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
- 30 19. A host cell, which has been transformed stably or transiently with the vector as claimed in claim 18 or the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 17.
20. An isolated Stress Related Protein (SRP) which is selected from the group comprising Fig. 1a, 1b or 1c and/or homologs thereof.
- 35

21. An isolated Stress Related Protein (SRP) of claim 20 which is selected from yeast, preferably *Saccharomyces cerevisiae*, or *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*.
22. A method of producing a transgenic plant with altered metabolic activity
5 compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by expression of a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell, comprising
- 10 a. transforming a plant cell with an expression vector according to claim 18 and
b. generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.
- 15 23. The method of claim 22, wherein the SRP coding nucleic acid is selected from the group comprising the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.
24. The method of any of claims 22 or 23, wherein the SRP coding nucleic acid is at least about 50% homologous to one of the nucleic acids of Fig. 1a, 1b or 1c.
- 20 25. A method of modifying stress tolerance of a plant comprising, modifying the level of expression of an SRP in the plant.
26. The method of claim 25, wherein the SRP encoding nucleic acid is selected from the group comprising the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.
- 25 27. The method of any of claims 25 or 26, wherein the SRP coding nucleic acid is at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c.
28. The method of any of claims 25 - 27, wherein an expression vector is used according to any of claims 17 or 18.
29. The method of any of claims 25 - 28, wherein the stress tolerance is decreased.
- 30 30. The method of any of claims 25 - 29, wherein the plant is transgenic.
31. The method of any of claims 25 - 30, wherein the plant is transformed with an inducible promoter that directs expression of the SRP.
32. The method of any of claims 25 - 31, wherein the promoter is tissue specific.
33. The method of any of claims 25 - 32, wherein the promoter is developmentally
35 regulated.
34. The method of any of claims 25 - 33, wherein SRP expression is modified by administration of an targeting nucleic sequence complementary to the regulatory region

of the SRP encoding nucleic acid and/or by a transcription factor and/or by a zinc finger protein.

35. A method of detecting environmental stress in plant cells or plants comprising screening the plant cells for altered metabolic activity as compared to non-stress conditions.

36. A method of screening plant cells or plants for increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions.

37. A method of breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress.

38. The method of one of claims 35 - 37, wherein metabolite activity is altered concerning one or more metabolites selected from the group consisting of 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4-dihydroxyphenylalanine (= dopa), 3-hydroxy-palmitic acid, 5-oxoprolino, alanine, alpha linolenic acid (c18:3 (c9, c12, c15)), alpha-tocopherol, aminoadipic acid, anhydroglucose, arginine, aspartic acid, beta-apo-8' carotenal, beta-carotens, beta-sitosterol, beta-tocopherol, (delta-7-cis,10-cis)-hexadecadienic acid, hexadecatrienic acid, margaric acid, delta-15-cis-tetracosenic acid, nerulic acid, campesterol, cerotic acid (c26:0), citrulline, cryptoxanthine, elcosenoic acid (20:1), fructose, fumarates, galactose, gamma-aminobutyric acid, gamma-tocopherol, gluconic acid, glucose, glutamic acid, glutamine, glycerate, glycerinaldehyd, glycerol, glycerol-3-phosphate, glycine, homoserine, inositol, isoleucine, iso-mallose, isopentenyl pyrophosphate, leucine, lignoceric acid (c24:0), linoleic acid (c18:2 (c9, c12)), luteine, lycopene, malates, mannose, methionine, methylgalactofuranoside, methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate, proline, putrescine, pyruvat, raffinose, ribonic acid, serine, shikimate, sinapine acid, stearic acid (c18:0), succinates, sucrose, threonine, triacontenic acid, tryptophane, tyrosine, ubiquinone, udp-glucose, valine, zeaxanthine.

39. The method of one of the claims 35 - 38, wherein the altered metabolic activity is by transformation with a Stress-Related Protein (SRP) coding nucleic acid.

40. The method of one of the claims 35 - 39, wherein metabolic activity is altered by transformation with one or more Stress-Related Protein (SRP) coding nucleic acids selected from the group comprising at least one of the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.

41. Use of a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences for preparing a plant cell with increased environmental stress tolerance.
42. Use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants or plant cells with increased tolerance to environmental stress.
43. Use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for detection of stress in plants or plant cells.
44. A nucleic acid construct which confers the expression of the nucleic acid molecule of claim 15 or 16, comprising one or more regulatory elements, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
45. A vector comprising the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 44, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
46. A plant cell comprising a nucleic acid construct of claim 44 or a vector of claim 45.
47. A plant comprising a cell of claim 46.
48. An isolated nucleic acid, comprising a polynucleotide selected from the group consisting of:
- a. a nucleic acid sequence of Fig. 1c;
 - b. a polynucleotide encoding a polypeptide of Fig. 1c;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1c, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1c, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant.
49. A vector comprising the isolated nucleic acid of claim 48.

50. A plant stably transformed with the isolated nucleic acid of claim 48.
51. A plant stably transformed with the vector of claim 49.
52. A seed of the plant of claim 50, wherein said seed comprises the isolated nucleic acid of claim 48.
53. A seed of the plant of claim 50, wherein said seed comprises the vector of claim 49.
54. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with an isolated nucleic acid of claim 48.
55. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with a vector of claim 49.
56. A plant transformed with a nucleic acid selected from the group consisting of:
- a. a nucleic acid sequence of Fig. 1a or Fig. 1b;
 - b. a polynucleotide encoding a polypeptide of Fig. 1a or Fig. 1b;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant.
57. A seed of the plant of claim 56.
58. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with a nucleic acid selected from the group consisting of:
- a. a nucleic acid sequence of Fig. 1a or Fig. 1b;
 - b. a polynucleotide encoding a polypeptide of Fig. 1a or Fig. 1b;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant.

SEQUENCES

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 Leu Ser Ile Ile Thr Trp Ser Asn Arg Asn Val Ser Ala Asn Leu Leu
 85 90 95
 Gly Ile Phe Leu Phe Thr Val Cys Val Leu Tyr Phe Gly Phe Ile Thr
 100 105 110
 Arg Tyr Phe Gly His Leu Met Ile Val Gly Ile Ile Trp Val Tyr Leu
 115 120 125
 Leu Ile Asp Lys His Val Gln Glu Thr Met Ala Ser Cys Pro Ser Leu
 130 135 140
 Asp Asp Ile Ile His Val Met Asp Arg Val Ser Met Lys Ser Ser Ala
 145 150 155 160
 Val Leu Ser Pro Ile Thr Ile Leu Ser Ala Gln Asp Val Arg Arg Leu
 165 170 175
 Leu Phe Thr Ile Ala Phe Leu Ser Pro Val Tyr Ile Phe Leu Thr Val
 180 185 190
 Phe Val Leu Ser Pro Asn Tyr Leu Met Leu Ile Gly Gly Leu Tyr Val
 195 200 205
 Leu Thr Tyr His Ser Lys Leu Ile Arg Arg Met Arg Arg Tyr Leu Trp
 210 215 220
 Lys Phe Arg Val Val Arg Leu Leu Val Thr Phe Ile Thr Gly Leu Asp

225	230	235	240
Leu Gly Gly Pro Asp Asn Asn Arg Arg Leu Phe Ala Ser Val Asn Lys			
245	250	255	
Lys Ile Arg Ser Phe Val Trp Asn Glu Val Gly Asn Thr Ser Asn Thr			
260	265	270	
Lys Lys Thr Val Leu Phe Lys Val Ala Leu Phe Glu Asn Gln Arg Arg			
275	280	285	
Trp Leu Gly Ile Gly Trp Thr Ser Thr Met Leu Ser Tyr Glu Arg Ala			
290	295	300	
Ser Trp Thr Asp Glu Phe Leu Asn Thr Ser Pro Ser Pro Glu Val Phe			
305	310	315	320
Thr Leu Pro Glu Glu Gln Ser Gly Met Ala Trp Glu Trp His Asp Lys			
325	330	335	
Asp Trp Met Leu Asp Leu Thr Asn Arg Gly Ile Ile Gln Leu Pro Ala			
340	345	350	
Ser Ala Ala Lys Thr Lys Val Lys Pro Gly Ala Asp Glu Gly Phe Ile			
355	360	365	
Tyr Tyr Asp Asn Thr Trp Asn Asn Pro Ser Ala Thr Asp Thr Tyr Lys			
370	375	380	
Lys Tyr Thr Arg Arg Arg Arg Trp Ile Arg Thr Ala Thr Val Thr Thr			
385	390	395	400
Thr Tyr Asp Asp Glu Pro Thr Val Glu Lys Ala Thr Pro Asn Ser His			
405	410	415	
Ala Leu Lys Ser Glu Glu Asn Asn Arg Val Arg Lys Arg Lys Val Ser			
420	425	430	
Phe Ser Thr Ala Asn Glu Val His Ile Ile Pro Ser Ser Asp Ser Ser			
435	440	445	
Lys Leu Ile Gln Ile Ser Asp Val Ser Met Ser Pro Ser Leu			

450

455

460

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<212> DNA

<213> Saccharomyces cerevisiae

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1			5						10			15			

tct	tgg	gac	agg	gac	acc	ttc	gac	ttt	ata	ttc	ggc	aat	gys	acc	96
Ser	Leu	Ala	Arg	Ala	Ser	Pro	Phe	Asp	Phe	Ile	Phe	Gly	Asn	Gly	Thr
			20				25					30			

caa	caa	gct	cag	agc	caa	agc	gag	agt	caa	ggc	caa	gtt	tct	ttc	acc	144
Gln	Gln	Ala	Glu	Ser	Gln	Ser	Glu	Ser	Glu	Gly	Gln	Val	Ser	Phe	Thr	
			35				40					45				

aat	gaa	gct	tct	cag	gat	agt	tcc	acc	ccc	tct	tgg	gta	acc	gac	tat	192
Asn	Glu	Ala	Ser	Gln	Asp	Ser	Thr	Thr	Ser	Leu	Val	Thr	Ala	Tyr		
			50			55				60						

tct	caa	ggc	gtt	cat	tcc	caa	acc	gag	gta	agt	gac	acc	240		
Ser	Gln	Gly	Val	His	Ser	His	Gln	Ser	Ala	Thr	Ile	Val	Ser	Ala	Thr
65					70				75			80			

atc	tct	tcc	ctc	cca	tct	act	tgg	tat	gat	ggc	agc	tcc	act	tcc	cag	288
Ile	Ser	Ser	Leu	Pro	Ser	Thr	Trp	Tyr	Asp	Ala	Ser	Ser	Thr	Ser	Gln	
			85					90				95				

aat	tct	gtg	tca	tat	gac	agt	caa	gaa	tcc	gac	tat	gac	gtt	aat	caa	336
Thr	Ser	Val	Ser	Tyr	Ala	Ser	Gln	Glu	Ser	Asp	Tyr	Ala	Val	Asn	Gln	
					100				105				110			

aac tct tgg agc ggc tct act aat caa atg cca tct acc agt acg aca	584
Asn Ser Trp Ser Ala Ser Thr Asn Gln Leu Pro Ser Thr Ser Thr Thr	
115 120 125	
agc tac tat ggc cca acc ttc agt aca tgg gcc gat ttt gct gct tct	432
Ser Tyr Tyr Ala Pro Thr Phe Ser Thr Ser Ala Asp Phe Ala Ala Ser	
130 135 140	
agt gta aat gca gct tct gac gtc tcc act gcc agt gtt odc att gat	480
Ser Val Asn Ala Ala Ser Asp Val Ser Thr Ala Ser Val Pro Ile Asp	
145 150 155 160	
acg agt got aat tct atc cct ttc aca act aca agt aac ata gag act	528
Thr Ser Ala Asn Ser Ile Pro Phe Thr Thr Thr Ser Asn Ile Glu Thr	
165 170 175	
aca acg agt gca cct ctc act tgg gac act cca ctt alt tcc act agt	576
Thr Thr Ser Ala Pro Leu Thr Ser Asp Thr Pro Leu Ile Ser Thr Ser	
180 185 190	
acg atg tcc gca got gat aac gta ttt tgg tca gca aac cct att tct	624
Thr Met Ser Ala Ala Asp Asn Val Phe Ser Ser Ala Asn Pro Ile Ser	
195 200 205	
gcc tcc cta aca aac acc gat agt tca gaa agt ttt gac cca act tgg	672
Ala Ser Leu Thr Thr Thr Asp Ser Ser Glu Ser Phe Asp Glu Thr Ser	
210 215 220	
act got ggt gcc att ccy gty caa agt tca gaa gat ttt agt agt tct	720
Thr Ala Gly Ala Ile Pro Val Gln Ser Ser Ala Asp Phe Ser Ser Ser	
225 230 235 240	
agt gaa att tta gta caa agt tgg ggc gat ttc agt agc cct agt tct	768
Ser Glu Ile Leu Val Gln Ser Ser Ala Asn Phe Ser Ser Pro Ser Ser	
245 250 255	
cca act act acc gat ata tgg cta tca get gcc cca atg caa aca agt	816
Pro Thr Thr Thr Asp Ile Ser Leu Ser Ala Ala Pro Leu Gln Thr Ser	
260 265 270	
gaa tca agc agt ttt acc act gca tcc gaa gct cta cca gta agt lua	864
Glu Ser Ser Ser Phe Thr Thr Ala Ser Ala Ala Leu Pro Val Ser Ser	

275	280	285	
ada gac gtt gat ggc tca agc gcc tca cct gta ggc agc atg agc gcc			912
Thr Asp Val Asp Gly Ser Ser Ala Ser Pro Val Val Ser Met Ser Ala			
290	295	300	
gca gga caa ata gct agc tca agc agc aca gat aat cca aat atg tca			960
Ala Gly Gln Ile Ala Ser Ser Ser Ser Thr Asp Asn Pro Thr Met Ser			
305	310	315	320
gaa acc ttt tgc tta aca tct aca gaa g-t gat ggt tcc gat gtt tca			1008
Glu Thr Phe Ser Leu Thr Ser Thr Gln Val Asp Gly Ser Asp Val Ser			
325	330	335	
tca aca gtc ago gca tta tta tgc gct cct ttt tta caa aca ayt act			1056
Ser Thr Val Ser Ala Leu Leu Ser Ala Pro Phe Leu Gln Thr Ser Thr			
340	345	350	
tca aac agt ttc ago att gtt ago caa tgc gta tct ttt gtt cca tca			1104
Ser Asn Ser Phe Ser Ile Val Ser Pro Ser Val Ser Phe Val Pro Ser			
355	360	365	
cag agt leu tca gac gtt gct ago tcc agt act gca aat gta gtt agt			1152
Gln Ser Ser Ser Asp Val Ala Ser Ser Ser Thr Ala Asn Val Val Ser			
370	375	380	
tca tcc ttt tct gat att cca cag caa act agt acc tca ggg ago gta			1200
Ser Ser Phe Ser Asp Ile Pro Pro Gln Thr Ser Thr Ser Gly Ser Val			
385	390	395	400
gtt tgc gta ggc caa tcc gaa tct gcc ctc gca ttt caa agt leu aca			1248
Val Ser Val Ala Gln Ser Ala Ser Ala Leu Ala Phe Gln Ser Ser Thr			
405	410	415	
gag gta tat ggt gcc agt gcc tgc ago aca atg agt tca tta ata tca			1296
Glu Val Tyr Gly Ala Ser Ala Ser Ser Thr Met Ser Ser Leu Leu Ser			
420	425	430	
act act tgc cta cug tct act act ttg gat ago tca agt tta gct agc			1344
Thr Thr Ser Leu Gln Ser Thr Thr Leu Asp Ser Ser Ser Leu Ala Ser			
435	440	445	

tcc tct ggc tgg agc tca gac ctt aca gat tat ggc gtc tcc agt aca Ser Ser Ala Ser Ser Ser Asp Leu Thr Asp Tyr Gly Val Ser Ser Thr 450 455 460	1332
gca agc ata cgg ctg ttg tca gcc tca gaa caa gca agt act tcc agc Alu Ser Ile Pro Leu Leu Ser Ala Ser Glu Gln Ala Ser Thr Ser Ser 465 470 475 480	1440
agc ttt agc gtt gtt agc cct tgg gta tct ttt gtt cca tca caa agt Ser Phe Ser Val Val Ser Pro Ser Val Ser Phe Val Pro Ser Gln Ser 485 490 495	1488
tcc tca gat gtt gct acc acc agt gct cca agt gta gtt agt tca tcc Ser Ser Asp Val Ala Ser Thr Ser Ala Pro Ser Val Val Ser Ser Ser 500 505 510	1536
ttt tct tat act tca ctg caa gca ggt ggc tct agc atg acc aat ccc Phe Ser Tyr Thr Ser Leu Gln Ala Gly Gly Ser Ser Met Thr Asn Pro 515 520 525	1584
tct tca tcc act ata gta tct tcc agt agt act ggc agt tct gag gaa Ser Ser Ser Thr Ser Val Tyr Ser Ser Ser Thr Gly Ser Ser Glu Glu 530 535 540	1632
tcc gct gca tct aca gcc tct gca aca ctg tgg ggc tcc tgg tct act Ser Ala Ala Ser Thr Ala Ser Ala Thr Leu Ser Gly Ser Ser Ser Thr 545 550 555 560	1680
tat atg gca gga aat ttg caa tca cag cct cca tcc act tca agt ttg Tyr Met Ala Gly Asn Leu Gln Ser Gln Pro Pro Ser Thr Ser Ser Leu 565 570 575	1728
ctt tgg gag tct caa gcc aca agc act tca gct gtg cta gct agc agt Leu Ser Glu Ser Gln Ala Thr Ser Thr Ser Ala Val Leu Ala Ser Ser 580 585 590	1776
tct gtt tct aca act tca ccc tat acc act gca ggt ggt gca tct aca Ser Val Ser Thr Thr Ser Pro Tyr Thr Thr Ala Gly Gly Ala Ser Thr 595 600 605	1824
gag gcc tca tcc ctc ata tca tct acc tct ggc gaa act tcc cag gta Glu Ala Ser Ser Leu Ile Ser Ser Thr Ser Ala Glu Thr Ser Gln Val 610 615 620	1872

610	615	620	
agt lut tcn caa agc aca act goa ttg caa act tcc tca ttc gca tgg			1920
Ser Tyr Ser Gln Ser Thr Thr Ala Leu Gln Thr Ser Ser Phe Ala Ser			
625	630	635	640
tct tca aca aca gaa gga agt gaa aca tct agt caa ggt tct tct acc			1968
Ser Ser Thr Thr Glu Gly Ser Glu Thr Ser Ser Gln Gly Phe Ser Thr			
645	650	655	
agc tct gtt tta gtt caa atg cct tct tgg all tcc agc gaa ttc tca			2016
Ser Ser Val Leu Val Glu Met Pro Ser Ser Ile Ser Ser Glu Phe Ser			
660	665	670	
ccc tct cug arg aca act caa atg aat tct goa agc tca tca tct cag			2064
Pro Ser Gln Thr Thr Thr Glu Met Asn Ser Ala Ser Ser Ser Ser Gln			
675	680	685	
tac aat ata tca tcc act ggt ata ctt tct cug gtt tca gac acc tgg			2112
Tyr Thr Ile Ser Ser Thr Cys Ile Leu Ser Gln Val Ser Asp Thr Ser			
690	695	700	
gtg tct tal aca act tca agt tcc tct gtt tct caa gtt tca gan aca			2160
Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp Thr			
705	710	715	720
caa gtt tct tat aca act tca agt tgg tct gtt tct caa gtt tca gac			2208
Pro Val Ser Tyr Thr Thr Ser Ser Ser Val Ser Gln Val Ser Asp			
725	730	735	
aca cgg gtt tct tat aca act tca agt tgg tct gtt tct caa gtt tca			2256
Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Val Ser Gln Val Ser			
740	745	750	
gac aca aca gtt tct tat aca act tca agt tca tct gtt tct caa gtt			2304
Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val			
755	760	765	
tca gac aca cgg gtt tct tat aca act tca agt tgg tcc gtt tct caa			2352
Ser Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln			
770	775	780	

ggt	tca	gac	acg	tca	gta	ctt	ctt	aca	agt	tcc	aca	tgg	tcc	gtt	tct	2400
Val	Ser	Asp	Thr	Ser	Val	Pro	Ser	Thr	Ser	Ser	Arg	Ser	Ser	Val	Ser	
785				790						795				800		
caa	gta	tca	gac	act	cag	gtg	act	tct	aca	agt	tca	agg	tgg	tcc	gtt	2448
Gln	Val	Ser	Asp	Thr	Pro	Val	Pro	Ser	Thr	Ser	Ser	Arg	Ser	Ser	Val	
				805						810				815		
tct	caa	acc	tct	agc	tca	cta	cag	ccc	acc	act	aca	tcc	tcc	caa	cgt	2496
Ser	Gln	Thr	Ser	Ser	Ser	Leu	Gln	Pro	Thr	Thr	Thr	Ser	Ser	Gln	Arg	
				820						825				830		
ttc	acc	att	tcc	act	cat	gga	gag	ctt	tct	gaa	agt	aga	tct	gtt	agc	2544
Phe	Thr	Ile	Ser	Thr	His	Gly	Ala	Leu	Ser	Glu	Ser	Ser	Ser	Val	Ser	
				835						840				845		
caa	caa	gct	tct	gag	att	act	agc	tca	atc	aat	gca	aca	gct	tcc	gaa	2592
Gln	Gln	Ala	Ser	Glu	Ile	Thr	Ser	Ser	Ile	Asn	Ala	Thr	Ala	Ser	Glu	
				850						855				860		
tac	cat	agc	atc	cag	aca	acc	gag	gct	act	caa	tcc	aca	act	cta	tct	2640
Tyr	His	Ser	Ile	Gln	Thr	Thr	Ala	Ala	Thr	Gln	Ser	Thr	Thr	Leu	Ser	
865				870						875				880		
ttt	acc	gac	gca	aac	agc	agt	tct	gct	tcc	gct	cca	tgg	gaa	gtg	gaa	2688
Phe	Thr	Asp	Ala	Asn	Ser	Ser	Ser	Ala	Ser	Ala	Pro	Leu	Glu	Val	Ala	
				885						890				895		
acg	tct	acg	cca	acc	cca	tct	tca	aaq	gca	tcc	tct	ctg	tgg	ctt	aca	2736
Thr	Ser	Thr	Pro	Thr	Pro	Ser	Ser	Lys	Ala	Ser	Ser	Leu	Leu	Leu	Thr	
				900						905				910		
cca	tca	aca	tcc	tct	tta	agt	cag	gtt	gct	aca	aat	act	aat	gtc	cag	2784
Pro	Ser	Thr	Ser	Ser	Leu	Ser	Gln	Val	Ala	Thr	Asn	Thr	Asn	Val	Gln	
				915						920				925		
acg	agt	tta	aca	acg	gaa	tgg	acg	acc	gtt	tta	gaa	cca	tca	acg	act	2832
Thr	Ser	Leu	Thr	Thr	Glu	Ser	Thr	Thr	Val	Leu	Glu	Pro	Ser	Thr	Thr	
				930						935				940		
aac	agt	tcc	agt	acg	ttt	agt	ctg	gtc	act	tca	agt	gac	aac	aat	tgg	2880
Asn	Ser	Ser	Ser	Thr	Phe	Ser	Leu	Val	Thr	Ser	Ser	Asp	Asn	Asn	Tyr	

945	950	955	960	
tgg att cca act gag tta atc acg cag gca cca gaa gct gca tcc acc				2928
Trp Ile Pro Thr Glu Leu Ile Thr Glu Ala Pro Glu Ala Ala Ser Thr				
	965	970	975	
gca tct tct acc gtt gga gga aca caa acg atg act ttg ccc cag gca				2975
Ala Ser Ser Thr Val Gly Gly Thr Glu Thr Met Thr Leu Pro His Ala				
	980	985	990	
att gca gcc gag aca caa gtc ccc gag cct gag ggc tac acc cta atc				3024
Ile Ala Ala Ala Thr Glu Val Pro Glu Pro Glu Gly Tyr Thr Leu Ile				
995	1000	1005		
aca ata ggg ttc aca aaa gct ttg aac tac gaa ttt gtt gta tca				3069
Thr Ile Gly Phe Lys Lys Ala Leu Asn Tyr Glu Phe Val Val Ser				
1010	1015	1020		
gaa cca aca tca tgg gct caa atc ttc gga tac ttg cct gaa gct				3114
Glu Pro Lys Ser Ser Ala Glu Ile Phe Gly Tyr Leu Pro Glu Ala				
1025	1030	1035		
ctg aac aca cct ttt aag aac gta ttc aca aac att acg gta cta				3159
Leu Asn Thr Pro Phe Lys Asn Val Phe Thr Asn Ile Thr Val Leu				
1040	1045	1050		
caa ata gtg ccc tta cag gat gac tca atc aac tac tta gla agt				3204
Gln Ile Val Pro Leu Glu Asp Asp Ser Leu Asn Tyr Leu Val Ser				
1055	1060	1065		
gtt gct gaa gta tac ttt cca act gca gaa ata gag gag ctg tca				3249
Val Ala Glu Val Tyr Phe Pro Thr Ala Glu Ile Glu Glu Leu Ser				
1070	1075	1080		
aat cta att acg aac tct tca agc gct ttt tac acg gat gga atg				3294
Asn Leu Ile Thr Asn Ser Ser Ser Ala Phe Tyr Thr Asp Gly Met				
1085	1090	1095		
ggc aca gca aca tct atg gct gca atg gtt gat tcc tca ata cgc				3339
Gly Thr Ala Lys Ser Met Ala Ala Met Val Asp Ser Ser Ile Pro				
1100	1105	1110		

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Leu Thr Gly Leu Leu His Asp Ser Asn Ser Asn Ser Gly Gly Ser	
1115 1120 1125	
tcg gac gga tcc tcc tcc agt aat tgg aac tca gga tct tca ggt	3429
Scr Asp Gly Ser Ser Ser Scr Asn Ser Asn Ser Gly Ser Ser Gly	
1130 1135 1140	
tca gga tct aat tgg aac tcc ggt gtg tct tca tct tcc gga aat	3474
Ser Gly Ser Asn Ser Asn Ser Gly Val Ser Ser Ser Ser Gly Asn	
1145 1150 1155	
tcc tac cca gat gcc ggt aat ttg gaa tat tca tcc aaa tct aac	3519
Ser Tyr Gln Asp Ala Gly Thr Leu Glu Tyr Ser Ser Lys Ser Asn	
1160 1165 1170	
tcc aac gta tcc aat tct agc aaa tca aag aaa aaa atc aat ggt	3564
Ser Asn Val Ser Thr Ser Ser Lys Ser Lys Lys Lys Ile Ile Gly	
1175 1180 1185	
tta gtt atc ggc gtt gtt gtt ggt gga tgc tta tct att tta ttc	3603
Leu Val Ile Gly Val Val Val Gly Gly Cys Leu Tyr Ile Leu Phe	
1190 1195 1200	
atg att ttt gct ttc aag tat atc ata aga agg agg aat cca agt	3654
Met Ile Phe Ala Phe Lys Tyr Ile Ile Arg Arg Arg Ile Gln Ser	
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caa gaa att atc aag aac cca gaa att tcc agt atc agt tca agt	3699
Gln Glu Ile Ile Lys Asn Pro Glu Ile Ser Ser Ile Ser Ser Ser	
1220 1225 1230	
gaa ttt ggt gga gag aaa aat tac aat aat gaa aag aga atg agc	3744
Glu Phe Gly Gly Glu Lys Asn Tyr Asn Asn Glu Lys Arg Met Ser	
1235 1240 1245	
ggt caa gaa tcc ata aca caa tct atg cga att caa aat tgg atg	3789
Val Gln Glu Ser Ile Thr Gln Ser Met Arg Ile Gln Asn Trp Met	
1250 1255 1260	
gat gat agt tac tat ggt ccc ggg ttg aca aat aat gac tca act	3834
Arg Arg Ser Tyr Tyr Gly His Gly Leu Thr Asn Asn Asp Ser Thr	

1265	1270	1275	
cca acc agy cac aat ada tgg agt tcc ata cca aac att taa aga			2870
Pro Thr Arg His Asn Thr Ser Ser Ser Ile Pro Lys Ile Ser Arg			
1280	1285	1290	
cca att gct ago caa aac tcc ctg ggt tgg aac gaa gtt tga			2871
Pro Ile Ala Ser Gln Asn Ser Leu Gly Trp Asn Glu Val			
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20	25	30	
Gln Gln Ala Gln Ser Gln Ser Glu Ser Gln Gly Ala Val Ser Phe Thr			
35	40	45	
Asn Glu Ala Ser Gln Asp Ser Ser Thr Phe Ser Leu Val Thr Ala Tyr			
50	55	60	
Ser Gln Gly Val His Ser His Gln Ser Ala Thr Ile Val Ser Ala Thr			
65	70	75	80
Ile Ser Ser Leu Pro Ser Thr Trp Tyr Asp Ala Ser Ser Thr Ser Gln			
85	90	95	
Thr Ser Val Ser Tyr Ala Ser Gln Gln Ser Asp Tyr Ala Val Asn Gln			
100	105	110	
Asn Ser Trp Ser Ala Ser Thr Asn Gln Leu Pro Ser Thr Ser Thr Thr			
115	120	125	

Ser Tyr Tyr Ala Pro Thr Phe Ser Thr Ser Ala Asp Phe Ala Ala Ser
 130 135 140

Ser Val Asn Ala Ala Ser Asp Val Ser Thr Ala Ser Val Pro Ile Asp
 145 150 155 160

Thr Ser Ala Asn Ser Ile Pro Phe Thr Thr Thr Ser Asn Ile Glu Thr
 165 170 175

Thr Thr Ser Ala Pro Leu Thr Ser Asp Thr Pro Leu Ile Ser Thr Ser
 180 185 190

Thr Met Ser Ala Ala Asp Asn Val Phe Ser Ser Ala Asn Pro Ile Ser
 195 200 205

Ala Ser Leu Thr Thr Thr Asp Ser Ser Glu Ser Phe Asp Glu Thr Ser
 210 215 220

Thr Ala Gly Ala Ile Pro Val Gln Ser Ser Ala Asp Phe Ser Ser Ser
 225 230 235 240

Ser Glu Ile Leu Val Gln Ser Ser Ala Asp Phe Ser Ser Pro Ser Ser
 245 250 255

Pro Thr Thr Thr Asp Ile Ser Leu Ser Ala Ala Pro Leu Gln Thr Ser
 260 265 270

Glu Ser Ser Ser Phe Thr Thr Ala Ser Ala Ala Leu Pro Val Ser Ser
 275 280 285

Thr Asp Val Asp Gly Ser Ser Ala Ser Pro Val Val Ser Met Ser Ala
 290 295 300

Ala Gly Gln Ile Ala Ser Ser Ser Ser Thr Asp Asn Pro Thr Met Ser
 305 310 315 320

Glu Thr Phe Ser Leu Thr Ser Thr Glu Val Asp Gly Ser Asp Val Ser
 325 330 335

Ser Thr Val Ser Ala Leu Leu Ser Ala Pro Phe Leu Gln Thr Ser Thr
 340 345 350

Ser Asn Ser Phe Ser Ile Val Ser Pro Ser Val Ser Phe Val Pro Ser
 355 360 365

Gln Ser Ser Ser Asn Val Ala Ser Ser Ser Thr Ala Asn Val Val Ser
 370 375 380

Ser Ser Phe Ser Asp Ile Pro Pro Gln Thr Ser Thr Ser Gly Ser Val
 385 390 395 400

Val Ser Val Ala Gln Ser Ala Ser Ala Leu Ala Phe Gln Ser Ser Thr
 405 410 415

Glu Val Tyr Gly Ala Ser Ala Ser Ser Thr Met Ser Ser Leu Leu Ser
 420 425 430

Thr Thr Ser Leu Gln Ser Thr Thr Leu Asp Ser Ser Ser Leu Ala Ser
 435 440 445

Ser Ser Ala Ser Ser Ser Asp Leu Thr Asp Tyr Cys Val Ser Ser Thr
 450 455 460

Ala Ser Ile Pro Leu Leu Ser Ala Ser Glu Gln Ala Ser Thr Ser Ser
 465 470 475 480

Ser Phe Ser Val Val Ser Pro Ser Val Ser Phe Val Pro Ser Gln Ser
 485 490 495

Ser Ser Asp Val Ala Ser Thr Ser Ala Pro Ser Val Val Ser Ser Ser
 500 505 510

Phe Ser Tyr Thr Ser Leu Gln Ala Gly Gly Ser Ser Met Thr Asn Pro
 515 520 525

Ser Ser Ser Thr Ile Val Tyr Ser Ser Ser Thr Gly Ser Ser Glu Glu
 530 535 540

Ser Ala Ala Ser Thr Ala Ser Ala Thr Leu Ser Gly Ser Ser Ser Thr
 545 550 555 560

Tyr Met Ala Gly Asn Leu Gln Ser Gln Pro Pro Ser Thr Ser Ser Leu
 565 570 575

Leu Ser Glu Ser Gln Ala Thr Ser Thr Ser Ala Val Leu Ala Ser Ser
530 585 590

Ser Val Ser Thr Thr Ser Pro Tyr Thr Thr Ala Gly Gly Ala Ser Thr
595 600 605

Glu Ala Ser Ser Leu Ile Ser Ser Thr Ser Ala Glu Thr Ser Gln Val
610 615 620

Ser Tyr Ser Gln Ser Thr Thr Ala Leu Gln Thr Ser Ser Phe Ala Ser
625 630 635 640

Ser Ser Thr Thr Glu Gly Ser Glu Thr Ser Ser Gln Gly Phe Ser Thr
645 650 655

Ser Ser Val Leu Val Gln Met Pro Ser Ser Ile Ser Ser Glu Phe Ser
660 665 670

Pro Ser Gln Thr Thr Thr Gln Met Asn Ser Ala Ser Ser Ser Ser Gln
675 680 685

Tyr Thr Ile Ser Ser Thr Gly Ile Leu Ser Glu Val Ser Asp Thr Ser
690 695 700

Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp Thr
705 710 715 720

Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp
725 730 735

Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser
740 745 750

Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val
755 760 765

Ser Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln
770 775 780

Val Ser Asp Thr Ser Val Pro Ser Thr Ser Ser Arg Ser Ser Val Ser
785 790 795 800

Glu Val Ser Asp Thr Pro Val Pro Ser Thr Ser Ser Arg Ser Ser Val
805 810 815

Ser Gln Thr Ser Ser Ser Leu Gln Pro Thr Thr Thr Ser Ser Gln Arg
820 825 830

Phe Thr Ile Ser Thr His Gly Ala Leu Ser Glu Ser Ser Ser Val Ser
835 840 845

Gln Gln Ala Ser Glu Ile Thr Ser Ser Ile Asn Ala Thr Ala Ser Glu
850 855 860

Tyr His Ser Ile Gln Thr Thr Ala Ala Thr Cln Ser Thr Thr Leu Ser
865 870 875 880

Phe Thr Asp Ala Asn Ser Ser Ser Ala Ser Ala Pro Leu Glu Val Ala
885 890 895

Thr Ser Thr Pro Thr Pro Ser Ser Lys Ala Ser Ser Leu Leu Leu Thr
900 905 910

Pro Ser Thr Ser Ser Leu Ser Gln Val Ala Thr Asn Thr Asn Val Gln
915 920 925

Thr Ser Leu Thr Thr Glu Ser Thr Thr Val Leu Glu Pro Ser Thr Thr
930 935 940

Asn Ser Ser Ser Thr Phe Ser Leu Val Thr Ser Ser Asp Asn Asn Trp
945 950 955 960

Trp Ile Pro Thr Glu Leu Ile Thr Glu Ala Pro Glu Ala Ala Ser Thr
965 970 975

Ala Ser Ser Thr Val Gly Gly Thr Gln Thr Met Thr Leu Pro His Ala
980 985 990

Ile Ala Ala Ala Thr Gln Val Pro Glu Pro Glu Gly Tyr Thr Leu Ile
995 1000 1005

Thr Ile Gly Phe Lys Lys Ala Leu Asn Tyr Glu Phe Val Val Ser
1010 1015 1020

Gln Pro	Lys Ser Ser Ala Gln	Ile Phe Gly Tyr Leu	Pro Glu Ala
1023	1030	1035	
Leu Asn	Thr Pro Phe Lys Asn	Val Phe Thr Asn Ile	Thr Val Leu
1040	1045	1050	
Gln Ile	Val Pro Leu Gln Asp	Asp Ser Leu Asn Tyr	Leu Val Ser
1055	1060	1065	
Val Ala	Glu Val Tyr Phe Pro	Thr Ala Glu Ile Glu	Glu Leu Ser
1070	1075	1080	
Asn Leu	Ile Thr Asn Ser Ser	Ser Ala Phe Tyr Thr	Asp Gly Met
1085	1090	1095	
Gly Thr	Ala Lys Ser Met Ala	Ala Met Val Asp Ser	Ser Ile Pro
1100	1105	1110	
Leu Thr	Gly Leu Leu His Asp	Ser Asn Ser Ser Ser	Gly Gly Ser
1115	1120	1125	
Ser Asp	Gly Ser Ser Ser Ser	Asn Ser Asn Ser Gly	Ser Ser Gly
1130	1135	1140	
Ser Gly	Ser Asn Ser Asn Ser	Gly Val Ser Ser Ser	Ser Gly Asn
1145	1150	1155	
Ser Tyr	Gln Asp Ala Gly Thr	Leu Glu Tyr Ser Ser	Lys Ser Asn
1160	1165	1170	
Ser Asn	Val Ser Thr Ser Ser	Lys Ser Lys Lys Lys	Ile Ile Gly
1175	1180	1185	
Leu Val	Ile Gly Val Val Val	Gly Gly Cys Leu Tyr	Ile Leu Phe
1190	1195	1200	
Met Ile	Phe Ala Phe Lys Tyr	Ile Ile Arg Arg Arg	Ile Gln Ser
1205	1210	1215	
Gln Glu	Ile Ile Lys Asn Pro	Glu Ile Ser Ser Ile	Ser Ser Ser
1220	1225	1230	

Glu Phe Gly Gly Glu Lys Asn Tyr Asn Asn Glu Lys Arg Met Ser
1235 1240 1245

Val Gln Glu Ser Ile Thr Gln Ser Met Arg Ile Gln Asn Trp Met
1250 1255 1260

Asp Asp Ser Tyr Tyr Gly His Gly Leu Thr Asn Asn Asp Ser Thr
1265 1270 1275

Pro Thr Arg His Asn Thr Ser Ser Ser Ile Pro Lys Ile Ser Arg
1280 1285 1290

Pro Ile Ala Ser Gln Asn Ser Leu Gly Trp Asn Glu Val
1295 1300 1305

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<211> 315

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(315)

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Met Lys Phe Leu Lys Asn Lys Ala Pro Ala Asn Leu Val Asp Asn Gly
1 5 10 15

agg ttt gtg gaa gca ata acg tgc aat aca gtt aac cag aat cca tct 36
Arg Phe Val Gly Ala Ile Thr Cys Asn Lys Val Lys Pro Asn Pro Ser
20 25 30

tgc gtc tcc aac tgc ctg aaa ttt att tcc gaa gtt tta gcg gta gaa 144
Cys Val Ser Asn Cys Leu Lys Phe Leu Ser Glu Val Leu Ala Val Glu
35 40 45

gca ata aat gat tgg gcc aga aat tta gct acg gtt tcc aaa tgg gac 192
Ala Ile Thr Asp Ser Ala Arg Asn Leu Ala Thr Val Ser Lys Ser Asp
50 55 60

alu ala ala ttt tct att cta caa ttg agt agc aat aaa cag agc ggg 240
 tta leu leu phe ser leu leu glu leu ser ser asn lys gln ser gly
 65 70 75 80

tcc tct ttg cca att ttt gat att ggg ttt ata ata att toa act ttt 288
 ser ser leu pro leu phe asp leu val phe ile leu leu ser thr phe
 85 90 95

ttt tta ttc cat aat ccc tgc aat tga 315
 phe leu phe his asn pro cys asn
 100

<210> 8
 <211> 104
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 8

Met Lys Phe Leu Lys Asn Lys Ala Pro Ala Asn Leu Val Asp Asn Gly
 1 5 10 15

Arg Phe Val Glu Ala Ile Thr Cys Asn Lys Val Lys Pro Asn Pro Ser
 20 25 30

Cys Val Ser Asn Cys Leu Lys Phe Leu Ser Glu Val Leu Ala Val Glu
 35 40 45

Ala Ile Thr Asp Ser Ala Arg Asn Leu Ala Thr Val Ser Lys Ser Asp
 50 55 60

Ile Leu Leu Phe Ser Leu Leu Gln Leu Ser Ser Asn Lys Gln Ser Gly
 65 70 75 80

Ser Ser Leu Pro Leu Phe Asp Leu Val Phe Ile Leu Leu Ser Thr Phe
 85 90 95

Phe Leu Phe His Asn Pro Cys Asn

100

<210> 9

<211> 2064

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2064)

<400> 9

atg tgc gcc agt tta aac gag gta aca aag aat gac acc tat ggg gtc 48
Met Cys Ala Ser Leu Asn Glu Val Lys Lys Asn Asp Thr Tyr Gly Val

1

5

10

15

tca caa aag ggc tac aat gac aat tta agt gaa aat gac ggc gta aat 96
Ser Glu Lys Gly Tyr Asn Asp Asn Phe Ser Glu Ser Glu Gly Val Leu

20

25

30

cat ggt agt aag tct atg acc act agc atg aca aat atg cta cag tct 144
His Gly Ser Lys Ser Met Pro Thr Ser Met Lys Asn Met Leu Glu Ser

35

40

45

ccc atg atg gtc aac atg tgt gat att tta caa aac aag gaa got got 192
Pro Thr Met Val Asn Met Cys Asp Ile Leu Glu Asn Lys Glu Ala Ala

50

55

60

aat gac gaa aca cct gtg ata cct act aag gat acc gcc act gag ggg 240
Asn Asp Glu Lys Pro Val Ile Pro Thr Thr Asp Thr Ala Thr Ala Gly

65

70

75

80

act ggt act gaa gat att agc tcc act caa tcc gag gaa act gat aag 288
Thr Gly Thr Glu Asp Ile Ser Ser Thr Glu Ser Glu Glu Thr Asp Glu

85

90

95

aat agt cat att att gcc tca gag ata ttg gaa ggc act ttc aca gat 336
Asn Ser His Leu Ile Ala Ser Glu Ile Leu Glu Gly Thr Phe Lys Asp

100

105

110

gta tct tac aag gaa tat gca aat ttc l-g gga aac gac aac aat aat	384
Val Ser Tyr Lys Glu Tyr Ala Asu Phe Leu Gly Asn Asp Asn Asn Asn	
115 120 125	
caa gtc ttg aat gag ttt gta aag tta ttg agt cct ttg cag tog lua	432
Gln Val Leu Thr Glu Phe Val Lys Leu Leu Ser Pro Ieu Pro Ser Ser	
130 135 140	
cta tta gaa aag ctt ttc aat lla tgg aaa agt ata tat ttc att gca	480
Leu Leu Glu Thr Leu Phe Asn Leu Ser Lys Ser Ile Tyr Phe Ile Ala	
145 150 155 160	
gaa gag caa aat atc gac cgg ala cta gag lyc lly agc ala gaa tgg	528
Glu Ala Gln Asn Ile Asp Arg Ile Leu Glu Cys Leu Ser Ile Glu Trp	
165 170 175	
ata gct tgc cac cag cac cca cct tgg aag tca ggc tat aag tca tgl	576
Ile Ala Cys His Pro Asn Thr His Trp Lys Ser Gly Tyr Lys Ser Cys	
180 185 190	
cct ata gtc tta ttt tcc ctg ttg atc ctt aat tgg gat ttg cac aac	624
His Ile Val Leu Phe Ser Leu Leu Ile Leu Asu Ser Asp Leu His Asn	
195 200 205	
aaa ttt caa gtt gac cat aaa aag att aag ttt tcc atg gtt gca ttt	672
Asn Phe Gln Val Asp His Lys Lys Ile Lys Phe Ser Met Val Ala Phe	
210 215 220	
atc aac aat aca cly agg gaa cta aya gag gaa ant gaa tac gaa gaa	720
Ile Asn Asn Thr Leu Arg Ala Leu Arg Glu Glu Asn Gln Tyr Gln Gln	
225 230 235 240	
ttg aaa ata tac tcc cgc gaa cct lly atc atc gaa gaa ctt tcc gaa	768
Leu Lys Ile Tyr Ser Arg Glu His Leu Ile Ile Glu Glu Leu Ser Glu	
245 250 255	
taa tat aaa aag tta aat gaa aag cct tta cag tta tgc aca gaa tct	816
Tyr Tyr Lys Thr Leu Asn Glu Thr Pro Leu Pro Leu Cys Thr Glu Ser	
260 265 270	

aga aca tca ata aat ata tca gat aac caa tct tcc ttg aaa agg ttc	864
Arg Thr Ser Ile Asn le Ser Asp Asn Gln Ser Ser Leu Lys Arg Phe	
275 280 285	
tct act cta gga tca cgg gaa ttt agt aca tca aat tta cgt agt gtt	912
Ser Thr Leu Gly Ser Arg Glu Phe Ser Thr Ser Asn Leu Arg Ser Val	
290 295 300	
aac tct aat lol act aca ata tat tca aga gat ggt caa gta tct gta	960
Asn Ser Asn Ser Thr Thr Leu Tyr Ser Arg Asp Gly Gln Val Ser Val	
305 310 315 320	
cga gaa atg agc gcu aaa tca aat aaa acc ttt cac aat aat caa ccc	1008
Arg Glu Met For Ala Lys Ser Asn Lys Asn Phe His Asn Asn His Pro	
325 330 335	
atg gat gaa ctc tac ctt aaa gag tct ttt gat gac ggt tta aat acc	1056
Met Asp Ala Leu Tyr Leu Lys Glu Ser Phe Asp Asp Gly Leu Ile Thr	
340 345 350	
gaa aac ggc tcc agt tgg tlu atg gat gat tta att ctt ata agc aag	1104
Gln Asn Gly Ser Ser Trp Phe Met Asp Asp Leu Ile Leu Ile Ser Lys	
355 360 365	
aaa ttt tta cca cgt aca tat tct aac agc gac aac gat caa gtc ggc	1152
Lys Ser Leu Pro Arg Lys Tyr Ser Lys Arg Asp Lys Asp Gln Val Ala	
370 375 380	
gca cca aaa atg acc tct aag aga aac aaa tcc ttc ttc gga tgg cta	1200
Ala Pro Lys Met Thr Ser Lys Arg Asn Lys Ser Phe Phe Gly Trp Leu	
385 390 395 400	
aaa cca tct aaa acg act aca ctt att gag cac aca tct aga agg act	1248
Lys Pro Ser Lys Thr Thr Thr Leu Ile Glu His Thr Ser Arg Arg Thr	
405 410 415	
tct tta tgg tat ttg aat ang gat tct gaa tgg gag agn gtc aaa ata	1296
Ser Leu Ser Tyr Leu Asn Lys Asp Ser Glu Trp Glu Arg Val Lys Ile	
420 425 430	

cag gtc aag gag ggc aga att ttt att ttc aaa att aaa cca gat ggt	1344
Gln Val Lys Glu Gly Arg Ile Phe Ile Phe Lys Ile Lys Pro Asp Val	
435 440 445	
aag gat atc atc caa tca agt gaa aca gac agt gct acc atc gac tat	1392
Lys Asp Ile Ile Gln Ser Ser Glu Thr Asp Ser Ala Thr Ile Asp Tyr	
450 455 460	
ttc aaa gat atc agt agc tct tat ttt gct tac tca ctg ctt gaa gct	1440
Phe Lys Asp Ile Ser Ser Ser Tyr Phe Ala Tyr Ser Leu Leu Glu Ala	
465 470 475 480	
gaa gca cat gtc gtg caa gat aat ata att ata ggt agt gga gca atg	1488
Glu Ala His Val Val Gln Asp Asn Ile Ile Ile Gly Ser Gly Ala Met	
485 490 495	
aaa tca aat gtg tgt aac aaa aac acc aag agg aaa agt ggc aac LL	1536
Lys Ser Asn Val Cys Asn Lys Asn Thr Lys Arg Lys Ser Gly Asn Phe	
500 505 510	
acc gtt agt ttt ccc gag aat atc aac gga ccc aag ctt gtt ctg gag	1584
Thr Val Ser Phe Pro Glu Asn Ile Asn Gly Pro Lys Leu Val Leu Glu	
515 520 525	
ttc cag acg aga agt gtt gca gca gcc ccc aag ttt atg gac tgt atc	1632
Phe Gln Thr Arg Ser Val Glu Glu Ala His Lys Phe Met Asp Cys Ile	
530 535 540	
aac ttc tgg gca ggt agg att tct cca gtt cct tta acc caa ttc gaa	1680
Asn Phe Trp Ala Gly Arg Ile Ser Pro Val Pro Leu Thr Gln Phe Glu	
545 550 555 560	
gcc gta tct aac gca gaa tac gga tgg agt gac aag atc ttg aca gag	1728
Ala Val Ser Asn Ala Glu Tyr Gly Trp Ser Asp Lys Ile Asn Thr Glu	
565 570 575	
cac gct tuc ctg aat ctt aaa aat att gtt gta agt gaa tgg aag cca	1776
His Ala Ser Leu Asn Leu Lys Asn Ile Val Val Ser Glu Trp Lys Pro	
580 585 590	
cta ttg ggg cta gag cta cta tac gaa gat ggg aaa gat gta gag atg	1824

Leu Leu Gly Leu Glu Leu Leu Tyr Glu Asp Ala Lys Asp Val Glu Met
 595 600 605

gtc gaa cta aaa gaa agg cta aag gaa ttg atg aac lio aca aga cag 1872
 Val Glu Leu Lys Glu Arg Leu Lys Glu Leu Met Asn Phe Thr Arg Gln
 610 615 620

ctt ggt ata tgg ata gac aaa cat aac gaa ata aag gat aag ctg gtc 1920
 Leu Gly Ile Trp Ile Asp Lys His Asn Glu Ile Lys Asp Lys Leu Val
 625 630 635 640

gaa att tgg agc ttt gac gat aac tat ttt gaa gca gtc atg aat aat 1968
 Glu Ile Trp Ser Phe Asp Asp Asn Tyr Phe Glu Ala Val Met Asn Asn
 645 650 655

tgg aat tog aga tat ttg tat atg aat aac tat aag aca cga ctg 2016
 Trp Asn Ser Arg Tyr Leu Tyr Met Asn Asn Glu Tyr Lys Lys Arg Leu
 660 665 670

agc tac ttg aaa got ttg caa aaa gcc atg ggt tct gtt cag ttc taa 2064
 Ser Tyr Leu Lys Ala Leu Glu Lys Ala Met Gly Ser Val Glu Phe
 675 680 685

<210> 10
 <211> 687
 <212> FRT
 <213> *Saccharomyces cerevisiae*
 <400> 10

Met Cys Ala Ser Leu Asn Glu Val Lys Lys Asn Asp Thr Tyr Gly Val
 1 5 10 15

Ser Glu Lys Gly Tyr Asn Asp Asn Phe Ser Glu Ser Glu Gly Val Leu
 20 25 30

His Gly Ser Lys Ser Met Pro Thr Ser Met Lys Asn Met Ser Glu Ser
 35 40 45

Pro Thr Met Val Asn Met Cys Asp Ile Leu Glu Asn Lys Glu Ala Ala

50	55	60	
Asn Asp Glu Iyo Pro Val Ile Pro Thr Tar Asp Thr Ala Tar Ala Gly			
65	70	75	80
Thr Gly Thr Glu Asp Ile Ser Ser Thr Gln Ser Glu Glu Tar Asp Glr			
	85	90	95
Asn Ser His Leu Ile Ala Ser Glu Ile Leu Glu Gly Thr Phe Lys Asp			
100	105	110	
Val Ser Tyr Lys Glu Tyr Ala Asn Phe Leu Gly Asn Asp Asn Asn Asn			
115	120	125	
Gln Val Leu Thr Glu Phe Val Lys Leu Leu Ser Pro Leu Pro Ser Ser			
130	135	140	
Leu Leu Glu Thr Leu Phe Asn Leu Ser Lys Ser Ile Tyr Phe Ile Ala			
145	150	155	160
Glu Ala Gln Asn Ile Asp Arg Le Asn Glu Cys Leu Ser Ile Glu Tyr			
165	170	175	
Ile Ala Cys His Pro Asn Thr His Trp Lys Ser Gly Tyr Lys Ser Cys			
180	185	190	
His Ile Val Leu Phe Ser Leu Leu Ile Leu Asn Ser Asp Leu His Asn			
195	200	205	
Asn Phe Gln Val Asp His Lys Lys Ile Lys Phe Ser Met Val Ala Phe			
210	215	220	
Ile Asn Asn Tar Leu Arg Ala Leu Arg Glu Glu Asn Glu Tyr Glu Glu			
225	230	235	240
Leu Lys Ile Tyr Ser Arg Glu His Leu Ile Ile Glu Glu Leu Ser Glu			
245	250	255	
Tyr Tyr Lys Thr Leu Asn Glu Thr Pro Leu Pro Leu Cys Thr Glu Ser			
260	265	270	
Arg Thr Ser Ile Asn Ile Ser Asp Asn Gln Ser Ser Leu Lys Arg Phe			

275	280	285
Ser Thr Leu Gly Ser Arg Glu Phe Ser Thr Ser Asn Leu Arg Ser Val		
290	295	300
Asn Ser Asn Ser Thr Thr Leu Tyr Ser Arg Asp Gly Gln Val Ser Val		
305	310	315
Arg Glu Met Ser Ala Lys Ser Asn Lys Asn Phe His Asn Asn His Pro		
325	330	335
Met Asp Ala Leu Tyr Leu Lys Glu Ser Phe Asp Asp Gly Leu Ile Thr		
340	345	350
Glu Asn Gly Ser Ser Trp Phe Met Asp Asp Leu Ile Leu Ile Ser Lys		
355	360	365
Lys Ser Leu Pro Arg Lys Tyr Ser Lys Arg Asp Lys Asp Gln Val Ala		
370	375	380
Ala Pro Lys Met Thr Ser Lys Arg Asn Lys Ser Phe Lys Gly Tyr Leu		
385	390	395
Lys Pro Ser Lys Thr Thr Thr Leu Ile Glu His Thr Ser Arg Arg Thr		
405	410	415
Ser Leu Ser Tyr Leu Asn Lys Asp Ser Glu Trp Glu Arg Val Lys Ile		
420	425	430
Gln Val Lys Glu Gly Arg Ile Phe Ile Phe Lys Ile Lys Pro Asp Val		
435	440	445
Lys Asp Ile Ile Gln Ser Ser Glu Thr Asp Ser Ala Thr Ile Asp Tyr		
450	455	460
Phe Lys Asp Ile Ser Ser Ser Tyr Phe Ala Tyr Ser Leu Leu Gln Ala		
465	470	475
Glu Ala His Val Val Gln Asp Asn Ile Ile Ile Gly Ser Gly Ala Met		
485	490	495
Lys Ser Asn Val Cys Asn Lys Asn Thr Lys Arg Lys Ser Gly Asn Phe		

500

595

510

Thr Val Ser Phe Pro Glu Asn Ile Asn Gly Pro Lys Leu Val Leu Glu
515 520 525

Phe Gln Thr Arg Ser Val Glu Glu Ala His Lys Phe Met Asp Cys Ile
530 535 540

Asn Phe Trp Ala Gly Arg Ile Ser Pro Val Pro Leu Thr Gln Phe Glu
545 550 555 560

Ala Val Ser Asn Ala Glu Tyr Gly Trp Ser Asp Lys Ile Leu Thr Glu
565 570 575

His Ala Ser Leu Asn Leu Lys Asn Ile Val Val Ser Glu Trp Lys Pro
580 585 590

Leu Leu Gly Leu Glu Leu Leu Tyr Glu Asp Ala Lys Asp Val Glu Met
595 600 605

Val Glu Leu Lys Glu Arg Leu Lys Glu Leu Met Asn Phe Thr Arg Gln
610 615 620

Leu Gly Ile Trp Ile Asp Lys His Asn Glu Ile Lys Asp Lys Leu Val
625 630 635 640

Glu Ile Trp Ser Phe Asp Asp Asn Tyr Phe Glu Ala Val Met Asn Asn
645 650 655

Trp Asn Ser Arg Tyr Leu Tyr Met Asn Asn Gln Tyr Lys Lys Arg Leu
660 665 670

Ser Tyr Leu Lys Ala Leu Gln Lys Ala Met Gly Ser Val Gln Phe
675 680 685

<210> 11

<211> 678

<212> DNA

<213> *Saccharomyces cerevisiae*

2.2.02

<221> CDS

<222> (1) . . (678)

<400> 11

atg gtc gta att aac ggg gtc aaa tat gcc tgt gaa acg tgt alc agg 48
Met Val Val Ile Asn Gly Val Lys Tyr Ala Cys Glu Thr Cys Ile Arg
1 5 10 15

ggc cac agg ggc ggc cag tgt act cac act gat ggt cag cta cag atg 36
Gly His Arg Ala Ala Gln Cys Thr His Thr Asp Gly Pro Leu Gln Met.
20 25 30

atc aga cgc aag gga aga uca fag acc aca tgt ggc cat tgt aaa gag 144
Ile Arg Arg Lys Gly Arg Pro Ser Phe Thr Cys Gly His Cys Lys Glu
35 40 45

ctg aga aga aac aag aac ttc aac cca tcc ggt ggg tgc atg tgl gcc 192
Leu Arg Arg Thr Lys Asn Phe Asn Pro Ser Gly Gly Cys Met Cys Ala
50 55 60

tct gca cga cgg cca gct gll ggc agc aag gaa gat gaa aca cga tgt 240
 ser ala arg arg pro ala val gly ser lys glt asp glu thr arg cys
 65 70 75 80

cgt tgt gnt gag ggt gaa cct tgt aaatgt cat acc aag agg naa aqc 288
Arg Tyr Asp Glu Gly Ala Pro Cys Lys Cys His Thr Leu Arg Lys Ser

95 90 85

GGU GGG AAA CCA AAG GGA GGG TCA TGC CAC AGA GYG GYA UUT GAT GAA 336
 Ser Arg Lys Ser Lys Gly Gly Ser Cys His Arg Arg Ala Asn Asp Glu
 100 105 110

gca ggc cat gtc aac ggt ctc ggt att gca gat ctg gac gtt ctt ttg 384
Ala Ala His Val Asn Gly Leu Gly Ile Ala Asp Leu Asp Val Leu Leu
115 220 325

990 gta aat ggt cgc tgc tgc gat gta gar atg aca acc aca ttg ccc 432
 Gly Leu Asn Gly Arg Ser Ser Asp Val Asp Met Thr Thr Thr Leu Phe
 120 135 140

agt ttg aaq cca cct ctg caa aac gga gaa att aag gcc gac agc att	480
Ser Leu Lys Pro Pro Leu Gln Asn Gly Gln Ile Lys Ala Asp Ser Ile	
145 150 155 160	

gac aat ctt gat ttg gct tcc ctc gat ccg ctt gag caa agc cct agt	528
Asp Asn Leu Asp Leu Ala Ser Leu Asp Pro Ser Glu Gln Ser Pro Ser	

165	170	175
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ata tct atg gaa cct gtt agt atc aat gaa aca gga agc gca tat aca	576
Ile Ser Met Glu Pro Val Ser Ile Asn Glu Thr Gly Ser Ala Tyr Thr	
180 185 190	

act acg aac aca gca cta aac gat att gac att cca ttc tcc atc aat	624
Thr Thr Asn Thr Ala Leu Asn Asp Ile Asp Ile Pro Phe Ser Ile Asn	
195 200 205	

gag ttg aac gag cta tac aaa caa gta tct tcg cat aac tca cat tca	672
Glu Ser Asn Glu Leu Tyr Lys Gln Val Ser Ser His Asn Ser His Ser	
210 215 220	

caa tca	678
Gln	
525	

<210> 12
 <211> 225
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 12

Met Val Val Ile Asn Gly Val Lys Tyr Ala Cys Glu Thr Cys Ile Arg
1 5 10 15

Gly His Arg Ala Ala Gln Cys Thr His Thr Asp Gly Pro Leu Gln Met
20 25 30

Ile Arg Arg Lys Gly Arg Pro Ser Thr Thr Cys Gly His Cys Lys Glu
35 40 45

Leu Arg Arg Thr Lys Asn Phe Asn Pro Ser Gly Gly Cys Met Cys Ala
50 55 60

Ser Ala Arg Arg Pro Ala Val Gly Ser Lys Glu Asp Glu Thr Arg Cys
65 70 75 80

Arg Cys Asp Glu Gly Glu Pro Cys Lys Cys His Thr Lys Arg Lys Ser
85 90 95

Ser Arg Lys Ser Lys Gly Gly Ser Cys His Arg Arg Ala Asn Asp Glu
100 105 110

Ala Ala His Val Asn Gly Leu Gly Ile Ala Asp Leu Asp Val Leu Leu
115 120 125

Gly Leu Asn Gly Arg Ser Ser Asp Val Asp Met Thr Thr Thr Leu Pro
130 135 140

Ser Leu Lys Pro Pro Leu Gln Asn Gly Glu Ile Lys Ala Asp Ser Ile
145 150 155 160

Asp Asn Leu Asp Leu Ala Ser Leu Asp Pro Leu Glu Gln Ser Pro Ser
165 170 175

Ile Ser Met Glu Pro Val Ser Ile Asn Glu Thr Gly Ser Ala Tyr Thr
180 185 190

Thr Thr Asn Thr Ala Leu Asn Asp Ile Asp Ile Pro Phe Ser Ile Asn
195 200 205

Glu Leu Asn Glu Leu Tyr Lys Gln Val Ser Ser His Asn Ser His Ser
210 215 220

Gln

225

<210> 13

<211> 750

<212> RNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (750)

<400> 13

atg ttg cag cta agg ttt atg cct gga tgg gtc ccc aga aat ggt ttt 48

Met Leu Gln Leu Arg Phe Met Pro Gly Trp Val Pro Arg Asn Gly Phe

1 5 10 15

ttt ggt ttg aag gag aca att ggt aca gta cat aag aga ttt Lal gcl 96

Phe Gly Leu Lys Gln Thr Ile Gly Thr Val His Lys Arg Phe Tyr Ala

20 25 30

ctg gct tct gaa caa ccc tca aga aag aca gta aag ccc ctg gac tgg 144

Leu Ala Ser Glu Gln Pro Ser Arg Lys Thr Val Lys Pro Leu Asp Ser

35 40 45

agg aag aag ttt ctg atc gat aca tac aag cat tta atg gag aac agt 192

Arg Lys Thr Phe Leu Ile Asp Thr Tyr Lys His Leu Met Glu Asn Ser

50 55 60

tcl atg all ttt ttt gtc cat tac aat aat ctt tcc aaa aca gaa gat 240

Ser Met Ile Phe Phe Val His Tyr Asn Asn Leu Ser Lys Thr Glu Asp

65 70 75 80

cac cat ttc aga ttc aag att aaa cag aca gga ggg aax ulc aca aca 288

His His Phe Arg Phe Lys Ile Lys Gln Thr Gly Gly Lys Leu Thr Lys

85 90 95

gta aga aac aac ctg ttc gaa gtc tac ttg aga aat tog cat ctg ccc 336

Val Arg Asn Asn Leu Phe Glu Val Tyr Leu Arg Asn Ser His Leu Pro

100 105 110

gac cca tgt gga ttc gtc aag cgt aaa gag caa aac tgg aaa cat cca 384

Asp Pro Cys Gly Phe Val Lys Arg Lys Glu Gln Asn Trp Lys His Pro

115 120 125

ctc ttg cca cta ctg aag ggt cat aag gcc aca att aca tac gaa gac 432

Leu Leu Pro Leu Leu Lys Gly Pro Thr Ala Thr Ile Thr Tyr Glu Asp

130 135 140

acc aac aat caa caa gta gcc aag cta ttg aag gtt ctg cag tca gca 480
 Thr Asa Pro Gln Gln Val Ala Lys Leu Leu Lys Val Leu Gln Ser Ala
 145 150 155 160

caa gac aag ctg atg gtg att ggt gcc aaa gta gaa aac gaa gtt ttg 528
 Gln Asp Lys Leu Met Val Phe Gly Ala Lys Val Glu Asn Glu Val Leu
 165 170 175

aat gtg gaa aac ata aac aat ttt aag aat ctg ccc aca aag cag gaa 576
 Asn Val Gln Lys Ile Asn Thr Phe Lys Thr Leu Pro Thr Lys Pro Glu
 180 185 190

atg cag tgg aag tta gtc agc gtt ttg aca atg cta agt ggg ttg ggt 624
 Met Gln Ser Gln Leu Val Ser Val Leu Gln Met Leu Ser Gly Leu Gly
 195 200 205

ttg gtt cgt acg ttg gaa aac agt tca aat gca ttg tat tta aca cta 672
 Leu Val Arg Thr Leu Glu Asn Ser Ser Asn Ala Leu Tyr Leu Thr Leu
 210 215 220

aaa tat cac aat gac aac caa aac cct aaa gag gat gtg gag tca act 720
 Lys Ser His Asn Asp Asn Gln Lys Pro Lys Glu Asp Val Glu Ser Thr
 225 230 235 240

aca gat gcc gaa tgg aag gga tca aag taa 760
 Thr Asp Ala Glu Ser Lys Gly Ser Lys
 245

<210> 14

<211> 249

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 14

Met Leu Gln Leu Arg Phe Met Pro Gly Tyr Val Pro Arg Asn Gly Phe
 1 5 10 15

Phe Gly Leu Lys Glu Thr Ile Gly Thr Val His Lys Arg Phe Tyr Ala
 20 25 30

Leu Ala Ser Glu Gln Pro Ser Arg Lys Thr Val Lys Pro Leu Asp Ser
35 40 45

Arg Lys Thr Phe Leu Ile Asp Thr Tyr Lys His Leu Met Glu Asn Ser
50 55 60

Ser Met Ile Phe Phe Val His Tyr Asn Asn Leu Ser Lys Thr Glu Asp
65 70 75 80

His His Phe Arg Phe Lys Ile Lys Gln Thr Gly Gly Lys Leu Thr Lys
85 90 95

Val Arg Asn Asn Leu Phe Glu Val Tyr Leu Arg Asn Ser His Leu Pro
100 105 110

Asp Pro Cys Gly Phe Val Lys Arg Lys Glu Gln Asn Trp Lys His Pro
115 120 125

Leu Leu Pro Leu Leu Lys Gly Pro Thr Ala Thr Ile Thr Tyr Glu Asp
130 135 140

Thr Asn Pro Glu Gln Val Ala Lys Leu Leu Lys Val Leu Glu Ser Ala
145 150 155 160

Gln Asp Lys Leu Met Val Ile Gly Ala Lys Val Glu Asn Glu Val Leu
165 170 175

Asn Val Glu Lys Ile Asn Thr Phe Lys Thr Leu Pro Thr Lys Pro Glu
180 185 190

Met Gln Ser Gln Leu Val Ser Val Leu Gln Met Leu Ser Gly Leu Gly
195 200 205

Leu Val Arg Thr Leu Glu Asn Ser Ser Asn Ala Leu Tyr Leu Thr Leu
210 215 220

Lys Ser His Asn Asp Asn Gln Lys Pro Lys Glu Asp Val Glu Ser Thr
225 230 235 240

Thr Asp Ala Glu Ser Lys Gly Ser Lys

245

<210> 15
 <211> 357
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
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 1 5 10 15

cgg tgg cca agg att ctg cgg ggc tca aag ctt tgg tac tca acg cag 26
 Arg Trp Pro Arg Ile Leu Thr Gly Ser Lys Leu Trp Tyr Ser Thr Gln
 20 25 30

atg gaa atg act cgg gag gag aag atg atc acc gat aaa cta caa cag 144
 Met Ala Met Thr Pro Gln Gln Lys Met Ile Thr Asp Lys Leu Gln Gln
 35 40 45

gaa ctg gaa cct gaa gtc tgt aac gtc aac gac gtt tcc ggt ggc tgc 192
 Glu Leu Glu Pro Glu Val Cys Lys Val Gln Asp Val Ser Gly Gly Cys
 50 55 60

gga tcc atg ttt gct atc aac ata aca agc aag aag ttc aac gga ctc 240
 Gly Ser Met Phe Ala Ile Asn Ile Thr Ser Lys Lys Phe Asn Gly Leu
 65 70 75 80

agt ctc atc aag cag aac cag ctg gtc aac aga att ttg agg gac gat 288
 Ser Leu Ile Lys Gln His Gln Leu Val Asn Arg Ile Leu Arg Asp Asp
 85 90 95

att tcc aga tgg cct ggc cta caa ttg acc act aag aag taa act ggg 336
 Ile Ser Arg Trp His Gly Leu Gln Leu Thr Thr Lys Lys Ser Thr Gly
 100 105 110

aug ggt cag gaa tca tca tga

357

Lys Gly Pro Ala Ser Ser

115

<210> 16

<211> 116

<212> PRT

<213> *Saccharomyces cerevisiae*

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Met Lys Leu Pro Gln Thr Met Leu Arg Ser Ile Ser Val Lys His Val

1

5

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15

Arg Trp Pro Arg Ile Leu Thr Gly Ser Lys Leu Trp Tyr Ser Thr Gln

20

25

30

Met Ala Met Thr Pro Gln Glu Lys Met Ile Thr Asp Lys Leu Gln Gln

35

40

45

Glu Leu Glu Pro Gln Val Cys Lys Val Gln Asp Val Ser Gly Gly Cys

50

55

60

Gly Ser Met Phe Ala Ile Asn Ile Thr Ser Lys Lys Phe Asn Gly Leu

65

70

75

80

Ser Leu Ile Lys Gln His Gln Leu Val Asn Arg Ile Leu Arg Asp Asp

85

90

95

Ile Ser Arg Trp His Gly Leu Gln Leu Thr Thr Iys Lys Ser Thr Gly

100

105

110

Lys Gly Pro Ala Ser Ser

115

<210> 17

<211> 1782

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1782)

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Met Ala Leu Ala Ile Ser His Glu Asp Thr Gln Ile Leu Leu Lys Asp

1 5 10 15

aaa aat att cta cag gaa tgg gtc ttg aac aaa tac aga act gat gga 96
Lys Asn Ile Leu Gln Glu Ser Val Leu Asn Lys Tyr Arg Thr Ala Gly

20 25 30

caa atc gca caa act gct ttg aaa tct gtt act tct ttg atc aat gat 144

Gln Ile Ala Gln Thr Ala Leu Lys Tyr Val Thr Ser Leu Ile Asn Asp

35 40 45

tca tat cac tct aag acc nca cag cgc caa tta aca gtc cca gag cta 132
Ser Tyr His Ser Lys Thr Thr Gln Arg Gln Leu Thr Val Pro Glu Leu

50 55 60

tgt ttg ctt acc gat tct ttt att ttg acc cgg ttg gaa aat tat tat 240

Cys Leu Leu Thr Asp Ser Phe Ile Leu Thr Arg Leu Glu Gln Tyr Tyr

65 70 75 80

aaa aac aaa gtt aat gaa aga ggt att ggc att cca acc act att gat 288

Lys Asn Lys Val Asn Glu Arg Gly Ile Ala Ile Pro Thr Thr Ile Asp

85 90 95

atc gac caa att tct ggt gga tgg tgc ccc gaa ata gat gat act caa 336

Ile Asp Gln Ile Ser Gly Gly Trp Cys Pro Glu Ile Asp Asp Thr Gln

100 105 110

aat ttg tta aac tgg aat aag ggg aaU guU tuc act ttt gca tca tct	384
Asn Leu Leu Asn Trp Asn Lys Gly Lys Asp Ser Thr Phe Ala Ser Ser	
115 120 125	
gtc act ggg act ttg aga gag ggg gat tta gtc aag att aca cta ggt	432
Val Thr Gly Thr Leu Arg Pro Gly Asp Leu Val Lys Phe Thr Leu Gly	
130 135 140	
gtt cat att gat ggt tac aac tct gaa gtt tct cat act aig gtt att	480
Val His Ile Asp Gly Tyr Thr Ser Glu Val Ser His Thr Met Val His	
145 150 155 160	
tac ccc gtt gat gaa acc aaa cct att ctt caa ccc act ggg cca cta	528
Tyr Pro Val Asp Glu Thr Lys Pro Ile Leu Gln Pro Thr Gly Pro Leu	
165 170 175	
cta ggt ggt aaa gag gal gct gta gct gct gct cac att gct atg gaa	576
Leu Gly Gly Lys Ala Asp Ala Val Ala Ala Ala His Ile Ala Met Glu	
180 185 190	
aca gtt gtt gct tta tta gcc tct cct ctg act cca gaa aag ctt cct	624
Thr Val Val Ala Leu Leu Ala Cys Ala Leu Thr Pro Glu Lys Leu Pro	
195 200 205	
gcc tca ctg gga gga act tca agt ggt atc acn ggc caa ttg att aga	672
Ala Ser Leu Gly Gly Thr Ser Ser Gly Ile Thr Gly Gln Leu Ile Arg	
210 215 220	
act ata gtg gat act att gcc aga tct tat aac tgt gcc gtt gtt cct	720
Thr Ile Val Asp Thr Ile Ala Arg Ser Tyr Asn Cys Gly Val Val Pro	
225 230 235 240	
ggg tct cgt gta aga gag atc aga aga ttc ctg gca ggc caa aac gaa	768
Gly Ser Arg Val Arg Arg Ile Arg Arg Phe Iasn Ala Gly Gln Asn Glu	
245 250 255	
ggg att gtt gcc gaa agg gaa tat aag ggt gtt gtt lgg aca aag tcc	816
Gly Ile Val Ala Glu Arg Glu Tyr Lys Gly Val Val Trp Thr Glu Ser	
260 265 270	
cat caa gaa gca gat ttg cta tct aat act gat gcc aag gat tta aca	864

His Glu Glu Ala Asp Leu Leu Ser Asn Thr Asp Ala Lys Asp Gln Thr	275	280	285	
gtg gta gat cgt gga caa ccg acc cca ttc acg aat gtt tct gct att				912
Val Val Asp Arg Gly Gln Ser Thr Pro Phe Thr Asn Val Ser Ala Ile	290	295	300	
cca agt gat gat ttc gtt gtt caa tca ggt gaa gtc tat tta att gat				960
Pro Ser Asp Asp Phe Val Val Gln Ser Gly Glu Val Tyr Leu Ile Asp	305	310	315	320
ttc aaa atg gca tct ttg gag cat tgt acc aaa aag ggt tta gta act				1008
Leu Lys Met Ala Ser Leu Glu His Cys Thr Lys Lys Gly Leu Val Thr	325	330	335	
tta gaa acc gtt gac tct tac aca ggt aaa tct cat aag gct gga gaa				1056
Leu Glu Thr Val Asp Ser Tyr Thr Gly Lys Ser His Lys Ala Gly Glu	340	345	350	
ttg att gca aga ccc ggt gca tat gtc aga gat ttt gct caa acc caa				1104
Leu Ile Ala Arg Pro Gly Ala Tyr Val Arg Asp Phe Ala Gln Thr His	355	360	365	
att ctt aag tta aaa cct tct cga caa ttc tta act aac atc gat aaa				1152
Ile Leu Lys Leu Lys Thr Ser Arg Gln Leu Leu Thr Lys Ile Asp Lys	370	375	380	
caa ggc gtt tat cca ttc aag tta tcc cat tta tct tct aac ttt acc				1200
Gln Gly Val Tyr Pro Phe Lys Leu Ser His Leu Ser Ser Asn Phe Pro	385	390	395	400
ttc gtt ccc gaa aat gaa gaa gaa ctg caa agc tta aag aac gat ttg				1248
Phe Val His Glu Asn Glu Glu Glu Leu Glu Ser Leu Lys Tyr Asp Asn	405	410	415	
aaa tca ttt aga ctt ggg atg agt gag att tcc aac aac tac tta tgt				1296
Lys Ser Phe Arg Leu Gly Met Ser Glu Ile Ser Asn Asn Tyr Leu Cys	420	425	430	
gtg gaa agt cca ata cca att gct aga tgg gtt cca tgg gac cat att				1344

Val Glu Ser Pro Ile Gln Ile Ala Arg Trp Val Pro Trp Asp His Ile	
435 440 445	
ttc aag gcc acc aat acc aac ggt aat tta agt tat gat gaa acc tct	1392
Leu Lys Ala Thr Asn Pro Asn Gly Asn Leu Ser Tyr Asp Ala Trp Ser	
450 455 460	
acc tta acc tta cct ggg cat gag tta cct tta cca aaa tgg ggt gtt	1440
Thr Leu Thr Leu Pro Gly His Glu Leu Pro Leu Pro Lys Leu Gly Val	
465 470 475 480	
tcc gcc atc aag ctt aaa tcc tta atg aat tca acc aag gaa tgg att	1488
Ser Ala Ile Lys Leu Lys Ser Leu Met Asn Ser Thr Lys Glu Ser Ile	
485 490 495	
tct tta acc gtt gct cgt gaa tgt aat acc atc gla tta tgt gac tct	1536
Ser Leu Pro Val Ala Arg Glu Cys Asn Thr Ile Val Leu Cys Asp Ser	
500 505 510	
agt gta agt acc acg gat aga ccc aac tta ttg aga tta act ggt ggt	1584
Ser Val Ser Thr Thr Asp Arg Pro Glu Leu Leu Arg Leu Thr Gly Gly	
515 520 525	
tct aag acc tgc aac ccg agc tgg att cac tct cag cac gaa tta aat	1632
Ser Lys Thr Cys Gln Pro Ser Trp Ile His Ser Gln His Glu Leu Asn	
530 535 540	
cca caa gat tca att gtt caa ggg atc ttt caa tta gat aat ttg gcc	1680
Pro Gln Asp Ser Ile Val Gln Gly Ile Phe Gln Leu Ala Thr Leu Ala	
545 550 555 560	
aag gat aag agg ttc ggt cta tta tta aag gan acc cag ccc atg aag	1728
Lys Asp Lys Arg Phe Gly Leu Leu Leu Lys Glu Thr Gln Pro Met Lys	
565 570 575	
cag aag agt gtt gag acc tca aat ggc gga gtt gaa gaa acc aig aaa	1776
Gln Lys Ser Val Glu Thr Ser Asn Gly Gly Val Glu Gln Thr Met Lys	
580 585 590	
atg tag	1782
Met	

<210> 13

<211> 593

<212> VRT

<213> *Saccharomyces cerevisiae*

<400> 18

Met Ala Leu Ala Ile Ser His Glu Asp Thr Gln Ile Leu Leu Lys Asp

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15

Lys Asn Ile Leu Gln Glu Ser Val Leu Asn Lys Tyr Arg Thr Ala Gly

20

25

30

Gln Ile Ala Gln Thr Ala Leu Lys Tyr Val Thr Ser Leu Ile Asn Asp

35

40

45

Ser Tyr His Ser Lys Thr Thr Gln Arg Gln Leu Thr Val Pro Glu Leu

50

55

60

Cys Leu Leu Lys Asp Ser Phe Ile Leu Thr Arg Leu Glu Gln Tyr Tyr

65

70

75

80

Lys Asn Lys Val Asn Glu Arg Gly Ile Ala Ile Pro Thr Thr Ile Asp

85

90

95

Ile Asp Gln Ile Ser Gly Gly Trp Cys Pro Gln Ile Asp Asp Thr Gln

100

105

110

Asn Leu Leu Asn Trp Asn Lys Gly Lys Asp Ser Thr Phe Ala Ser Ser

115

120

125

Val Thr Gly Thr Leu Arg Pro Gly Asp Leu Val Lys Ile Thr Ser Gly
 130 135 140

Val His Ile Asp Gly Tyr Thr Ser Glu Val Ser His Thr Met Val Ile
 145 150 155 160

Tyr Pro Val Asp Glu Thr Lys Pro Ile Leu Glu Pro Thr Gly Pro Leu
 165 170 175

Leu Gly Gly Lys Ala Asp Ala Val Ala Ala Ala His Ile Ala Met Gly
 180 185 190

Thr Val Val Ala Leu Leu Ala Cys Ala Leu Thr Pro Glu Lys Leu Pro
 195 200 205

Ala Ser Leu Gly Gly Thr Ser Ser Gly Ile Thr Gly Gln Leu Ile Arg
 210 215 220

Thr Ile Val Asp Thr Ile Ala Arg Ser Tyr Asn Cys Gly Val Val Pro
 225 230 235 240

Gly Ser Arg Val Arg Arg Ile Arg Arg Phe Leu Ala Gly Gln Asn Glu
 245 250 255

Gly Ile Val Ala Glu Arg Glu Tyr Lys Gly Val Val Trp Thr Glu Ser
 260 265 270

His Gln Glu Ala Asp Leu Leu Ser Asn Thr Asp Ala Lys Asp Leu Thr
 275 280 285

Val Val Asp Arg Gly Gln Ser Thr Pro Phe Thr Asn Val Ser Ala Ile
 290 295 300

Pro Ser Asp Asp Phe Val Val Gln Ser Gly Glu Val Tyr Leu Ile Asp
395 310 315 320

Leu Lys Met Ala Ser Leu Glu His Cys Thr Lys Lys Gly Leu Val Thr
325 330 335

Leu Gln Thr Val Asp Ser Tyr Thr Gly Lys Ser His Lys Ala Gly Glu
340 345 350

Leu Ile Ala Arg Pro Gly Ala Tyr Val Arg Asp Phe Ala Gln Thr His
355 360 365

Ile Leu Lys Leu Lys Thr Ser Arg Gly Leu Leu Thr Lys Ile Asp Lys
370 375 380

Gln Gly Val Tyr Pro Phe Lys Leu Ser His Val Ser Ser Asn Phe Pro
385 390 395 400

Phe Val His Glu Met Glu Glu Glu Leu Gln Ser Leu Lys Lys Asp Leu
405 410 415

Lys Ser Phe Arg Leu Gly Met Ser Glu Ile Ser Asn Asn Tyr Leu Cys
420 425 430

Val Gln Ser Pro Ile Gln Ile Ala Arg Trp Val Pro Trp Asp His His
435 440 445

Leu Lys Ala Thr Asn Pro Asn Gly Asn Leu Ser Tyr Asp Ala Thr Ser
450 455 460

Thr Leu Thr Leu Pro Gly His Glu Leu Pro Leu Pro Lys Leu Gly Val
 465 470 475 480

Ser Ala Ile Lys Leu Lys Ser Leu Met Asn Ser Thr Lys Glu Ser Ile
 485 490 495

Ser Leu Pro Val Ala Arg Glu Cys Asn Thr Ile Val Leu Cys Asp Ser
 500 505 510

Ser Val Ser Thr Thr Asp Arg Pro Glu Leu Leu Arg Leu Thr Gly Gly
 515 520 525

Ser Lys Thr Cys Gln Pro Ser Asp Ile His Ser Gln His Glu Leu Asn
 530 535 540

Pro Gln Asp Ser Ile Val Gln Gly Ile Phe Gln Leu Ala Thr Leu Ala
 545 550 555 560

Lys Asp Lys Arg Phe Gly Leu Leu Leu Lys Glu Thr Gln Pro Met Lys
 565 570 575

Gln Lys Ser Val Glu Thr Ser Asn Gly Gly Val Glu Glu Thr Met Lys
 580 585 590

Met

<210> 19

<211> 2099

<212> DNA

<213> *Saccharomyces cerevisiae*

«220»

<221> CDS

(222) (1) - (2997)

<100> 25

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1 5 10 15

Tac Arg Asn Gln Neg Gly Cys Ala Val Ile Ser
Asn Ser Lys Glu Thr Val Pro Phe Leu Tyr Arg His Met

20 25 30

TAT GGT ATA GGT CCT GTA ATA ACA GTT ACT TCA ACT CCG CTC CTC GAG 144
 ASN ALA ILE ALA PRO VAL ILE THR VAL THR SER THR PRO LEU PHE ASP
 35 40 45

aa cat att caa gaa aag tac aaa gta gat tct ctc tat atg ctg ctg 192
 Lys His Ile Glu Glu Thr Tyr Lys Val Asp Ser Ser Tyr Met Leu Leu
 50 55 60

aga ttc ttc ggc ggt tgt gtc lct gat gga gat cca gcc aat gaa gcg 240
Arg Phe Phe Gly Gly Cys Val Ser Asp Arg Asp Gln Ala Asn Glu Ala
65 75 80

tag gtt gga cag cat gay cat gag gtt tgt gat gca agt gac tog acg 188
 Lys Val Gly Gln His Glu His Glu Val Cys Asp Ala Ser Arg Sec Thr
 85 90 95

gat tca att ccc aaa aat aaa aat ttg gaa g'ig ddc aat tta tca aag 336
Asp Ser Ile Pro Lys Asa Lys Asn Leu Glu Val Pro Asn Leu Ser Lys
100 105 110

aa a ggt agt cgc agt agg tgg aat agt ctt ttc cag agt gat tca acg 381
 Lys Gly Ser Arg Ser Arg Ser Asn Ser Leu Phe Gln Arg Asp Ser Thr
 115 120 125

caa tct caa tat atc agg ttt cca agg cca tta ggt gac ttg atc gaa 432
Gln Ser Gln Tyr Ile Arg Phe Thr Arg Pro Leu Gly Asp Leu Ile Glu
130 135 140

aca aga gat gca aat gat atg tta ttc aat tac cat tct tta gag gta	480
Thr Arg Asp Ala Asn Asp Met Leu Phe Asn Tyr His Ser Leu Glu Val	
145 150 155 160	
ttc tta gat aat tat ttg aac ttg gtt gca gca aat act gat gaa atg	528
Phe Leu Asp Asn Tyr Leu Lys Leu Val Ala Ala Asn Thr Asp Glu Met	
165 170 175	
gtt cat cat aat ctt ctt aag aac tcc att tat cat agt ttc ttt tca	576
Val Pro His Asn Leu Leu Lys Lys Ser Ile Tyr His Ser Phe Phe Ser	
180 185 190	
cta gca att tca tcc aca aat cac tta tcg acc tat gaa act ttt aat	624
Leu Ala Ile Ser Ser Thr Asn Asn Leu Ser Pro Tyr Glu Thr Phe Asn	
195 200 205	
cac cat att ctt tcc ttg att gct tca gat ata tca aat ggc gaa gtt	672
His Pro Ile Leu Ser Leu Ile Ala Leu Asp Ile Ser Asn Gly Glu Val	
210 215 220	
tat gag gat gca aga gat ctt tta gtc cat ttc aag aat ctt aat cat	720
Tyr Glu Asp Ala Arg Asp Leu Leu Val Asn Phe Lys Asn Leu Asn His	
225 230 235 240	
aat act gaa aac ttt cct atc ttc atg aat aca aat gaa aly ctt cca	768
Asn Thr Glu Asn Phe Pro Ile Phe Met Asn Thr Asn Glu Met Leu Pro	
245 250 255	
gtt ttc tta ctc tcg tac aat cac gat tcc caa gaa gaa ttc gaa aac	816
Val Phe Leu Leu Cys Tyr Asn Asp Asp Ser Gln Glu Glu Phe Glu Lys	
260 265 270	
tgc cag gcg tta gct aag aac cta aag aag cag ttg ttt gtt gag agt	864
Cys Gln Ala Leu Ala Lys Lys Leu Lys Lys Gln Leu Phe Val Glu Ser	
275 280 285	
ata tta cta gca ctc tgg aag gat tct ttt att tac gac gaa aat tca	912
Ile Leu Leu Ala Leu Trp Lys Asp Ser Phe Ile Tyr Asp Glu Asn Ser	
290 295 300	
gta ata cag tta cac caa caa gta atg toa tcg ctt gaa gaa att ctc	960
Val Ile Gln Leu His Gln Pro Val Met Ser Ser Leu Glu Glu Ile Leu	

305	310	315	320
ttc ttc ctt caa gct cca act caa aca aca ctc tct ctg gct ttg ata			1003
Phe Phe Leu Gln Ala Pro Thr Gln Thr Thr Ser Ser Leu Ala Leu ile			
325	330	335	
aac tgg atc tat gat atg ctt gat tat ttg gtt tat gat tta atg ata			1053
asn ser ile tyr asp met leu asp tyr leu val tyr asp leu val ile			
340	345	350	
cca ttc atg aaa aga aaa gtg tca ttc tgg gaa gag aca att tta cag			1104
pro phe met lys arg lys val ser phe trp glu glu thr ile leu gln			
355	360	365	
caa aga aag tcy cta ttt aat ggt gca aag ttt tta aaa aca ttt atg			1152
pro arg lys ser leu phe asn gly ala lys phe phe lys lys phe met			
370	375	380	
aat aaa aat cct gtc aat ggt aat cac caa cat aat tat cta aag aga			1203
asn lys asn pro val asn gly asn his gln his asn ser leu thr arg			
385	390	395	400
gac agc cag gga aat gaa taa tlu gaa tgg tca tct tct gag ttt ttg			1248
asp ser glu gly asn glu tyr phe ala ser ser ser ser glu phe jasn			
405	410	415	
ctg aga aag tta gca gat tgg tct atg atg cta tcc gac ttc aaa act			1296
met arg lys leu ala asp trp ser met met leu ser asp phe lys thr			
420	425	430	
gct tat tcc aca tac gaa tgg ctt atg gat gac ata gat gca ttt caa			1344
ala tyr ser thr tyr glu ser leu met asp asp leu asp ala phe pro			
435	440	445	
aag taa cly gca tca tgc atc gaa tgg tgc ggg gta tca cta ttg atg			1392
lys tyr leu ala ser cyn ile glu trp cys ala val ser leu leu met			
450	455	460	
ggt ggg cag agc ata gtc acc gtg aaa atg atc aaa aac gat ata aat			1440
gly ala gln ser ile val thr val lys met ile lys asn asp ile asn			
465	470	475	480

oct att atc gaa agg gaa tta gcc aca tac gaa aac tgc tca cgs atx	1188
Pro Leu Ile Glu Arg Ala Leu Ala Thr Tyr Glu Asn Cys Ser Arg Ile	
485 490 495	
caa cgt ggt aaa ggc aaa gaa tca aac tot ttg gat gtt aca gag cca	1576
Gln Arg Gly Lys Gly Lys Glu Ser Asn Ser Leu Asp Val Thr Glu Pro	
500 505 510	
gtg cgt tgg tat gag aca cgt tgt atg att ttg gca tct gaa ttg ttt	1584
Val Arg Ser Tyr Glu Thr Arg Cys Met Ile Leu Ala Ser Glu Leu Phe	
515 520 525	
tta tot tta agc aat aag tgg aca tot aca cca taa gaa ala uaa tai	1632
Leu Ser Asn Ser Asn Thr Trp Thr Ser Thr Pro Tyr Ala Ile Gln Tyr	
530 535 540	
lta gaa aca att cia gac gag tgc aag ttg gga cct tgc tca cag ata	1580
Leu Glu Thr Ile Leu Asp Glu Cys Lys Leu Gly Pro Cys Ser Gln Ile	
545 550 555 560	
atg gtt tgg gaa agg att agt gac tgc tat aat ttg aga gtt gac cct	1728
Met Val Trp Glu Arg Leu Ser Asp Cys Tyr Asn Leu Arg Val Asp Phe	
565 570 575	
aga atc aac cat aga gtt ggc gca atg cag cag gac gct aac gac aac	1776
Arg Ile Lys His Arg Val Gly Ala Met Lys Lys Asp Ala Lys Asp Thr	
580 585 590	
gaa gat ctc cga ggt gag cat aag tat agc aac gat cat ttc uaa gaa	1824
Glu Asp Gln Arg Gly Gln His Lys Tyr Ser Thr Asn His Phe Thr Asp	
595 600 605	
gag gac ata tta tog gaa ggg tta aca aga aga cgc aag gca gct ttt	1872
Glu Asp Ile Leu Ser Glu Gly Leu Thr Arg Arg Arg Lys Ala Ala Phe	
610 615 620	
ttt agg tta ata gca gct aag aag tgg gca gag caa aaa caa tgg aga	1920
Phe Arg Asn Thr Ala Ala Lys Lys Trp Ala Glu Gln Lys Glu Trp Arg	
625 630 635 640	

dag gtt tot tqq tqc tta aaa gat att gaa agt acc tat tca gag atc 1968
 Glu Val Ser Trp Cys Leu Lys Asp Ile Glu Ser Thr Tyr Ser Glu Ile
 645 650 655

aaa ttt ttg cat ggt aac ggt tta att tta agc aaa ctg aaa aat cca 2016
 Lys Phe Leu His Gly Asn Gly Leu Ile Leu Ser Lys Leu Lys Asn Glu
 660 665 670

atc aat tta aag gac ggg gat tot gca cca cyg ccc tcc gaa aag aat 2064
 Leu Asn Leu Lys Asp Val Asp Ser Ala Pro Arg Pro Ser Glu Lys Asn
 675 680 685

ctt aca aga aca agt gtt ago ttt att gga lga 2197
 Leu Thr Arg Thr Ser Val Ser Phe Ile Gly
 690 695

<210> 20

<211> 698

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

Met Val Phe Ser Tyr Glu His Tyr Met Asn Leu Phe His Leu Asp
 1 5 10 15

Asn Ser Lys Glu Thr Val Pro Pro Glu Ile Ala Lys Arg Ile Ile Ser
 20 25 30

Asn Ala Ile Ala Pro Val Ile Thr Val Thr Ser Thr Pro Leu Phe Asp
 35 40 45

Lys His Ile Glu Glu Thr Tyr Lys Val Asp Ser Leu Tyr Met Leu Leu
 50 55 60

Arg Phe Phe Gly Gly Cys Val Ser Asp Arg Asp Glu Ala Asn Glu Ala

65	70	75	80
Lys Val Gly Gln His Glu His Glu Val Cys Asp Ala Ser Asp Ser Thr			
	85	90	95
Asp Ser Ile Pro Lys Asn Lys Asn Leu Glu Val Pro Asn Leu Ser Lys			
	100	105	110
Lys Gly Ser Arg Ser Arg Ser Asn Ser Leu Phe Gln Arg Asp Ser Thr			
	115	120	125
Gln Ser Gln Tyr Ile Arg Phe Thr Arg Pro Leu Gly Asp Leu Ile Glu			
	130	135	140
Thr Arg Asp Ala Asn Asp Met Leu Phe Asn Tyr Phe Ser Leu Glu Val			
	145	150	155
Phe Leu Asp Asn Tyr Leu Lys Leu Val Ala Ala Asn Thr Asp Glu Met			
	165	170	175
Val Pro His Asn Leu Leu Lys Lys Ser Ile Tyr His Ser Phe Phe Ser			
	180	185	190
Leu Ala Ile Ser Ser Thr Asn Asn Leu Ser Pro Tyr Glu Thr Phe Asn			
	195	200	205
His Pro Ile Leu Ser Leu Ile Ala Leu Asp Ile Ser Asn Gly Glu Val			
	210	215	220
Tyr Glu Asp Ala Arg Asp Leu Leu Val Asn Phe Lys Asn Leu Asn His			
	225	230	235
			240

Asn Thr Glu Asn Phe Pro Ile Phe Met Asn Thr Asn Glu Met Leu Pro
 345 250 355

Val Phe Leu Leu Cys Tyr Asn Asp Asp Ser Gln Glu Glu Phe Glu Lys
 260 265 270

Cys Gln Ala Leu Ala Lys Lys Leu Lys Lys Gly Asn Phe Val Glu Ser
 275 280 285

Ile Leu Leu Ala Leu Trp Lys Asp Ser Phe Ile Tyr Asp Glu Asn Ser
 290 295 300

Val Ile Gln Leu His Gln Pro Val Met Ser Ser Leu Glu Glu Ile Leu
 305 310 315 320

Phe Phe Leu Gln Ala Pro Thr Gln Thr Thr Leu Ser Leu Ala Leu Ile
 325 330 335

Asn Ser Ile Tyr Asp Met Leu Asp Tyr Leu Val Tyr Asp Leu Met Ile
 340 345 350

Pro Phe Met Lys Arg Lys Val Ser Phe Tyr Gln Glu Thr Val Leu Gln
 355 360 365

Pro Arg Lys Ser Leu Phe Asn Gly Ala Lys Phe Phe Lys Lys Phe Met
 370 375 380

Asn Lys Asn Pro Val Asn Gly Asn His Gln His Asn Ser Leu Thr Arg
 385 390 395 400

Asp Ser Gln Gly Asn Glu Tyr Phe Ala Ser Ser Ser Ser Glu Phe Leu

605

410

415

Met Arg Lys Leu Ala Asp Trp Ser Met Met Leu Ser Asp Phe Tyr Thr
420 425 430

Ala Tyr Ser Thr Tyr Glu Ser Leu Met Asp Asp Leu Asp Ala Phe Pro
435 440 445

Lys Tyr Leu Ala Ser Cys Ile Glu Trp Cys Ala Val Ser Leu Leu Met
450 455 460

Gly Ala Gln Ser Ile Val Thr Val Tyr Met Ile Lys Asn Asp Ile Asn
465 470 475 480

Pro Leu Ile Glu Arg Ala Leu Ala Thr Tyr Glu Asn Cys Ser Arg Ile
485 490 495

Glu Arg Gly Lys Gly Lys Glu Ser Asn Ser Leu Asp Val Thr Glu Pro
500 505 510

Val Arg Ser Tyr Glu Thr Arg Cys Met Ile Ser Ala Ser Glu Leu Phe
515 520 525

Leu Ser Leu Ser Asn Thr Trp Thr Ser Thr Pro Tyr Ala Ile Gln Tyr
530 535 540

Leu Glu Thr Ile Leu Asp Glu Cys Tyr Leu Gly Pro Cys Ser Gln Ile
545 550 555 560

Met Val Trp Glu Arg Leu Ser Asp Cys Tyr Asn Leu Arg Val Asp Pro
565 570 575

Arg Ile Lys His Arg Val Gly Ala Met Lys Lys Asp Ala Lys Asp Thr
580 585 590

Glu Asp Leu Arg Gly Glu His Lys Tyr Ser Thr Asp His Phe Thr Asp
595 600 605

Glu Asp Ile Leu Ser Glu Gly Leu Thr Arg Arg Arg Lys Ala Ala Phe
610 615 620

Phe Arg Leu Ile Ala Ala Lys Tyr Trp Ala Glu Glu Lys Glu Trp Arg
625 630 635 640

Glu Val Ser Trp Cys Leu Lys Asp Ile Glu Ser Thr Tyr Ser Glu Ile
645 650 655

Lys Phe Leu His Gly Asn Gly Leu Ile Leu Ser Lys Leu Lys Asn Glu
660 665 670

Leu Asn Leu Lys Asp Val Asp Ser Ala Pro Arg Pro Ser Glu Lys Asn
675 680 685

Leu Thr Arg Trp Ser Val Ser Phe Ile Gly
690 695

<210> 21

<211> 327

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(327)

<400> 21
 atg cga tat act gca act ttt cgg cct ttg caa cga ttt gta atg aat 48
 Met Arg Tyr Thr Ala Thr Phe Arg Pro Leu Gln Arg Phe Val Met Asn
 1 5 10 15
 cct ttt gca tgg cta gaa gga caa gat aat apt tct tct gtt ttt ttt 96
 Pro Phe Ala Ser Leu Glu Gly Gln Asp Asn Ile Ser Ser Val Thr Phe
 20 25 30
 tta cat atg caa caa ttt gaa agt cag gtc aaa gac aga ttc cgg ttc 144
 Leu His Met Gln Gln Phe Glu Ser Gln Val Lys Asp Arg Phe Arg Phe
 35 40 45
 ccc ata ttc aga ttg gag aga aaa act ttt ggc aac tca tgt tuc caa 192
 Pro Ile Phe Arg Leu Glu Arg Lys Thr Phe Gly Asn Ser Cys Tyr Gln
 50 55 60
 gtc gag acg ctt aaa gtt aag tgt cgg cca aaa cac gca aaa tct tgt 240
 Val Glu Thr Leu Lys Val Lys Cys Arg Pro Arg His Ala Lys Ser Cys
 65 70 75 80
 aat ctt tta acg ctg ctc ttc aaa tca cgg acg caa tca gta ctt gta 288
 Asn Leu Leu Thr Leu Leu Phe Lys Ser Arg Thr Gln Ser Val Leu Val
 85 90 95
 cct aat ttt ggt ttt cta ata ttg aat agc gaa cca tag 327
 Pro Asn Phe Gly Phe Leu Ile Leu Asn Ser Glu Pro
 100 105

<210> 32
 <211> 108
 <212> FRT
 <213> *Saccharomyces cerevisiae*
 <400> 22

Met Arg Tyr Thr Ala Thr Phe Arg Pro Leu Gln Arg Phe Val Met Asn
 1 5 10 15

Pro Phe Ala Ser Leu Glu Gly Gln Asp Asn Ile Ser Ser Val Phe Phe
20 25 30

Leu His Met Gln Gln Phe Glu Ser Gln Val Lys Asp Arg Phe Arg Phe
35 40 45

Pro Ile Phe Arg Leu Glu Arg Lys Thr Phe Gly Asn Ser Cys Tyr Gln
50 55 60

Val Glu Thr Leu Lys Val Lys Cys Arg Pro Arg His Ala Lys Ser Cys
65 70 75 80

Asn Leu Leu Thr Leu Leu Phe Lys Ser Arg Thr Gln Ser Val Leu Val
85 90 95

Pro Asn Phe Gly Phe Leu Ile Leu Asn Ser Glu Pro
100 105

<210> 23
<211> 411
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(411)

<400> 23
atg caa ttc tct acc gtc gct tat atc ggc gct att ggc gct gtt gcc 48
Met Gln Phe Ser Thr Val Ala Ser Ile Ala Ala Ile Ala Ala Val Ala
1 5 10 15

ccc gcc gct tct aac att acc act gct act gtc aca gaa gaa tct acc 96
Ser Ala Ala Ser Asn Ile Thr Thr Ala Thr Val Thr Glu Glu Ser Thr

20	25	30	
act ttg gtc act atc act tct tgt gag gac cac gtt tgt tct gaa aca			144
Thr Leu Val Thr Ile Thr Ser Cys Glu Asp His Val Cys Ser Glu Thr			
35	40	45	
gtt tcc cca gct ttg gtt tcc act gct acc gtc acc gta aat gac gll			192
Val Ser Pro Ala Leu Val Ser Thr Ala Thr Val Thr Val Asn Asp Val			
50	55	60	
atc act taa tac acc acc tgg tgt cca ttg cca acc act gaa gca cca			240
Ile Thr Tyr Thr Thr Trp Cys Pro Leu Pro Thr Thr Glu Ala Pro			
65	70	75	
aag aat acc act tct cca gct cca act gaa aag cca acc gaa aag cca			288
Lys Asn Thr Thr Ser Pro Ala Pro Thr Glu Lys Pro Thr Glu Lys Pro			
80	85	90	95
act gaa aag cca acc caa caa ggt tct agc act ccc gtt acc acc			336
Thr Glu Lys Pro Thr Glu Glu Gly Ser Ser Thr Glu Thr Val Thr Ser			
100	105	110	
tac act ggt gcc gct gtt aag gct ttg cca gct gcc ggt gct ttg ttg			384
Tyr Thr Gly Ala Ala Val Lys Ala Leu Pro Ala Ala Gly Ala Leu Leu			
115	120	125	
gct ggt gct gcc gct tta ttg ttg taa			411
Ala Gly Ala Ala Ala Leu Leu Leu			
130	135		
<210> 24			
<211> 66			
<212> ?RT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 24			
Met Glu Phe Ser Thr Val Ala Ser Ile Ala Ala Ile Ala Ala Val Ala			
1	5	10	15

Ser Ala Ala Ser Arg Ile Thr Thr Ala Thr Val Thr Glu Gln Ser Thr
20 25 30

Thr Leu Val Thr Ile Thr Ser Cys Glu Asp His Val Cys Ser Gln Thr
35 40 45

Val Ser Pro Ala Leu Val Ser Thr Ala Thr Val Thr Val Arg Asp Val
50 55 60

(1a Thr
65

<210> 25

<211> 69

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 25

Tyr Thr Thr Trp Cys Pro Leu Pro Thr Thr Glu Ala Pro Lys Asn Thr
1 5 10 15

Thr Ser Pro Ala Pro Thr Glu Lys Pro Thr Gln Lys Pro Thr Glu Lys
20 25 30

Pro Thr Gln Gln Gly Ser Ser Thr Gln Thr Val Thr Ser Tyr Thr Gly
35 40 45

Ala Ala Val Lys Ala Leu Pro Ala Ala Gly Ala Leu Leu Ala Gly Ala
50 55 60

Ala Ala Leu Leu Leu
65

<210> 26
 <211> 693
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> {1}..{693}

<400> 26
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 Met Glu Met Thr Asp Phe Glu Leu Thr Ser Asn Ser Gln Ser Asn Leu
 1 5 10 15
 gct atc cct acc aac ttc aag tgg aat ctg cct cca agg aaa aga gcc 96
 Ala Ile Pro Thr Asn Phe Lys Ser Thr Ien Pro Pro Arg Lys Arg Ala
 20 25 30
 aag acc aaa gag gaa aag gaa cag cga agg atc gag cgc att ttg aga 144
 Lys Thr Lys Glu Glu Lys Glu Glu Arg Arg Ile Glu Arg Ile Leu Arg
 35 40 45
 aac aga aga gct gct cgc cag agc aga gag aac aac aga cta cct ctg 192
 Asn Arg Arg Ala Ala His Gln Ser Arg Glu Lys Lys Arg Ien His Ien
 50 55 60
 cag tat ctc gag aga aaa tgt tct ctt ttg gaa aal tta ctg aac agc 240
 Gln Tyr Leu Glu Arg Lys Cys Ser Leu Leu Glu Asn Leu Ien Asn Ser
 65 70 75 80
 gtc aac ctt gaa aaa ctg gct gac cac gaa gac ggg ttg act tgc agc 288
 Val Asn Leu Glu Lys Leu Ala Asp His Glu Asp Ala Leu Thr Cys Ser
 85 90 95
 aac gaa gct ttt gtt gct tct ctt gaa gag tac agg gat ttc cag agc 336
 His Asp Ala Phe Val Ala Ser Leu Asp Glu Tyr Arg Asp Phe Gln Ser
 100 105 110
 aag agg ggc gct tca ctg gac acc agg gcc agt tgg aac tgg tgg tct 384
 Thr Arg Gly Ala Ser Leu Asp Thr Arg Ala Ser Ser His Ser Ser Ser

65/762

115	120	125	
gat aag ttc aca cct tca cct ctg aac tgt aca atg gag cct gag act			422
asp thr phe tle pro ser pro leu asn cys thr met glu pro ala thr			
130	135	140	
ttg tgg ccc aag agc atg cgc gat tcc gag tgg gac cca gag act tca			480
leu ser pro lys ser met arg asp ser ala ser asp gln glu thr ser			
145	150	155	160
tgg gag ctg cag atg ttt aag acg gaa aat gla cca gag tgg aag aag			520
trp glu leu gln met phe lys tar glu asn val pro gln ser thr thr			
165	170	175	
gla cct gcc gta gac aac aac aat ttg ttt gat ggg gtg gcc tgg aag			576
leu pro ala val asp asn asn asn leu phe asp ala val ala ser pro			
180	185	190	
ttg gcc gcc cca ctc tgc gac gat ata gag gga aac agt ata ccc ttt			624
leu ala asp pro leu cys asp asp ile ala gly asn ser leu pro phe			
195	200	205	
gac aat tca att ggt ctt gac aat tgg cgt aat cca gcc gtg att acc			672
asp asn ser ile asp leu asp asn trp arg asn pro ala val ile thr			
210	215	220	
atg acc agg aac cta cag tga			693
met thr arg lys leu glu			
225	230		
<210> 27			
<211> 230			
<212> FMT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 27			
met glu met thr asp phe glu leu thr ser asn ser glu ser asn leu			
1	5	10	15

Ala Ile Pro Thr Ser Phe Lys Ser Thr Leu Pro Pro Arg Lys Arg Ala
20 25 30

Lys Thr Lys Glu Glu Lys Glu Glu Arg Arg Ile Glu Arg Ile Leu Arg
35 40 45

Asn Arg Arg Ala Ala His Glu Ser Arg Glu Lys Lys Arg Leu His Leu
50 55 60

Glu Tyr Leu Glu Arg Lys Cys Ser Leu Ile Glu Asn Leu Leu Asn Ser
65 70 75 80

Val Asn Leu Glu Lys Leu Ala Asp His Glu Asp Ala Leu Thr Cys Ser
85 90 95

His Asp Ala Phe Val Ala Ser Leu Asp Glu Tyr Arg Asp Phe Glu Ser
100 105 110

Thr Arg Gly Ala Ser Leu Asp Thr Arg Ala Ser Ser His Ser Ser Ser
115 120 125

Asp Tyr Phe Thr Pro Ser Pro Leu Asn Cys Thr Met Glu Pro Ala Thr
130 135 140

Leu Ser Pro Lys Ser Met Arg Asp Ser Ala Ser Asp Glu Glu Thr Ser
145 150 155 160

Tyr Glu Leu Glu Met Phe Lys Thr Glu Asn Val Pro Glu Ser Thr Thr
165 170 175

Leu Pro Ala Val Asp Asn Asn Asn Leu Phe Asp Ala Val Ala Ser Pro
180 185 190

Leu Ala Asp Pro Leu Cys Asp Asp Ile Ala Gly Asn Ser Leu Pro Phe
 195 200 205

Asp Asn Ser Ile Asp Leu Asp Asn Trp Arg Asn Pro Ala Val Ile Thr
 210 215 220

Met Thr Arg Lys Leu Gln
 225 230

<213> 28

<211> 1398

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1398)

<400> 28

atg gcc cgc aat aga caa gag tgc gac tgt tgt tgc att tgt cgc gta 48
 Met Ala Arg Asn Arg Gln Ala Cys Asp Cys Cys Cys Ile Arg Arg Val
 1 5 10 15

aag tgt gat agt aaa aaa cca tgt aaa tgt tgt ctt caa cgc aat ctg 96
 Lys Cys Asp Arg Lys Lys Pro Cys Lys Cys Cys Leu Gln His Asn Leu
 20 25 30

caa tgt aca tat ctt cga cct ttg aag aaa aga ggt cca aaa ccc gtc 144
 Cln Cys Thr Tyr Leu Arg Pro Leu Lys Lys Arg Gly Pro Lys Pro Val
 35 40 45

aag gag aga aat tta aag aaa gta gat gat gta cag gta ttt agt aaa 192
 Lys Val Arg Asn Leu Lys Lys Val Asp Asp Val Gln Val Phe Ser Lys
 50 55 60

agt agt agt gag ggc ata atg aag gct cca aag gca cta att gat cag 240

Ser Ser Ser Gly Gly Ile Met Lys Val Pro Pys Ala Leu Ile Asp Glu	
65 70 75 80	
tgt ctg cgg ctg tct aat gat aag ttg tat gtg atc tgg cct ttg ctg	288
Cys Leu Arg Leu Tyr Asn Asp Lys Leu Tyr Val Ile Trp Pro Leu Leu	
85 90 95	
tgt tat gat gat ctt tac gaa ctt tta gag aaa aga tat gac gaa acc	336
Cys Tyr Asp Asp Leu Tyr Glu Leu Leu Glu Lys Arg Tyr Asp Glu Trp	
100 105 110	
tgt ggg tat tgg ttc ctg gta tct ctt tct gcc gcc acg ctt agc gat	384
Cys Val Tyr Tyr Phe Leu Val Ser Leu Ser Ala Ala Thr Leu Ser Asp	
115 120 125	
ttg cag act gaa att gag tgg gaa gga ggg gtt acc ttt act ggg ata	432
Leu Glu Thr Glu Ile Glu Ser Glu Gly Gly Val Thr Phe Thr Gly Ile	
130 135 140	
cag tta tcc agt ttc tgc atg tca tca cgc caa gaa ttt gac gat ttt	480
Glu Leu Ser Ser Phe Cys Met Ser Ser Arg Glu Glu Phe Asp Asp Phe	
145 150 155 160	
aac ggt agt gat ata ttc aag att atg acg tac tat tgt tca aac cgc	528
Asn Gly Ser Asp Ile Phe Lys Ile Met Thr Tyr Tyr Cys Leu Asn Arg	
165 170 175	
lgc tgc gaa cag atg aac aac tca aga act tgg tat cgg ctt tct tgt	576
Cys Tyr Ala Glu Met Ser Asn Ser Arg Thr Ser Tyr Arg Leu Ser Cys	
180 185 190	
gaa gcc gtg ggg ctg att aag ttg ggg ggg ttc cat cgc gag gaa act	624
Glu Ala Val Gly Leu Ile Lys Leu Ala Gly Phe His Arg Glu Glu Thr	
195 200 205	
ttg aaa ctt ctt cct ttc gat gag cag cag ctt gga agg aaa gtt tat	672
Leu Lys Leu Leu Pro Phe Asp Glu Glu Glu Leu Gly Arg Lys Val Tyr	
210 215 220	
tat ttg ctt ctg tta aag gaa aga tac ttt tct gtg tat acg cat tgc	720
Tyr Leu Leu Leu Leu Thr Glu Arg Tyr Phe Ser Val Tyr Thr His Cys	
225 230 235 240	

gac aag agc ctg gat acc acg att gct cca cca caa ccg gag aac gla Ala Thr Ser Leu Asp Thr Thr Ile Ala Pro Pro Gln Pro His Asn Val	768
243 250 255	
aag gac ccc cga cta tct ctg gac agc ttc ctg gag atg att agc gta Thr Asp Pro Arg Leu Ser Leu Asp Ser Phe Leu Glu Met Ile Arg Val	816
260 265 270	
ttt act gta ccg gga aac tgc ttc ttt gat gct cta gct acc gac tct Phe Thr Val Pro Gly Lys Cys Phe Phe Asp Ala Leu Ala Thr Asp Ser	864
275 290 285	
gct aat gta acc tgc act gaa gac tcc ctt aca aag ata tgg agg gaa Ala Asn Val Thr Cys Thr Glu Asp Ser Leu Lys Lys Ile Trp Arg Glu	912
290 295 300	
ctt cal aag ggg cca ctt gag ata gaa cca tgg tct tac ggc tal gta Leu His Thr Val Pro Leu Glu Ile Glu Pro Trp Ser Tyr Gly Tyr Val	960
305 310 315 320	
gac ata tct ttt tca cgg ctt tgg att aga acc ctt gct tgg aag cta Asp Ile Ser Phe Ser Arg His Trp Ile Arg Thr Leu Ala Trp Lys Leu	1008
325 330 335	
glg ctt cca aca agc ggt atg cga atc agt ttc ctt tca aat agc aag Val Leu Gln Ile Ser Gly Met Arg Ile Ser Phe Leu Ser Asn Ser Lys	1056
340 345 350	
aat aag cat att cca gta gaa att gct aga gac atg ttc gaa gac aca Asn Thr His Ile Pro Val Glu Ile Ala Arg Asp Met Leu Glu Asp Thr	1104
355 360 365	
ttt tta atc cca aaa aat ctt tat gca gtt cac ggt cca ggg ala tca Phe Leu Ile Pro Lys Asn Leu Tyr Ala Val His Gly Pro Gly Ile Ser	1152
370 375 380	
glg aaa gca cta gaa ata gcc gac gca tly gta gat gtt gtg aat cag Val Lys Ala Leu Glu Ile Ala Asp Ala Leu Val Asp Val Val Asn Gln	1200
385 390 395 400	
tac gat caa aat gca gag tgg gag gct tgg aat ttt ttg ttc gat ata	1248

Tyr Asp Gln Asn Ala Glu Ser Glu Ala Trp Asn Phe Leu Phe Asp His
 405 410 415
 too aaa ttt gtc ttc tct ctt aag oac tgt gat agc aca tta gtt gat 1296
 Ser Lys Phe Val Phe Ser Leu Lys His Cys Asp Ser Thr Leu Val Asp
 420 425 430
 aag ttt acg aca aag tgt cag tgt gac ctt atc acg ctt cct ctt tct 1344
 Lys Phe Thr Thr Lys Cys Gln Cys Ala Leu Ile Thr Leu Pro Leu Ser
 435 440 445
 aat ccg ctt gaa tcg aca gat ggt tct aaa gaa gat gta gat ggc ctt 1392
 Asn Pro Leu Glu Ser Thr Asp Gly Ser Lys Glu Asp Val Asp Ala Leu
 450 455 460
 cct taa 1398
 Pro
 165
 <210> 29
 <211> 485
 <212> DRT
 <213> *Saccharomyces cerevisiae*
 <400> 29
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 1 5 10 15
 Lys Cys Asp Arg Lys Lys Pro Cys Lys Cys Cys Leu Gln His Asn Leu
 20 25 30
 Gln Cys Thr Tyr Leu Arg Pro Leu Lys Lys Arg Gly Pro Lys Pro Val
 35 40 45
 Lys Val Arg Asn Leu Lys Lys Val Asp Asp val Gln val Phe Ser Lys
 50 55 60

Ser Ser Ser Gly Gly Ile Met Lys Val Pro Lys Ala Leu Ile Asp Gln
 65 70 75 80

Cys Leu Arg Leu Tyr Asn Asp Lys Leu Tyr Val Ile Trp Pro Leu Leu
 85 90 95

Cys Tyr Asp Asp Leu Tyr Glu Leu Leu Glu Lys Arg Tyr Asp Glu Thr
 100 105 110

Cys Val Tyr Trp Phe Leu Val Ser Leu Ser Ala Ala Thr Leu Ser Asp
 115 120 125

Leu Glu Thr Glu Ile Glu Ser Glu Gly Gly Val Thr Phe Thr Gly Ile
 130 135 140

Gln Leu Ser Ser Phe Cys Met Ser Ser Arg Gln Glu Phe Asp Asp Phe
 145 150 155 160

Asn Gly Ser Asp Ile Phe Lys Ile Met Thr Tyr Tyr Cys Leu Asn Arg
 165 170 175

Cys Tyr Ala Glu Met Ser Asn Ser Arg Thr Ser Tyr Arg Leu Ser Cys
 180 185 190

Glu Ala Val Gly Leu Ile Lys Leu Ala Gly Phe His Arg Glu Glu Thr
 195 200 205

Leu Lys Leu Leu Pro Phe Asp Glu Glu Glu Leu Gly Arg Lys Val Tyr
 210 215 220

Tyr Leu Leu Leu Leu Thr Glu Arg Tyr Phe Ser Val Tyr Thr His Cys

225	230	235	240
Ala Thr Ser Leu Asp Thr Thr Ile Ala Pro Pro Gln Pro Glu Asn Val			
245	250	255	
Thr Asp Pro Arg Leu Ser Leu Asp Ser Phe Leu Glu Met Ile Arg Val			
260	265	270	
Phe Thr Val Pro Gly Lys Cys Phe Phe Asp Ala Leu Ala Thr Asp Ser			
275	280	285	
Ala Asn Val Thr Cys Thr Glu Asp Ser Leu Lys Lys Ile Trp Arg Glu			
290	295	300	
Leu His Thr Val Pro Leu Glu Ile Glu Pro Trp Ser Tyr Gly Tyr Val			
305	310	315	320
Asp Ile Ser Phe Ser Arg His Trp Ile Arg Thr Leu Ala Trp Lys Leu			
325	330	335	
Val Leu Gln Ile Ser Gly Met Arg Ile Ser Phe Leu Ser Asn Ser Lys			
340	345	350	
Asn Thr His Ile Pro Val Glu Ile Ala Arg Asp Met Leu Glu Asp Thr			
355	360	365	
Phe Leu Ile Pro Lys Asn Leu Tyr Ala Val His Gly Pro Gly Ile Ser			
370	375	380	
Val Lys Ala Leu Glu Ile Ala Asp Ala Leu Val Asp Val Val Asn Gln			
385	390	395	400

Tyr Asp Cln Asn Ala Glu Ser Glu Ala Trp Asn Phe Leu Phe Asp Ile
 405 410 415

Ser Lys Phe Val Phe Ser Leu Gys His Cys Asp Ser Thr Leu Val Asp
 420 425 430

Lys Phe Thr Thr Lys Cys Glu Cys Ala Leu Ile Thr Leu Pro Leu Ser
 435 440 445

Asn Pro Leu Glu Ser Thr Asp Gly Ser Lys Glu Asp Val Asp Ala Leu
 450 455 460

Pro
 465

<210> 30
 <211> 2025
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(2025)

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 Met Ser Asp Val Asp Asn Trp Glu Pro Val Ser Asp Asn Glu Asp Ser
 1 5 10 15
 act gat tct gtg aaa caa ttg ggt ccc ccc ttt gag cat gca agt aac 96
 Thr Asp Ser Val Lys Glu Leu Gly Pro Pro Phe Glu His Ala Ser Asn
 20 25 30
 aat gac aat gcc ggc gat aat gaa gct gag tca ctg caa gaa glu ccc 144

Asn Asp Asn Ala Gly Asp Thr Glu Ala Glu Ser Leu Glu Glu Val Pro	35	40	45	
cta aat acc gag acc aac gac gta cgc aag aat tta gta gtg att aca				193
Leu Asn Thr Glu Thr Asn Asp Val Arg Tyr Asn Leu Val Val Ile Thr	50	55	60	
aac caa agt gcc gcc gat gaa cac cct acc gag atc aag cac gat caa				240
Asn Gln Ser Ala Ala Asp Glu His Pro Thr Glu Ile Lys His Asp Gln	65	70	75	80
tca agg act tct tgg cag tcc tgg tta ttc agt gga atg atc tct tgg				288
Ser Arg Thr Ser Ser Thr Ser Ser Phe Phe Ser Gly Met Ile Ser Ser	85	90	95	
ttt aag tca aac gtg aca tcc gaa gtt tct aga tca act acg cca act				336
Phe Lys Ser Asn Val Pro Ser Pro Val Ser Arg Ser Thr Thr Pro Thr	100	105	110	
tgg cca gtt tgg cca aca agc att ata tca cct aga agg ggg cct tcc				384
Ser Pro Val Ser Gln Pro Ser Ile Ile Ser His Arg Arg Glu Pro Ser	115	120	125	
atg ggg tcc aaa aga aya tca agc cgc cgt atc agt aat gcc uca att				432
Met Gly Ser Lys Arg Arg Ser Ser Arg Arg Ile Ser Asn Ala Thr Ile	130	135	140	
gct gaa ata ggc tct ccc ttg cca cag gtg gaa aag cct gat gag gtc				480
Ala Glu Ile Gly Ser Pro Leu Gln Gln Val Glu Lys Pro Asp Glu Val	145	150	155	160
aag aca aga ctc act cct tcc cca atg aca gaa gac aat tac gat cat				528
Lys Thr Arg Leu Thr Pro Ser Gln Met Lys Glu Asp Asn Tyr Asp His	165	170	175	
aga cga ttc gtg gaa gaa cgt tcc atg gac aca cct tat cac tat ggg				576
Arg Arg Phe Val Glu Glu Arg Tyr Met Asp Thr Pro Tyr His Tyr Ala	180	185	190	
tct gag cca aya aat aaa gac ttt cat gag aca ttc aag tcc gtt cct				624
Ser Glu Gln Arg Asn Lys Asp Phe His Glu Thr Phe Lys Ser Val Pro	195	200	205	

aaa gah gac aga cca ctg gat gat ttt aat tgt ggg ctg aat aga gag lys asp asp arg leu leu asp asp phe asn cys gly leu asn arg ala 210 215 220	673
ctg ctt tac cag ggg aaa cta tac ata aca gaa acg cat ctc tgc ttc leu leu tyr ala gly lys leu tyr ile thr glu thr his leu cys phe 225 230 235 240	720
aac tcc aat gtt ctt ggt tgg att gct aaa gta cta aat gag ttc gaa asn ser asn val leu gly trp phe ala lys val leu ile ala phe ala 245 250 255	768
gct gtc acg ttt atg gaa aaa act tct gct gct ggg tgg ttc ccc agc asp val thr phe met glu lys thr ser ala ala gly leu phe pro ser 260 265 270	816
gca ata tcc atc gaa aca aag atg ggc aaa act ctc ttt aat ggt ttt ala ile ser ile ala thr lys met gly lys thr leu phe asn gly phe 275 280 285	864
ata tcc agg gat gct gca ttt gga tta atg aaa gaa ggc tgg tca aga ile ser arg asp ala ala phe gly leu met lys glu val trp ser arg 290 295 300	912
acc tta tta cag aag gac atg gcc agc gaa aac atc aat acc aac gca thr leu leu ala lys asp met ala ser glu asn ile asn thr lys ala 305 310 315 320	960
gaa aag tca gga aat ggc aaa gag att gat gat gca ata aac tcc atc glu lys ser gly asn gly lys glu ile asp asp ala ile asn ser ile 325 330 335	1008
gat gag gaa aac aat gat aaa gac gct aat gat aat gac act aat gaa asp ala glu asn asn asp lys asp ala asn asp asn asp thr asn glu 340 345 350	1056
aat gac gat gaa aat atc tct aca aat gag act acc ccc aat agt acg asn asp asp glu asn ile ser thr asn glu thr thr pro asn ser thr 355 360 365	1104
agt ttc tgg cag gat aaa gaa aaa gag aaa gag tat aaa ctg cgt gcc 370 375 380	1152

Ser Ser Ser Pro Asp Lys Glu Lys Glu Lys Ala Tyr Lys Leu Arg Ala	
370	375 380
gat taa taa tat cag tat ggt ggt cca ata tat cgt cgt taa aca agc	1230
Asp Ser Ser Tyr Gln Tyr Asp Gly Pro Ile Tyr His His Ser Thr Ser	
385	390 395 400
ttt cag gct gaa cct atg gcc aat aac gag ttt gtt ctg aag gag tta	1240
Phe Pro Ala Glu Pro Met Ala Asn Asn Glu Phe Val Leu Lys Glu Leu	
405	410 415
cca ttc gat tgt gca cct ggt ata ctt ttt gag atc atg ttc aac taa	1296
Pro Phe Asp Cys Ala Pro Gly Ile Leu Phe Glu Ile Met Phe Asn Ser	
420	425 430
gag caa aac gaa ttt ctt cta gat ttt tta cgg ggt caa gaa ggt taa	1344
Glu Gln Asn Glu Phe Leu Leu Asp Phe Leu Arg Gly Gln Glu Gly Ser	
435	440 445
caa att acc act att cca aat ttc acg agc att gac gaa tct tcc atg	1392
Gln Ile Thr Thr Ile Pro Asn Phe Thr Ser Ile Asy Gly Ser Ser Met	
450	455 460
act ttg aag cgt gag tat tca tac gag aaa gca ttg cag ttt cct gag	1440
Thr Leu Lys Arg Glu Tyr Ser Tyr Glu Lys Ala Leu His Phe Pro Ala	
465	470 475 480
ggg ccc aag tcc acg aca tgt tat gtt gct gag gta ata aag aga aaa	1488
Gly Pro Lys Ser Thr Thr Cys Tyr Val Ala Glu Val Ile Lys Arg Lys	
485	490 495
gat act gat act tac tat gag gtt ctc agt agc ata cgc act cag aac	1536
Asp Pro Asp Thr Tyr Tyr Glu Val Ile Ser Ser Ile Arg Thr Pro Asn	
500	505 510
gtg ccc agt ggt ggt agt ttc taa act aag aca agg tat cta ctc cgt	1584
Val Pro Ser Gly Gly Ser Phe Ser Thr Lys Thr Arg Tyr Leu Ile Arg	
515	520 525
tgg aat gac gaa ata acg tgt ctg tta cgg gta tcc ttt tgg gtg gaa	1632
Trp Asn Asp Glu Ile Thr Cys Leu Leu Arg Val Ser Phe Trp Val Glu	
530	535 540

tgg act ggt tcc aqt tgg atc aaa ggt atg gtt gaa aat gga tga aag	1680
Trp Thr Gly Ser Ser Trp Ile Lys Gly Met Val Glu Asn Gly Cys Tyr	
545 550 555 560	
aat ggt aca ttg gag gct ggc cna tta atg gag cgt att ctt tcc aag	1728
Asn Gly Gln Leu Glu Ala Ala Gln Leu Met Glu Arg Ile Leu Ser Lys	
565 570 575	
ttc atc aag aac aat gtc gaa gag tgc aca att act atc agc aag gag	1776
Phe Ile Lys Asn Asn Val Glu Glu Cys Gln Ile Thr Ile Ser Lys Glu	
580 585 590	
gaa gag gag cna gat gat aca gaa gaa aca aat aag ttg aca gag gtt	1824
Glu Glu Glu Gln Asp Asp Lys Glu Val Lys Asn Lys Leu Lys Glu Val	
595 600 605	
gac ctt gaa caa caa aga gaa gag gtt gtt acg gct ccc gca att gca	1872
Asp Leu Glu Gln Pro Arg Glu Ala Val Val Thr Ala Pro Ala Ile Ala	
610 615 620	
gag acg caa ggt ctc aag gtc aca atg gaa aca tgg tgg ttc tta tcc	1920
Glu Gln Gln Gly Leu Lys Val Thr Met Glu Thr Trp Leu Phe Leu Tyr	
625 630 635 640	
ttg att tgg gtc gtt ttg cta ttg ttt aat ctg ttc tcc aca cgt tca	1968
Leu Ile Val Val Val Leu Leu Leu Phe Asn Leu Phe Tyr Ile Arg Met	
645 650 655	
att gct gtc tca tta cat caa ctg gta aag atg caa ttg gta gaa ctg	2016
Ile Ala Val Ser Leu His Gln Leu Val Lys Leu Gln Leu Val Glu Leu	
660 665 670	
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Lys Leu	

<210> 31

<211> 674

<212> PRT

<213> Saccharomyces cerevisiae

<400> 31

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 20 25 30

Asn Asp Asn Ala Gly Asp Thr Glu Ala Glu Ser Leu Glu Glu Val Pro
 35 40 45

Leu Asn Thr Glu Thr Asn Asp Val Arg Lys Asn Leu Val Val Ile Thr
 50 55 60

Asn Glu Ser Ala Ala Asp Glu His Pro Thr Glu Ile Lys His Asp Glu
 65 70 75 80

Ser Arg Thr Ser Ser Thr Ser Ser Phe Phe Ser Gly Met Ile Ser Ser
 85 90 95

Phe Lys Ser Asn Val Pro Ser Pro Val Ser Arg Ser Thr Thr Pro Thr
 100 105 110

Ser Pro Val Ser Gln Pro Ser Ile Ile Ser His Arg Arg Glu Pro Ser
 115 120 125

Met Gly Ser Lys Arg Arg Ser Ser Arg Arg His Ser Asn Ala Thr Ile
 130 135 140

Ala Glu Ile Gly Ser Pro Leu Gln Gln Val Glu Lys Pro Asp Glu Val
 145 150 155 160

Lys Thr Arg Leu Thr Pro Ser Gln Met Lys Glu Asp Asn Tyr Asp His
165 170 175

Arg Arg Phe Val Glu Glu Arg Tyr Met Asp Thr Pro Tyr His Tyr Ala
180 185 190

Ser Glu Gln Arg Asn Lys Asp Phe His Glu Thr Phe Lys Ser Val Pro
195 200 205

Lys Asp Asp Arg Leu Leu Asp Asp Phe Asn Cys Gly Leu Asn Arg Glu
210 215 220

Leu Leu Tyr Gln Gly Lys Leu Tyr His Thr Gln Thr His Leu Cys Phe
225 230 235 240

Asn Ser Asn Val Leu Gly Trp Ile Ala Lys Val Leu Tyr Ala Phe Glu
245 250 255

Asp Val Thr Phe Met Glu Lys Thr Ser Ala Ala Gly Leu Phe Pro Ser
260 265 270

Ala Ile Ser Ile Glu Thr Lys Met Gly Lys Thr Leu Phe Asn Gly Phe
275 280 285

Ile Ser Arg Asp Ala Ala Phe Gly Leu Met Lys Glu Val Trp Ser Arg
290 295 300

Thr Leu Leu Cln Lys Asp Met Ala Ser Glu Asn Ile Asn Thr Lys Ala
305 310 315 320

Glu Lys Ser Gly Asn Gly Lys Glu Ile Asp Asp Ala Ile Asn Ser Ile
325 330 335

Asp Glu Glu Asn Asn Asp Lys Asp Ala Asn Asp Asn Asp Thr Asn Glu
340 345 350

Asn Asp Asp Glu Asn Ile Ser Thr Asn Glu Thr Thr Pro Asn Ser Thr
355 360 365

Ser Ser Ser Pro Asp Lys Glu Gln Glu Lys Ala Tyr Lys Leu Arg Ala
370 375 380

Asp Ser Ser Tyr Glu Tyr Asp Gly Pro Ile Tyr His His Ser Thr Ser
385 390 395 400

Phe Pro Ala Glu Pro Met Ala Asn Asn Glu Phe Val Leu Lys Glu Leu
405 410 415

Pro Phe Asp Cys Ala Pro Gly Ile Leu Phe Glu Ile Met Phe Asn Ser
420 425 430

Glu Glu Asn Glu Phe Leu Leu Asp Phe Leu Arg Gly Glu Glu Gly Ser
435 440 445

Gln Ile Thr Thr Ile Pro Asn Phe Thr Ser Ile Asp Gly Ser Ser Met
450 455 460

Thr Leu Lys Arg Glu Tyr Ser Tyr Glu Lys Ala Leu His Phe Pro Ala
465 470 475 480

Gly Pro Lys Ser Thr Thr Cys Tyr Val Ala Glu Val Ile Lys Arg Lys
485 490 495

Asp Pro Asp Thr Tyr Tyr Glu Val Ile Ser Ser His Arg Thr Pro Asn
 560 565 570

Val Pro Ser Gly Gly Ser Phe Ser Thr Lys Thr Arg Tyr Leu Ile Arg
 575 580 585

Trp Asn Asp Glu Ile Thr Cys Leu Leu Arg Val Ser Phe Trp Val Glu
 590 595 600

Trp Thr Gly Ser Ser Trp Ile Lys Gly Met Val Glu Asn Gly Cys Lys
 605 610 615 620

Asn Gly Glu Leu Glu Ala Ala Gln Leu Met Glu Arg Ile Leu Ser Lys
 625 630 635

Phe Ile Lys Asn Asn Val Glu Glu Cys Gln Ile Thr Ile Ser Lys Glu
 635 640 645

Glu Glu Glu Gln Asp Asp Lys Glu Val Lys Asn Lys Leu Lys Glu Val
 650 655 660

Asp Leu Glu Gln Pro Arg Glu Ala Val Val Thr Ala Pro Ala Ile Ala
 665 670 675

Glu Gln Gln Gly Leu Lys Val Thr Met Glu Thr Trp Leu Phe Leu Tyr
 680 685 690 695

Leu Ile Val Val Val Leu Leu Leu Phe Asn Leu Phe Tyr Ile Arg Ser
 700 705 710

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Lys Leu

<210> 32

<211> 1185

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1185)

<400> 32

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cca ggt aat aca ttg aca gcc ggt att gtc ggt ttg gcc aat ggt ggt 96
 Pro Gly Asn Asn Leu Lys Ala Gly Ile Val Gly Leu Ala Asn Val Gly
 20 25 30

aag cct acc lll lll cca gcc atc act aga tgt cca ttg ggt aac cca 144
 Lys Ser Thr Phe Phe Gln Ala Ile Thr Arg Cys Pro Leu Gly Asn Pro
 35 40 45

gct aac tat cca ttc gct acc att gat cca gaa gaa gcc cgt gtt aat 192
 Ala Asn Tyr Pro Phe Ala Thr Ile Asp Pro Glu Glu Ala Arg Val Ile
 50 55 60

gcc cca cct cca aga ttt gat aag ttg tgt gaa atc tac aag aag cca 240
 Val Pro Ser Pro Arg Phe Asp Lys Ser Cys Glu Ile Tyr Lys Lys Thr
 65 70 75 80

gct ttg gaa gtt cca gct aat ttg acc gtt tac gat att gct ggt ttg 288
 Ala Ser Glu Val Pro Ala His Leu Thr Val Tyr Asp Ile Ala Gly Leu

85	90	95	
act aag ggt gcc tct gct ggt gaa ggt ttg ggt aat gct ttc ttg tct			335
Thr Lys Gly Ala Ser Ala Gly Glu Gly Leu Gly Asn Ala Phe Leu Ser			
130	105	110	
cac atc aga tca gtc gat tct atc tac caa gtc gtt cgt tgt ttc gat			384
His Ile Arg Ser Val Asp Ser Ile Tyr Glu Val Val Arg Cys Phe Asp			
115	120	125	
gat gct gaa att atc cac gtt gag ggt gac gtt gat cca gtt cgt gat			432
Asp Ala Glu Ile Ile His Val Glu Gly Asp Val Asp Pro Val Arg Asp			
130	135	140	
tta gaa ttt att aac caa gaa cta aga ttg aaa gat att gaa ttc gca			480
Leu Glu Ile Ile Asn Glu Glu Lys Arg Asn Tyr Asp Ile Glu Phe Ala			
145	150	155	150
caa aag gct ttg gaa ggt gct gaa aag att gcc aaa aga cgt ggt caa			528
Glu Lys Ala Leu Glu Gly Ala Glu Lys Ile Ala Lys Arg Gly Gly Glu			
165	170	175	
tct ttg gaa gtc aaa caa aag aag gaa gaa atg gat ttg att acg aaa			576
Ser Leu Glu Val Lys Glu Lys Lys Glu Glu Met Asp Leu Ile Thr Lys			
180	185	190	
atc att aaa ttg cta gag agt ggt caa aga gtt gct aat aac tcc tgg			624
Ile Ile Lys Leu Leu Glu Ser Gly Glu Arg Val Ala Asn His Ser Thr			
195	200	205	
act tca aaa gaa gtt gaa att atc aac tcc atg ttc ttg ttg act gct			672
Thr Ser Lys Glu Val Glu Phe Ile Asn Ser Met Phe Leu Leu Thr Ala			
210	215	220	
aag cca tgt atc tat ttg att aat tta tct gaa aga gat tac atc aga			720
Lys Pro Cys Ile Tyr Leu Ile Asn Leu Ser Glu Arg Asp Tyr Ile Arg			
225	230	235	240
aag aaa aac aag cat ctg cta aga atc aag gaa tgg gta gac aag tac			768
Lys Lys Asn Lys His Leu Leu Arg Ile Lys Glu Trp Val Asy Lys Tyr			
245	250	255	

<p> tct cca ggt gac ttg atc att cca ttc agt gtt tct cta gaa gaa aga Ser Pro Gly Asp Leu Ile Ile Pro Phe Ser Val Ser Leu Glu Glu Arg 260 265 270 </p>	816
<p> cta tct cat atc tcc cca gaa gat gct gaa gaa gaa ttg aag aza ctg Leu Ser His Met Ser Pro Glu Asp Ala Glu Glu Glu Leu Lys Lys Leu 275 280 285 </p>	864
<p> aag aca ata tct gcc ttg cca aag att atc act acc atg aga aza aag Glu Thr Ile Ser Ala Leu Pro Lys Ile Ile Thr Thr Met Arg Glu Tyr 290 295 300 </p>	912
<p> tta gat ttg att tcc ttt ttc acc tgc ggt cca gat gaa gtt ag- gaa Leu Asp Leu Ile Ser Phe Phe Thr Cys Gly Pro Asp Glu Val Arg Glu 305 310 315 320 </p>	960
<p> tgg acc atc aga aga ggt act aaa gct cca caa gct gct ggt gtt att Trp Thr Phe Arg Arg Gly Thr Lys Ala Pro Gln Ala Ala Gly Val Ile 325 330 335 </p>	1008
<p> cat aac gat tta atg act acc ttt att ttg gct caa gtt atg aza tgt His Asn Asp Leu Met Asn Thr Thr Ile Leu Ala Gln Val Met Lys Cys 340 345 350 </p>	1056
<p> gaa ggt gtc ttc gaa ttc aag gac gat tct gcc atc aag gcc gct ggt Glu Asp Val Phe Glu Tyr Lys Asp Asp Ser Ala Ile Lys Ala Ala Gly 355 360 365 </p>	1104
<p> aag ttg atg caa aag ggt aaa aac tat gtc gtc gaa gaa ggt gat atc Lys Leu Met Glu Lys Gly Lys Asp Tyr Val Val Glu Asp Gly Asp Phe 370 375 380 </p>	1152
<p> att taa ttc aga gct ggt gct ggt aag act tga Ile Tyr Phe Arg Ala Gly Ala Gly Lys Asn 385 390 </p>	1188

<210> 33

<211> 394

<212> PRT

<213> Saccharomyces cerevisiae

<400> 33

Met Pro Pro Lys Lys Glu Val Glu Glu Lys Lys Val Leu Leu Gly Arg
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Pro Gly Asn Asn Leu Lys Ala Gly Ile Val Gly Leu Ala Asn Val Gly
 20 25 30

Lys Ser Thr Phe Phe Gln Ala Ile Thr Arg Cys Pro Leu Gly Asn Pro
 35 40 45

Ala Asn Tyr Pro Phe Ala Thr Ile Asp Pro Glu Glu Ala Arg Val Ile
 50 55 60

Val Pro Ser Pro Arg Phe Asp Lys Leu Cys Glu Ile Tyr Lys Lys Thr
 65 70 75 80

Ala Ser Glu Val Pro Ala His Leu Thr Val Tyr Asp Ile Ala Gly Leu
 85 90 95

Thr Lys Gly Ala Ser Ala Gly Glu Gly Leu Gly Asn Ala Phe Leu Ser
 100 105 110

His Ile Arg Ser Val Asp Ser Ile Tyr Gln Val Val Arg Cys Phe Asp
 115 120 125

Asp Ala Glu Ile Ile His Val Glu Gly Asp Val Asp Pro Val Arg Asp
 130 135 140

Leu Glu Ile Ile Asn Glu Glu Leu Arg Leu Lys Asp Ile Glu Phe Ala
 145 150 155 160

Gln Lys Ala Leu Glu Gly Ala Glu Lys Ile Ala Lys Arg Gly Gly Gln
 165 170 175

Ser Leu Glu Val Lys Gln Lys Lys Gln Glu Met Asp Leu Ile Thr Lys
 180 185 190

Ile Ile Lys Leu Leu Glu Ser Gly Gln Arg Val Ala Asn His Ser Thr
 195 200 205

Thr Ser Lys Gln Val Glu Ile Ile Asn Ser Met Phe Leu Leu Thr Ala
 210 215 220

Lys Pro Cys Ile Tyr Leu Ile Asn Leu Ser Glu Arg Asp Tyr Ile Arg
 225 230 235 240

Lys Lys Asn Lys His Leu Leu Arg Ile Lys Glu Trp Val Asp Lys Tyr
 245 250 255

Ser Pro Gly Asp Leu Ile Ile Pro Phe Ser Val Ser Leu Glu Glu Arg
 260 265 270

Leu Ser His Met Ser Pro Glu Asp Ala Glu Glu Glu Leu Lys Lys Leu
 275 280 285

Gln Thr Ile Ser Ala Leu Pro Lys Ile Ile Thr Thr Met Arg Gln Lys
 290 295 300

Leu Asp Leu Ile Ser Phe Phe Thr Cys Gly Pro Asp Glu Val Arg Glu
 305 310 315 320

Trp Thr Ile Arg Arg Gly Thr Lys Ala Pro Gln Ala Ala Gly Val Ile

325

330

335

His Asn Asp Leu Met Asn Thr Phe Ile Leu Ala Gln Val Met Lys Cys
 340 345 350

Glu Asp Val Phe Glu Tyr Lys Asp Asn Ser Ala Ile Lys Ala Ala Gly
 355 360 365

Lys Leu Met Gln Lys Gly Lys Asp Tyr Val Val Glu Asp Gly Asp Ile
 370 375 380

Tle Tyr Phe Arg Ala Gly Ala Gly Lys Asn
 385 390

<210> 34

<211> 735

<212> HNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (735)

<400> 34

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 1 5 10 15

act aca aac gct gct aat aaa ctc att gtc tta tat ttt aaa gct caa 96
 Thr Thr Asn Ala Ala Asn Lys Leu ile Val Leu Tyr Phe Lys Ala Gln
 20 25 30

tgg gct gat cct tgc aaa act atg agc cag gtc cta gaa gct gtt agt 144
 Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
 35 40 45

gaa aaa gtt agg caa gag gat gtc cgg ttt tta tca ata gat gca gaa Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp 50 55 60	192
gaa cat cca gaa ata tca gac ctt ttt gag att gca gcc gta cca tac Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr 65 70 75 80	240
Llu gtc ttc att cca aat ggt act att gta aaa gaa ata tca gcc gca Phe Val Phe Ile Glu Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala 95 90 95	288
gat cct aag gag lll ytg aaa agc tta gaa att ctt tcg aat gct tct Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser 100 105 110	336
gcc tca cta gcg aac aat guu aag ggt cct aaa tct acg tct gat gag Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu 115 120 125	384
gaa agc agc ggg tct tcc gat gat gaa gag gac gaa act gaa gaa gaa Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu 130 135 140	432
ata aat gct agg ctg ctg aag cta gta caa gct gca cct gty atg ctg Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu 145 150 155 160	480
ttc atg aaa gga agc cca tca gaa cct aaa tgc gga ttt tct aqa cag Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Glu 165 170 175	528
tta gtt ggt atc ctc aga gaa sac caa ata agg ttc gga ttt ttt gat Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asp 180 185 190	576
ata tta aga gac gaa aac gtt aga caa agc ttg aag aag ttt tct gat Ile Leu Arg Asp Glu Asn Val Arg Gln Ser Leu Lys Lys Phe Ser Asp 195 200 205	624
agg cct act ttt cct cag tta tat atc aat ggg gag ttc cag gga ggt Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly 210 215 220 225 230 235 240	672

210	215	220	
ttg gat att atc aag gaa tct ata gaa gaa gat cct gaa tat ttc cca			720
Leu Asp Ile Ile Lys Glu Ser Ile Glu Glu Asp Pro Glu Tyr Phe Gln			
225	230	235	240
cat gct cta cag laa			735
His Ala Leu Gln			

<210> 35
 <211> 244
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 35

Met Thr Val Val Glu Ile Lys Ser Thr Asp Gln Phe Thr Gln Leu Thr
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Thr Thr Asn Ala Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
20 25 30

Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
35 40 45

Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp
50 55 60

Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr
65 70 75 80

Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala
85 90 95

Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser
 100 105 110

Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu
 115 120 125

Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu
 130 135 140

Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu
 145 150 155 160

Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Gln
 165 170 175

Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asy
 180 185 190

Ile Leu Arg Asp Glu Asp Val Arg Gln Ser Leu Lys Lys Phe Ser Asp
 195 200 205

Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly
 210 215 220

Leu Asp Ile Ile Lys Glu Ser Ile Glu Glu Asp Pro Glu Tyr Phe Gln
 225 230 235 240

His Ala Leu Gln

<211> 351

4212 LIMA

<313> *Saccharomyces cerevisiae*

e2202

<221> CDS

<222> (1) , , (351)

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 1 5 10 15

Ttg att ttt ttt aag cna tac gta oca ttt gaa gag gag gga gga tat 96
 Leu Ile Phe Phe Lys Gln Tyr Val Pro Phe Ala Ala Ala Gly Gly Tyr
 20 25 30

ccg ata tgg ttt cta ctc atc aaa gtt cly acc ggc tca aag aat tta 144
Pro Ile Ser Phe Leu Phe Ile Lys Val Leu Thr Ala Ser Thr Asn Leu
35 40 45

cta ctt tct tct tcc tct gga ggg tcc tgg aat aag tta tcc aaa gag 192
Leu Lau Ser Ser Ser Ser Gly Gly Ser Trp Aan Lys Leu Ser Lys Glu
50 55 60

240
 65 70 75 80
 GCG GAA TTA CTC AAA GTC ATT CTC ACA CAC TAT GTT GGT CCG ATT CTT
 GCG GGA LAA LAA LYS VAL ILE LEU THR HIS PHE LEU VAL PRO ILE PHE

Uct tta tta ttc caa tat att att tta tta gaa gac aga cag caa gaa 90
 Phe Phe Leu Phe Glu Tyr Ile Ile Leu Ser Glu Asp Arg Gln Gln Glu 95

Arg Gln Pro Lys Phe Arg Asp Asn Ala Lys Phe Asp Gly His Ala Lys

aca tgc cat ata taa 35
Thr Cys His Ile
115

<210> 37
<211> 116
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 37

Met His Ile Leu Phe Leu Phe Ile Phe His Cys Leu Ala Phe Tyr Asp
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20 25 30

Pro Ile Ser Phe Leu Phe Ile Lys Val Leu Thr Ala Ser Thr Asp Leu
35 40 45

Leu Leu Ser Ser Ser Ser Gly Gly Ser Trp Asn Lys Leu Ser Lys Glu
50 55 60

Ser Gln Leu Leu Lys Val Ile Leu Thr His Phe Leu Val Pro Ile Phe
65 70 75 80

Phe Phe Leu Phe Gln Tyr Ile Ile Leu Ser Glu Asp Arg Gln Gln Glu
85 90 95

Arg Gln Pro Lys Phe Arg Asp Asn Ala Lys Phe Asp Gly His Ala Lys
100 105 110

Thr Cys His Ile
115

<210> 38

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<211> 900
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(900)

<400> 38
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1 5 10 15

tca aga cct tct tat ccc tcc gat ttt taa aag atg akt gat gaa tac      96
Ser Arg Pro Ser Tyr Pro Ser Asp Phe Tyr Lys Met Ile Asp Glu Tyr
20 25 30

cac gac gga gaa agg cca tta ctc gta gat gtt ggc tgt gga cca ggt      144
His Asp Gly Glu Arg Tyr Leu Met Val Asp Val Clr Cys Gly Pro Gly
35 40 45

act gcc act tta cca atg gct cag gag tta aaa cca ttc gaa cca att      192
Thr Ala Thr Leu Glu Met Ala Gln Glu Leu Lys Pro Phe Glu Gln Ala
50 55 60

atc gga agc gat ctc tcc gct acc atg att aag act gca gaa gta ata      240
Ile Gly Ser Asp Leu Ser Ala Thr Met Ile Lys Thr Ala Glu Val Ile
65 70 75 80

aag gaa gga agt cct gat aca tac aza aac gtt tca ttc aag att tct      288
Lys Glu Gly Ser Pro Asp Thr Tyr Lys Asn Val Ser Phe Lys Ile Ser
85 90 95

tca agt gat gat ttt aaa ttc cta ggc gag gat tca gta gac aca cag      336
Ser Ser Asp Asp Phe Lys Phe Leu Gly Ala Asp Ser Val Asp Lys Glu
100 105 110

aaa att gat atg att acc gaa gla gaa tgt gct cat tgg ttc gat ttc      384
Lys Ile Asp Met Ile Thr Ala Val Glu Cys Ala His Trp Phe Asp Phe
115 120 125

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gaa aaa ttt cag cga tct gct tat gcc aac ttg aga aaa gat ggt act Glu Lys Phe Gln Arg Ser Ala Tyr Ala Asn Leu Arg Lys Asp Gly Thr 130 135 140	432
atc gct att tgg ggt tat gcg gac cca att ttc cgg gac tac cct gaa Ile Ala Ile Trp Gly Tyr Ala Asp Pro Ile Phe Pro Asp Tyr Pro Glu 145 150 155 160	440
ttt gat gat ctg atg att gaa gtt cct tac ggg aag caa gga ctg gga Phe Asp Asp Leu Met Ile Glu Val Pro Tyr Gly Lys Gln Gly Leu Gly 165 170 175	528
ccc tat tgg gaa caa ccg ggg aga tct cgc ctt cgt aat atg ctg aaa Pro Tyr Trp Glu Gln Pro Gly Arg Ser Arg Leu Arg Asn Met Leu Lys 180 185 190	576
gac tct cac tta gac cca gaa ctt ttc cat gat ata caa gtt tca tat Asp Ser His Leu Asp Pro Glu Leu Phe His Asp Ile Gln Val Ser Tyr 195 200 205	624
ttt tgt gcc gcc gat gtg aga gac aaa gta aaa ctc cac cag cat aca Phe Cys Ala Glu Asp Val Arg Asp Lys Val Lys Leu His Gln His Thr 210 215 220	672
aag aag ccc tly ctc atc aga aag cag gtc acc cta gtc gag ttt gca Lys Lys Pro Leu Leu Ile Arg Lys Gln Val Thr Leu Val Glu Phe Ala 225 230 235 240	720
gat tat qtc aqa adc tgg aqc qct tac cat cag tgg aaq cag qat cca Asp Tyr Val Arg Thr Trp Ser Ala Tyr His Gln Thr Lys Gln Asp Pro 245 250 255	768
aag aac aaa gat aac gaa gat gta gca gat tgg ttt att aaa gag tca Lys Asn Lys Asp Lys Glu Asp Val Ala Asp Trp Phe Ile Lys Glu Ser 260 265 270	816
cta agg agg agg ccg gaa ctt tcc acc acc acc aaa att gaa gtt gtt Leu Arg Arg Arg Pro Glu Leu Ser Thr Asn Thr Lys Ile Glu Val Val 275 280 285	864
tgg aat act ttt tac aaa ctt gcc aaa agg gtc tga Trp Asn Thr Phe Tyr Lys Leu Gly Lys Arg Val	900

290

295

<210> 39

<211> 299

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 39

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Ser	Arg	Pro	Ser	Tyr	Pro	Ser	Asp	Phe	Tyr	Lys	Met	Ile	Asp	Glu	Tyr
		20						25						30	

His	Asp	Gly	Glu	Arg	Lys	Leu	Leu	Val	Asp	Val	Gly	Cys	Gly	Pro	Gly
		35						40					45		

Thr	Ala	Thr	Leu	Glu	Met	Ala	Gln	Glu	Leu	Lys	Pro	Phe	Glu	Gln	Ile
	50						55					60			

Ile	Gly	Ser	Asp	Leu	Ser	Ala	Thr	Met	Ile	Lys	Thr	Ala	Glu	Val	Ile
65					70					75					80

Lys	Glu	Gly	Ser	Pro	Asp	Thr	Tyr	Lys	Asn	Val	Ser	Phe	Lys	Ile	Ser
					85					90				95	

Ser	Ser	Asp	Asp	Phe	Lys	Phe	Leu	Gly	Ala	Asp	Ser	Val	Asp	Lys	Gln
					100				105					110	

Lys	Ile	Asp	Met	Ile	Thr	Ala	Val	Glu	Cys	Ala	His	Trp	Phe	Asp	Phe
			115					120						125	

Ser Lys Phe Gln Arg Ser Ala Tyr Ala Asn Leu Arg Lys Asp Gly Thr
 130 135 140

Ile Ala Ile Trp Gly Tyr Ala Asp Pro Ile Phe Pro Asp Tyr Pro Glu
 145 150 155 160

Phe Asp Asp Leu Met Ile Glu Val Pro Tyr Gly Lys Gln Gly Leu Gly
 165 170 175

Pro Tyr Trp Glu Gln Pro Gly Arg Ser Arg Leu Arg Asn Met Leu Lys
 180 185 190

Asp Ser His Leu Asp Pro Glu Leu Phe His Asp Ile Gln Val Ser Tyr
 195 200 205

Phe Cys Ala Glu Asp Val Arg Asp Lys Val Iys Leu His Gln His Thr
 210 215 220

Lys Lys Pro Leu Leu Ile Arg Lys Gln Val Thr Leu Val Glu Phe Asn
 225 230 235 240

Asp Tyr Val Arg Thr Trp Ser Ala Tyr His Gln Trp Lys Gln Asp Pro
 245 250 255

Lys Asn Lys Asp Lys Glu Asp Val Ala Asp Trp Phe Ile Lys Glu Ser
 260 265 270

Leu Arg Arg Arg Pro Glu Leu Ser Thr Asn Thr Lys Ile Glu Val Val
 275 280 285

Trp Asn Thr Phe Tyr Lys Leu Gly Lys Arg Val
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<210> 40
 <211> 336
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
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 Met Lys Gly Ser Lys Ser His Leu Val Phe Thr Leu Leu Gln Val Ser
 1 5 10 15
 caa cta aat gtt ttt ctt ttc ttt cta ggt ttt ttg ttg cca tta tgc 96
 Gln Leu Asn Val Phe Leu Phe Phe Leu Gly Phe Leu Leu Pro Leu Phe
 20 25 30
 tta gga cly ttc gtt tca ctg ggc tct ttg gct att gca cta tcc tct 144
 Leu Gly Leu Phe Val Ser Leu Arg Ser Leu Ala Leu Ala Leu Ser Ser
 35 40 45
 gga tgg ttt att aag gat ctg ata cta ttt ggc aac ttt cca gaa gca 192
 Gly Trp Phe Ile Met Asp Leu Ile Leu Phe Arg Thr Phe Pro Glu Ala
 50 55 60
 gaa tta ttt cca gca ctc atc ggt aaa cca tat ggt ctg ggg att aat 240
 Glu Leu Tyr Pro Ala Val Ile Gly Lys Pro Ser Gly Leu Gly Leu Thr
 65 70 75 80
 gag gaa ttt gag ttt ata tcc att ttt ttc cct gat gtt cag caa aac 288
 Glu Ala Phe Glu Phe Ile Ser Ile Phe Phe Pro Asp Val Gln Gln Thr
 85 90 95
 gaa aga aal ala aua tac aac tgg gaa aga tgt ttt aat ggt gag taa 336
 Glu Arg Asn Ile Lys Tyr Asn Trp Glu Arg Cys Phe Asn Gly Glu
 100 105 110

<210> 41
 <211> 111
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 41

Met Lys Gly Ser Lys Ser His Leu Val Phe Thr Leu Leu Gln Val Ser
 1 5 10 15

Gln Leu Asn Val Phe Leu Phe Phe Leu Gly Phe Leu Leu Pro Leu Phe
 20 25 30

Leu Gly Leu Phe Val Ser Leu Arg Ser Leu Ala Leu Ala Leu Ser Ser
 35 40 45

Gly Trp Phe Ile Met Asp Leu Ile Leu Phe Arg Thr Phe Pro Glu Ala
 50 55 60

Glu Leu Tyr Pro Ala Val Ile Gly Lys Pro Ser Gly Leu Gly Leu Thr
 65 70 75 80

Glu Ala Phe Glu Phe Ile Ser Ile Phe Phe Pro Asp Val Gln Glu Thr
 85 90 95

Glu Arg Asn Ile Lys Tyr Asn Trp Glu Arg Cys Phe Asn Gly Glu
 100 105 110

<210> 42
 <211> 2556
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (2556)

<400> 42

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Met	Pro	Lys	Asn	Ser	His	His	His	Arg	Ser	Ser	Ser	Val	Asn	Ser	Thr	
1			5					10					15			

aag	agt	cgt	tct	acg	gaa	tct	acg	aat	aaa	tgg	aaa	att	ccg	cac	tat	96
Lys	Ser	Arg	Ser	Thr	Glu	Ser	Thr	Asn	Lys	Trp	Lys	Ile	Pro	His	Tyr	
			20					25				30				

Lal	cgc	aya	ccc	gct	agc	ggc	agc	aca	caa	gct	tgg	ccg	gac	acg	aac	144
Tyr	Arg	Arg	Ser	Ala	Ser	Gly	Ser	Thr	Gln	Ala	Ser	Pro	Asp	Arg	Asn	
			35					40				45				

ccc	cca	aca	ggc	cca	tgt	agc	act	cca	gta	ata	ccc	act	atg	aat	ggt	192
Ser	Ser	Thr	Gly	Ser	Cys	Ser	Thr	Pro	Val	Leu	Pro	Thr	Met	Asn	Val	
			50				55					60				

atg	tct	agc	cgc	aaa	aaa	gtt	tgg	cta	gag	gat	ccc	aga	gac	aac	cat	240
Ile	Ser	Ser	Pro	Lys	Lys	Val	Leu	Leu	Glu	Asp	Pro	Arg	Asp	Asn	Ile	
65					70					75				80		

act	aag	gag	aag	aag	agt	agt	aga	aag	aaa	cca	ggc	gaa	atg	gtc	ttc	288
Thr	Lys	Ala	Lys	Lys	Ser	Ser	Arg	Lys	Cys	Ser	Gly	Glu	Met	Val	Phe	
			85					90				95				

gtc	aat	tat	act	gta	cag	gac	acg	gct	aac	gaa	aat	gat	act	gac	tgg	336
Val	Asn	Tyr	Thr	Val	Gln	Asp	Thr	Ala	Asn	Glu	Asn	Asp	Thr	Asp	Leu	
			100					105				110				

caa	acc	cag	ccg	gtt	tct	gtg	ccc	gca	cca	aag	gag	aaa	tta	aag	aag	384
Gln	Thr	Gln	Pro	Val	Ser	Val	Pro	Ala	Pro	Lys	Ala	Lys	Leu	Lys	Lys	
			115				120					125				

aaa	ccc	ccc	aaa	agg	aga	atg	cly	aaa	ata	ttt	gga	tgg	cca	aag	aac	432
Lys	Ser	Ser	Lys	Arg	Met	Leu	Lys	Ile	Phe	Gly	Ser	Ser	Lys	Asn		
			130				135				140					

gaa	cac	ata	gag	gac	ttc	gtt	gaa	gag	caa	cca	atg	gtg	ctt	caa	atg	480
Glu	His	Ile	Glu	Asp	Ile	Val	Glu	Glu	Gln	Pro	Met	Val	Leu	Gln	Met	

100/762

145	150	155	160	
gat. tca gaa tct aaa ccc ctt tgg gga acc cct atc tca gaa agc gga				528
Asp Ser Glu Ser Lys Pro Leu Ser Gly Thr Pro Ile Ser Glu Ser Gly				
	165	170	175	
atc gac gcc tgg tca cta aca acc aaa aga tct tat aac tgg ttc tta				576
Ile Asp Ala Ser Ser Leu Thr Thr Lys Arg Ser Tyr Asn Ser Phe Leu				
	180	185	190	
aaa cac aat agg cta aac ggt aaa act cgg ttc tct gga aac ttg tca				624
Lys His Asn Arg Leu Asn Gly Lys Thr Pro Phe Ser Gly Asn Leu Ser				
	195	200	205	
ttt cca tcn tta aac atg atg ggt aac act act gat cag cct att gac				672
Phe Pro Ser Leu Asn Met Met Gly Asn Thr Thr Asp Leu Pro Phe Asp				
	210	215	220	
aat aac gat ttt tgt tcc gag aaa gaa gtc gtt cgg aaa tca act cat				720
Asn Asn Arg Phe Cys Ser Glu Lys Glu Val Val Pro Lys Ser Thr His				
	225	230	235	240
gat cct tca cta gca aaa cgg cca tca cgg ttc act gaa agc gaa aca				768
Asp Pro Ser Leu Ala Lys Pro Pro Ser Arg Phe Thr Glu Ser Glu Thr				
	245	250	255	
aat tct act ccc aac tta tca agt aca cct ctc atg aac aca aaa aat				816
Asp Ser Thr Thr Pro Asn Leu Ser Ser Ile Pro Leu Met Asn Thr Lys Asn				
	260	265	270	
aca aga ttg aag tac aat aaa gtg gag cct cag ayt leu gac cga caa				864
Thr Arg Leu Lys Tyr Asn Lys Val Ala Pro Gln Ser Ser Asp Arg Gln				
	275	280	285	
acg tca cag gaa agt ggg cta tat cat tct acc gaa tca ttc aac ttc				912
Lys Ser Gln Glu Ser Gly Leu Tyr His Ser Thr Glu Ser Phe Asn Phe				
	290	295	300	
aaa gat caa aac tac agt aac aat aaa tcn tct tta agt ctg aac tcc				960
Lys Asp Gln Asn Tyr Ser Asn Asn Lys Ser Ser Leu Ser Leu Asn Ser				
	305	310	315	320

gat tta agt aca ccc cac ttt gca aag cat tca cct gat tca cca aga	1908
Asp Leu Ser Thr Pro His Phe Ala Lys His Ser Pro Asp Ser Pro Arg	
335 339 335	
act tca aga tct ttc aac tgc gga gac tca caa agt aaa gtt aaa tta	1056
Thr Ser Arg Ser Phe Asn Cys Gly Asp Ser Gln Ser Lys Val Lys Leu	
340 345 350	
ccg gaa gaa aat gac gct tct att gca ttt agt aag atg ttt act aga	1104
Pro Gln Glu Asn Asp Ala Ser Ile Ala Phe Ser Lys Met Phe Thr Arg	
355 360 365	
aac cga gcc aac act ggc ggg tcc aag tgt tgg cta gcc tca ccc act	1152
Lys Arg Ala Asn Thr Gly Gly Ser Thr Cys Ser Leu Ala Ser Pro Thr	
370 375 380	
att gcc aac act att cag aac tca aat ata aaa gtt aat aaa ttg cca	1200
Ile Ala Gln Thr Ile Gln Gln Ser Asp Ile Lys Val Asn Lys Leu Pro	
385 390 395 400	
act cag cga acc act tca gtt ggc tca tta tca tcc atg tca aat cgt	1248
Thr Gln Arg Thr Thr Ser Val Gly Ser Leu Ser Ser Met Ser Asn Arg	
405 410 415	
tat tca cca ata aga gtt gca tgg cca gga aga gcc aga tcc gcc act	1296
Tyr Ser Pro Ile Arg Val Ala Ser Pro Gly Arg Ala Arg Ser Ala Thr	
420 425 430	
cgt ggg tct tcc ctt tct aqa tta tcc aqa gac ctt aat tct tta cca	1344
Arg Gly Ser Ser Leu Tyr Arg Leu Ser Arg Asp Leu Asn Ser Leu Pro	
435 440 445	
agc gtc act gat cta cca gaa atg gat agt aca acc cca gtt aac gan	1392
Ser Val Thr Asp Leu Pro Gln Met Asp Ser Thr Thr Pro Val Asn Glu	
450 455 460	
ata ttc ttg gat ggc caa cca cag cat aaa agt ggc agt gtc aaa gga	1440
Ile Phe Leu Asp Gly Gln Pro Gln His Lys Ser Gly Ser Val Lys Gly	
465 470 475 480	
ggg cat agg aag aaa caa gaa tct atc tct gat gct caa aga att caa	1488
Gly His Arg Lys Lys Gln Glu Ser Ile Ser Asp Ala Gln Arg Ile Gln	

485	490	495	
cat tct aat tct tac ttc aca aca cct tca tct tct ctg gtg act cct			1536
His Ser Asn Ser Tyr Ile Thr Thr Pro Ser Ser Ser Leu Val Thr Pro			
500	505	510	
cct tac tac atg aca ggt tac aca tta cca agt tct gca tct gct tct			1538
Pro Tyr Tyr Met Thr Gly Tyr Thr Leu Pro Ser Ser Ala Ser Ala Ser			
515	520	525	
tca aat cca aat ggg ctt gaa aca cac aat atg aac ttt gtt cca agt			1542
Ser Thr Pro Asn Val Leu Glu Thr His Asn Met Asn Phe Val Pro Ser			
530	535	540	
acc agt act gtt aca agt tat cgc cca tct cgc aat ttt tcc tca ttt			1546
Thr Ser Thr Val Thr Ser Tyr Arg Pro Ser Ser Asn Phe Ser Ser Phe			
545	550	555	560
gac aac gac tac agt tac gaa aac gac gct agt ggg gaa ttc tct gct			1728
Asp Lys Glu Tyr Ser Asn Glu Asn Asp Ala Ser Gly Glu Phe Ser Ala			
565	570	575	
ttc aat act cca atg gag aat ata ccg gca cta aau ggt ata cct agu			1776
Phe Asn Thr Pro Met Glu Asn Ile Pro Ala Leu Lys Gly Ile Pro Arg			
580	585	590	
tcc acc tta gaa gaa aat gaa gaa gag gat gtc cta gta caa gat att			1824
Ser Thr Leu Glu Glu Asn Glu Glu Asp Val Leu Val Glu Asp Ile			
595	600	605	
ccg aat acg gca cac ttc caa aga agg gat att atc ggg atg gat act			1872
Pro Asn Thr Ala His Phe Glu Arg Arg Asp Ile Met Gly Met Asp Thr			
610	615	620	
caa aga aag gat gac agt tta gat ttt aac tct ttg atg cca cac ggt			1920
His Arg Lys Asp Asp Ser Leu Asp Phe Asn Ser Leu Met Pro His Gly			
625	630	635	640
agt aca act agt agc ago abc gta gat tct gtt atg acg aac tca ata			1968
Ser Thr Thr Ser Ser Ser Ile Val Asp Ser Val Met Thr Asn Ser Ile			
645	650	655	

tcc act aca aca agc aac gag aac gga aac tac ttt caa gat caa gat	2016
Ser Thr Thr Thr Ser Asn Ala Thr Gly Asn Tyr Phe Gln Asp Gln Asp	
660 665 670	
aag tat aca ttg gta aat acg gga ttg gga ttg agt gal gca aac ctg	2064
Lys Tyr Thr Leu Val Asn Thr Gly Leu Gly Leu Ser Asp Ala Asn Leu	
675 680 685	
gat cat ttt att aga tct caa tgg aaa cag gcc tct cga tca gaa tcc	2112
Asp His Phe Ile Arg Ser Gln Trp Lys His Ala Ser Arg Ser Glu Ser	
690 695 700	
aat aat aat aac gga aat cgc gtt tct tac agt ggc tca aca cca aac	2160
Asn Asn Asn Thr Gly Asn Arg Val Ser Tyr Ser Gly Ser Thr Pro Asn	
705 710 715 720	
aat gtt gat aca aca aag act aat ttg caa atg tat acc gag ttc gat	2208
Asn Val Asp Thr Thr Lys Thr Asn Leu Gln Val Tyr Thr Glu Phe Asp	
725 730 735	
ttt gaa aac cca gag tgg ttt ttc cat gag caa tgg aag cta cta ggt	2256
Thr Glu Asn Pro Glu Ser Phe Phe His Glu Gln Ser Lys Leu Leu Gly	
740 745 750	
gag atg ggc caa agc aat aac aac agc tac agc ggc atc acc atg aat	2304
Glu Met Gly His Ser Asn Asn Asn Ser Asn Ser Ala Ile Asn Met Asn	
755 760 765	
gaa ccc aag tct cgc gat aca tac att gga aal ala tct ccg gat act	2352
Glu Pro Lys Ser Ala Asp Thr Tyr Ile Gly Asn Ile Ser Pro Asn Thr	
770 775 780	
tca gca act gtt tca tta ggc gaa ctg atg ggc tca aac gtt tca aac	2400
Ser Ala Thr Val Ser Leu Gly Asp Leu Met Gly Ser Asn Val Ser Asn	
785 790 795 800	
aan agt gaa aga aat ttt tac gat ggt cat acb ttc gct cca cag tat	2448
Asn Ser Glu Arg Asn Phe Tyr Asp Gly His Thr Phe Val Pro Gln Tyr	
805 810 815	
cag gag aac tca tct gtg gaa aac tca aat aat caa aat gaa gaa cca	2496
Gln Ala Asn Ser Ser Val Glu Asn Ser Asn Asn Gln Asn Ala Ala Pro	

820

825

830

att gca att aac gac att gat aat aat tta cag rct ttt tat ttt gal 2544

Ile Ala Asn Asn Asp Ile Asp Asn Asn Leu Gln Ser Phe Tyr Phe Asp

835

840

845

aat agc aac taa

2556

Asn Ser Asn

850

<210> 43

<211> 851

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 43

Met Pro Lys Asn Ser His Ala His Arg Ser Ser Ser Val Asn Ser Thr

1

5

10

15

Lys Ser Arg Ser Thr Glu Ser Thr Asn Lys Arg Lys Ile Pro His Tyr

20

25

30

Tyr Arg Arg Ser Ala Ser Gly Ser Thr Cln Ala Ser Pro Arg Arg Asn

35

40

45

Ser Ser Thr Gly Ser Cys Ser Thr Pro Val Leu Pro Thr Met Asn Val

50

55

60

Met Ser Ser Pro Lys Lys Val Leu Leu Glu Asp Pro Arg Asp Asn His

65

70

75

80

Thr Lys Ala Lys Lys Ser Ser Arg Lys Lys Ser Gly Glu Met Val Phe

85

90

95

Val Asn Tyr Thr Val Gln Asp Thr Ala Asn Glu Asn Asp Thr Asp Leu
 100 105 110

Gln Thr Gln Pro Val Ser Val Pro Ala Pro Lys Ala Lys Leu Lys Lys
 115 120 125

Lys Ser Ser Lys Arg Arg Met Leu Lys Ile Phe Gly Ser Ser Lys Asn
 130 135 140

Glu His Ile Glu Asp Ile Val Glu Glu Gln Pro Met Val Leu Gln Met
 145 150 155 160

Asp Ser Glu Ser Lys Pro Leu Ser Gly Thr Pro Ile Ser Glu Ser Gly
 165 170 175

Ile Asp Ala Ser Ser Leu Thr Thr Lys Arg Ser Tyr Asn Ser Phe Leu
 180 185 190

Lys His Asn Arg Leu Asn Gly Lys Thr Pro Phe Ser Gly Asn Leu Ser
 195 200 205

Phe Pro Ser Leu Asn Met Met Gly Asn Thr Thr Asp Leu Pro Ile Asp
 210 215 220

Asn Asn Asp Phe Cys Ser Glu Lys Glu Val Val Pro Lys Ser Thr His
 225 230 235 240

Asp Pro Ser Leu Ala Lys Pro Pro Ser Arg Phe Thr Glu Ser Glu Thr
 245 250 255

Asn Ser Thr Pro Asn Leu Ser Ser Ile Pro Leu Met Asn Thr Lys Asn

260

265

270

Thr Arg Leu Lys Tyr Asn Lys Val Ala Pro Gln Ser Ser Asp Arg Gln
 275 280 285

Lys Ser Gln Glu Ser Gly Leu Tyr His Ser Thr Glu Ser Phe Asn Phe
 290 295 300

Lys Asp Gln Asn Tyr Ser Asn Asn Lys Ser Ser Leu Ser Leu Asn Ser
 305 310 315 320

Asp Leu Ser Thr Pro His Phe Ala Lys His Ser Pro Asp Ser Pro Arg
 325 330 335

Thr Ser Arg Ser Phe Asn Cys Gly Asp Ser Gln Ser Lys Val Lys Leu
 340 345 350

Pro Glu Glu Asn Asp Ala Ser Ile Ala Phe Ser Lys Met Phe Thr Arg
 355 360 365

Lys Arg Ala Asn Thr Gly Gly Ser Thr Cys Ser Leu Ala Ser Pro Thr
 370 375 380

Ile Ala Gln Thr Ile Gln Gln Ser Asn Ile Lys Val Asn Lys Leu Pro
 385 390 395 400

Thr Glu Arg Thr Thr Ser Val Gly Ser Leu Ser Ser Met Ser Asn Arg
 405 410 415

Tyr Ser Pro Ile Arg Val Ala Ser Pro Gly Arg Ala Arg Ser Ala Thr
 420 425 430

Arg Gly Ser Ser Leu Tyr Arg Leu Ser Arg Asp Ser Asn Ser Leu Pro
 435 440 445

Ser Val Thr Asp Leu Pro Glu Met Asp Ser Thr Thr Pro Val Asn Glu
 450 455 460

Ile Phe Leu Asp Gly Gln Pro Gln His Lys Ser Gly Ser Val Lys Gly
 465 470 475 480

Gly His Arg Lys Lys Gln Glu Ser Ile Ser Asp Ala Gln Arg Ile Gln
 485 490 495

His Ser Asn Ser Tyr Ile Thr Thr Thr Pro Ser Ser Ser Leu Val Thr Pro
 500 505 510

Pro Tyr Tyr Met Thr Gly Tyr Thr Leu Pro Ser Ser Ala Ser Ala Ser
 515 520 525

Ser Thr Pro Asn Val Leu Glu Thr His Asn Met Asn Phe Val Pro Ser
 530 535 540

Thr Ser Thr Val Thr Ser Tyr Arg Pro Ser Ser Asn Phe Ser Ser Phe
 545 550 555 560

Asp Lys Glu Tyr Ser Asn Glu Asn Asp Ala Ser Gly Glu Phe Ser Ala
 565 570 575

Phe Asn Thr Pro Met Glu Asn Ile Pro Ala Leu Lys Gly Ile Pro Arg
 580 585 590

Ser Thr Leu Glu Glu Asn Glu Glu Glu Asp Val Leu Val Gln Asp Ile

535

600

605

Pro Asn Thr Ala His Phe Gln Arg Arg Asp Ile Met Gly Met Asp Thr
 610 615 620

His Arg Lys Asp Asp Ser Leu Asp Phe Asn Ser Leu Met Pro His Gly
 625 630 635 640

Ser Thr Thr Ser Ser Ser Ile Val Asp Ser Val Met Thr Asn Ser Ile
 645 650 655

Ser Thr Thr Thr Ser Asn Ala Thr Gly Asn Tyr Phe Gln Asp Gln Asp
 660 665 670

Asp Tyr Thr Leu Val Asn Thr Gly Leu Gly Leu Ser Asp Ala Asn Ser
 675 680 685

Asp His Phe Ile Arg Ser Glu Thr Lys His Ala Ser Arg Ser Glu Ser
 690 695 700

Asn Asn Asn Thr Cys Asn Arg Val Ser Tyr Ser Gly Ser Thr Pro Asn
 705 710 715 720

Asn Val Asp Thr Thr Lys Thr Asn Ser Gln Val Tyr Thr Glu Phe Asp
 725 730 735

Phe Glu Asn Pro Glu Ser Phe Phe His Glu Gln Ser Lys Leu Leu Gly
 740 745 750

Glu Met Gly His Ser Asn Asn Asn Ser Asn Ser Ala Ile Asn Met Asn
 755 760 765

Glu Pro Tyr Ser Ala Asp Thr Tyr Ile Gly Asn Ile Ser Pro Asp Thr
770 775 780

Ser Ala Thr Val Ser Ser Gly Asp Leu Met Gly Ser Asn Val Ser Asn
785 790 795 800

Asn Ser Glu Arg Asn Phe Tyr Asp Gly His Thr Phe Val Pro Gln Tyr
805 810 815

Glu Ala Asn Ser Ser Val Glu Asn Ser Asn Asn Gln Asn Ala Ala Pro
820 825 830

Ile Ala Asn Asn Asp Ile Asp Asn Asn Leu Glu Ser Phe Tyr Phe Asp
835 840 845

Asn Ser Asn
850

<210> 44

<211> 1575

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1575)

<400> 44

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1 5 10 15

gga cct aag att ggc gaa ggg tct ttc gga gta ata ttt gag gga gag 96

Gly Pro Lys Ile Gly Glu Gly Ser Phe Gly Val Ile Phe Glu Gly Glu	
20	25
30	
aac att ctt cat tct tgt caa gcg cag acc ggt agt aag aag gac tct	144
Asn Ile Leu His Ser Cys Gln Ala Gln Thr Gly Ser Lys Arg Asp Ser	
35	40
45	
agt aba ata atg gcg aac gag cca gtc gca att aaa ttc gaa ccg cga	192
Ser Ile Ile Met Ala Asn Glu Pro Val Ala Ile Lys Phe Glu Pro Arg	
50	55
60	
cat tgg gac gaa ucc cag ttg cgt gac gca ttt aga gcc tat agg ata	240
His Ser Asp Ala Pro Gln Leu Arg Asp Gln Phe Arg Ala Tyr Arg Ile	
65	70
75	80
ttg aat ggc tgc gtt gga att ccc caa gcc tat ttt ggt caa gaa	288
Leu Asn Gly Cys Val Gly Ile Pro His Ala Tyr Tyr Phe Gly Gln Glu	
85	90
95	
ggt atg cac aac atc ttg att atc gat cta cta ggg cca tca ttg gaa	336
Gly Met His Asn Ile Leu Ile Ile Asp Leu Leu Gly Pro Ser Leu Glu	
100	105
110	
gat ctc ttt gag tgg tgt ggt aga aaa ttt tca gly aaa acc tgt	384
Asp Leu Phe Glu Trp Cys Gly Arg Lys Phe Ser Val Tyr Thr Thr Cys	
115	120
125	
atg gtt gaa aag caa atg att gat aga gtt aga gca att cat gat cac	432
Met Val Ala Lys Gln Met Ile Asp Arg Val Arg Ala Ile His Asp His	
130	135
140	
gac tta atu tat cgc gat att aaa ccc gat aac ttt tta att xct caa	480
Asp Leu Ile Tyr Arg Asp Ile Lys Pro Asp Asn Phe Leu Ile Ser Gln	
145	150
155	160
tat caa aga att tca cct gaa gga aaa gtc att aaa tca tgt gcc tcc	528
Tyr Gln Arg Ile Ser Pro Glu Gly Lys Val Ile Tyr Ser Cys Ala Ser	
165	170
175	
tct tct aat aat gat ccc aat tta ata taa atg gtt gac ttt ggt atg	576
Ser Ser Asn Asn Asp Pro Asn Leu Ile Tyr Met Val Asp Phe Gly Met	
180	185
190	

gca aaa caa tat aga gat cca aga acg aaa caa nat ata cca tac cgt	624
Ala Lys Gln Tyr Arg Asp Pro Arg Val Lys Glu His Ile Pro Tyr Arg	
195 200 205	
 gaa aga aaa tca tlg agc ggt acc gcc aga tat atg tct att aat act	672
Glu Arg Lys Ser Leu Ser Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr	
210 215 220	
 cat ttt gga aga gaa cag tca cgt agc gat gat tta gaa tgg cta ggt	720
His Phe Gly Arg Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly	
225 230 235 240	
 cac gtt ttt ttt tat ttc ttg agc gga tcc tly cca tgg cua ggt ttg	768
His Val Phe Phe Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu	
245 250 255	
 aaa gca cca aac aac aaa cly acg tat gaa aag att ggt atg act aaa	816
Lys Ala Pro Asn Asn Lys Leu Lys Tyr Glu Lys Ile Gly Met Thr Lys	
260 265 270	
 cag aaa tlg aat cct gat gat ctt tta tta aat aat gct att cct tac	864
Gln Lys Leu Asn Pro Asp Asp Leu Leu Leu Asn Asn Ala Ile Pro Tyr	
275 280 285	
 cag ttt gcc acc tat tta aac tat gca cgt tcc tly acg ttc gac gaa	912
Gln Phe Ala Val Tyr Leu Lys Tyr Ala Arg Ser Leu Lys Phe Asp Glu	
290 295 300	
 gat cag gat tat gac tat tta atc tgg tta atg gat gac gct ttg aga	960
Asp Pro Asp Tyr Asp Tyr Leu Ile Ser Leu Met Asp Asp Ala Leu Arg	
305 310 315 320	
 tta aac gac tta aag gat gat gga ctc tat gac tgg atg gat ttg aat	1008
Leu Asn Asp Leu Lys Asp Asp Gly His Tyr Asp Trp Met Asp Leu Asn	
325 330 335	
 ggt ggt aaa gcc tgg aat atc aag att aat aga aga gct aac ttg cat	1056
Gly Gly Lys Gly Trp Asn Ile Lys Ile Asn Arg Arg Ala Asn Leu His	
340 345 350	
 ggt tac gga aat cca aat cca aga gtc aat gcc aat act gca aga aac	1104

<p> Gly Tyr Gly Asn Pro Asn Pro Arg Val Asn Gly Asn Thr Ala Arg Asn 353 360 365 </p>	
<p> aat glg aat aoy aat lca ung acn cga aat aca aeg cca gtt gcg aca Acn Val Asn Thr Asn Ser Lys Thr Arg Asa Thr Thr Pro Val Ala Thr 370 375 380 </p>	1152
<p> oct aag caa caa gct caa aac agt tat aac aag gac aat tog aaa tgg Pro Lys Gln Gln Ala Gln Asn Ser Tyr Asn Lys Asp Asn Ser Lys Ser 385 390 395 400 </p>	1200
<p> aga att tct tog aac uoy cag agc ttt act aaa cca cca cnc gtc ttg Arg Ile Ser Ser Asn Pro Gln Ser Phe Thr Lys Gln Thr His Val Leu 405 410 415 </p>	1248
<p> aaa aaa atc gaa ccc aat agt aaa tat att cct gaa aca cat tcc aat Lys Lys Ile Glu Pro Asn Ser Lys Tyr Ile Pro Glu Thr His Ser Asn 420 425 430 </p>	1296
<p> ctt caa cgg cca att aaa agt caa agt caa acg tac gac ttc atc agt Leu Gln Arg Pro Ile Lys Ser Gln Ser Gln Thr Tyr Asp Ser Ile Ser 435 440 445 </p>	1344
<p> cat aca caa aat tca cca ttt gta cca tat tca ayt lol aaa gct aac His Thr Gln Asn Ser Pro Phe Val Pro Tyr Ser Ser Ser Lys Asn Asn 450 455 460 </p>	1392
<p> oct aaa aga agt aat aat gag cac aac tta cca aac ccc tac aca aac Pro Lys Arg Ser Asn Asn Glu His Asn Leu Pro Asn His Tyr Thr Asn 465 470 475 480 </p>	1440
<p> cll gaa aat aag aat atc aat tat caa agt can cga aat tac gaa caa Leu Ala Asn Lys Asn Ile Asn Tyr Gln Ser Gln Arg Asn Tyr Glu Glu 485 490 495 </p>	1488
<p> gaa aat gat gct tat tct gat gac gag aat gat aca ttt tgt tct aaa Glu Asn Asp Ala Tyr Ser Asp Asp Glu Asn Asp Thr Phe Cys Ser Lys 500 505 510 </p>	1536
<p> ata tac aaa tat tgt tgt tgc tgt ttt tgt tgc tgt tga Ile Tyr Lys Tyr Cys Cys Cys Cys Phe Cys Cys Cys 515 520 </p>	1575

<210> 45

<211> 521

<212> CBT

<213> *Saccharomyces cerevisiae*

<400> 45

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Gly Pro Lys Ile Gly Glu Gly Ser Phe Gly val Ile Phe Glu Gly Glu
 20 25 30

Asn Ile Leu His Ser Cys Gln Ala Gln Thr Gly Ser Lys Arg Asp Ser
 35 40 45

Ser Ile Ile Met Ala Asn Glu Pro Val Ala Ile Lys Phe Glu Pro Arg
 50 55 60

His Ser Asp Ala Pro Gln Leu Arg Asp Glu Phe Arg Ala Tyr Arg Ile
 65 70 75 80

Leu Asn Gly Cys Val Gly Ile Pro His Ala Tyr Tyr Phe Gly Gln Glu
 85 90 95

Gly Met His Asn Ile Leu Ile Ile Asp Leu Leu Gly Pro Ser Leu Glu
 100 105 110

Asp Leu Phe Glu Trp Cys Gly Arg Lys Phe Ser Val Lys Thr Thr Cys
 115 120 125

Met Val Ala Lys Gln Met Ile Asp Arg Val Arg Ala Ile His Asp His
130 135 140

Asp Leu Ile Tyr Arg Asp Ile Lys Pro Asp Asn Phe Leu Ile Ser Gln
145 150 155 160

Tyr Glu Arg Ile Ser Pro Glu Gly Lys Val Ile Lys Ser Cys Ala Ser
165 170 175

Ser Ser Asn Asn Asp Pro Asn Leu Ile Tyr Met Val Asp Phe Gly Met
180 185 190

Ala Lys Gln Tyr Arg Asp Pro Arg Thr Lys Cln His Ile Pro Tyr Arg
195 200 205

Glu Arg Lys Ser Leu Ser Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr
210 215 220

His Phe Gly Arg Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly
225 230 235 240

His Val Phe Phe Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu
245 250 255

Lys Ala Pro Asn Asn Lys Leu Lys Tyr Glu Lys Ile Gly Met Thr Lys
260 265 270

Gln Lys Leu Asn Pro Asp Asp Leu Leu Leu Asn Asn Ala Ile Pro Tyr
275 280 285

Gln Phe Ala Thr Tyr Leu Lys Tyr Ala Arg Ser Leu Lys Phe Asp Glu

290

295

300

Asp Pro Asp Tyr Asp Tyr Leu Ile Ser Leu Met Asp Asp Ala Leu Arg
 305 310 315 320

Leu Asn Asp Leu Lys Asp Asp Gly His Tyr Asp Trp Met Asp Leu Phe
 325 330 335

Gly Gly Lys Gly Trp Asn Ile Lys Ile Asn Arg Arg Ala Asn Leu His
 340 345 350

Gly Tyr Gly Asn Pro Asn Pro Arg Val Asn Gly Asn Thr Ala Arg Asn
 355 360 365

Asn Val Asn Thr Asn Ser Lys Thr Arg Asn Thr Thr Pro Val Ala Thr
 370 375 380

Pro Lys Gln Gln Ala Gln Asn Ser Tyr Asn Lys Asp Asn Ser Lys Ser
 385 390 395 400

Arg Ile Ser Ser Asn Pro Gln Ser Phe Thr Lys Gln Gln His Val Asn
 405 410 415

Lys Lys Ile Glu Pro Asn Ser Lys Tyr Ile Pro Glu Thr His Ser Asn
 420 425 430

Leu Gln Arg Pro Ile Lys Ser Gln Ser Gln Thr Tyr Asp Ser Ile Ser
 435 440 445

His Thr Gln Asn Ser Pro Phe Val Pro Tyr Ser Ser Ser Lys Ala Asn
 450 455 460

Pro Lys Arg Ser Asn Asn Glu His Asn Leu Pro Asn His Tyr Thr Asn
465 470 475 480

Leu Ala Asn Lys Asn Ile Asn Tyr Glu Ser Gln Arg Asn Tyr Glu Gln
485 490 495

Glu Asn Asp Ala Tyr Ser Asp Asp Glu Asn Asp Thr Phe Cys Ser Lys
500 505 510

Ile Tyr Lys Tyr Cys Cys Cys Cys Phe Cys Cys Cys
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<210> 48

<211> 1125

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1125)

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1 5 10 15

tgg tca tat cca tat gag cct tta agg gtt tta caa gta gga gag aat 96
Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
20 25 30

gag gta atg gag gtt ccc gaa tca gaa aeg cta aac tta cga aga aga 144
Glu Val Met Glu Val Pro Glu Ser Glu Lys Leu Asn Leu Arg Arg Arg
35 40 45

ggt gtc aag ttc ttt gat gbg acc aag cac act tct ttc tta cct ttc 192

117/762

Gly Val Lys Phe Phe Asp Val Thr Lys His Tyr Ser Phe Leu Pro Phe	
50 55 60	
ttt aac aag gag gaa gag cca aua gta cca acg tat aac tat cct cct	240
Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro	
65 70 75 80	
gag ata tcg aac aaa gaa gta gtg gat gat tcg att aag aat aua gac	288
Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp	
85 90 95	
aag ggc tct atg cac aag aac lly gca aag ttt aca agt ttt tac acc	316
Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr	
100 105 110	
agt tac tac aag tcc gat cac ggc ttt gaa tct gac gag tgg tta gct	384
Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala	
115 120 125	
gaa aat atc gct aat att aca aaa gat att ccg caa gat acg lly aat	432
Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Glu Asp Thr Leu Thr	
130 135 140	
att gaa cat ttt gat cag aau gaa tgg aag caa tat tca att ata gtc	480
Ile Glu His Phe Asp His Lys Glu Trp Lys Glu Tyr Ser Ile Ile Val	
145 150 155 160	
agt gtc acg gga tct aat aag cca gaa gat att ata ata atg ggt ttt	528
Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser	
165 170 175	
cat caa gat tct atc aat ctg cta ctg cca tcc ata atg gca gct cca	576
His Glu Asp Ser Ile Asn Leu Leu Leu Pro Ser Ile Met Ala Ala Pro	
180 185 190	
ggt gag gac gac aat ggg tca ggc acg gtg aat aat atg gag gct ctg	624
Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Gly Ala Leu	
195 200 205	
aga tta tat aag gaa aat ttt ttg aag aga gga ttt aga cct aac aac	672
Arg Leu Tyr Thr Gly Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn	
210 215 220	

act gtg gaa ttt cac tct tat tcc gcc gaa gag ggg gga ttg ttg ygt	720
Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Thr Gly	
225 230 235 240	
tct ctt gat gtt ttt acc gat tat gcc aaa cag aaa aag cat gtg aga	768
Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Gln Lys Lys His Val Arg	
245 250 255	
gag atg ctt cag aac gac atg aag gga tat gtt tct gat cca gaa gat	816
Ala Met Leu Gln Gln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp	
260 265 270	
gaa cat gtg ggg att gtc acc gac tac act act ccc gaa tta act gat	864
Glu His Val Gly Ile Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp	
275 280 285	
ttt ata aca cta att atc aac tct tat cta tcc att cct tac agt gat	912
Phe Ile Lys Leu Ile Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp	
290 295 300	
aca caa tgt ggt tct gct tgt agt gat cat ggg agt gcc acc aga aac	960
Thr Gln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn	
305 310 315 320	
gga ttt cca gcc tcc ttc gta att gaa agt gag ttc aac aap acc aac	1008
Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn	
325 330 335	
aag tat att cac agc aac atg gat act ttg gaa aga tta agt ctc gat	1056
Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala	
340 345 350	
cat atg gag gaa aac aca aaa att gta tta ggg gta atc att gaa ctc	1104
His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu	
355 360 365	
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Gly Ser Trp Ser Ala Trp	
370	

<210> 47
 <211> 374
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 47

Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
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Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
 20 25 30

Glu Val Met Glu Val Pro Glu Ser Glu Lys Leu Asn Leu Arg Arg Arg
 35 40 45

Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe
 50 55 60

Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
 65 70 75 80

Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp
 85 90 95

Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr
 100 105 110

Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala
 115 120 125

Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Gln Asp Thr Leu Thr
 130 135 140

Lie Glu His Phe Asp His Lys Glu Trp Lys Gln Tyr Ser Ile Ile Val
145 150 155 160

Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser
165 170 175

His Gln Asp Ser Ile Asn Leu Leu Phe Pro Ser Thr Met Ala Ala Pro
183 185 190

Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu
195 200 205

Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Ser Asn
210 215 220

Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly
225 230 235 240

Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Glu Lys Lys His Val Arg
245 350 355

Ala Met Leu Gln Gln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp
260 265 270

Glu His Val Gly Ile Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
275 280 285

Phe Ile Lys Leu Ile Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
390 295 300

Thr Gln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
 305 310 315 320

Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
 325 330 335

Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
 340 345 350

His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu
 355 360 365

Gly Ser Trp Ser Ala Trp
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<210> 48
 <211> 1530
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 <221> CDS
 <222> (1)..(1530)

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 Met Ile Ala Leu Lys Pro Asn Ala Val Arg Thr Phe Arg Gln Val Gln
 1 5 10 15
 cat tgc agc ttt cgc att tgt cgg tat caa tct acg aag tca aat aag 96
 His Cys Ser Phe Arg Ile Cys Arg Tyr Gln Ser Thr Lys Ser Asn Lys
 20 25 30
 tgt ctg acg ccc ttg cna gag tac gac aga ctg gtg aag ttg ggg aag 144
 Cys Leu Thr Pro Leu Gln Gln Tyr Asp Arg Leu Val Lys Leu Gly Lys
 35 40 45

cta cgg gat gat aca tat cag cgt ggt ile ala tct tcc tta ggg gat	192
Leu Arg Asp Asp Thr Tyr Gln Arg Gly Ile Ile Ser Ser Leu Gly Asp	
50 55 60	
ctg tat gat tca ctg gtt aau tat gta cct cgg gtt gtc aag aca ccc	240
Leu Tyr Asp Ser Leu Val Lys Tyr Val Pro Pro Val Val Lys Thr Pro	
65 70 75 80	
aat gct gtc gac caa gtt ggc ggt tgg ctg aat ggt ctt aaa tcc gta	288
Asn Ala Val Asp Gln Val Gly Gly Tyr Leu Asn Gly Leu Lys Ser Val	
85 90 95	
ttt agc cgt ggc aaa cct aag aac att ggg cgg tat gtc gat gta tcc	336
Phe Ser Arg Gly Lys Pro Lys Asn Ile Gly Ala Tyr Val Asp Val Ser	
100 105 110	
aaa att ggt aac tcg ata cct cga gga gtt tcc cta tat gga gat gtt	384
Lys Ile Gly Asn Ser Ile Pro Arg Gly Val Tyr Leu Tyr Gly Asp Val	
115 120 125	
ggc tgc gga cag aca atg ttg atg gac ctt ttt tat act aca att ccc	432
Gly Cys Gly Lys Thr Met Leu Met Asp Leu Phe Tyr Thr Thr Ile Pro	
130 135 140	
aat cat tta acc aac cag aga ata cat ttt cac cag ttt arg caa tat	480
Asn His Leu Thr Lys Lys Arg Ile His Phe His Gln Phe Met Gln Tyr	
145 150 155 160	
gtt cac aaa agg tcg cat gaa att gtt aga gag caa aat ttg aaa gaa	528
Val His Lys Arg Ser His Gln Trp Val Arg Gln Gln Asn Leu Lys Gln	
165 170 175	
cta ggt gat gca aaa gga aaa gag atc gat acg gtt cca ttt ttg gcc	576
Leu Gly Asp Ala Lys Gly Lys Gln Ile Asp Thr Val Pro Phe Leu Ala	
180 185 190	
gca gag att gca aat aat tcg cat gtt ctt tgt ttt cag gag ttt caa	624
Ala Gln Ile Ala Asn Asn Ser His Val Leu Cys Phe Asp Gln Phe Gln	
195 200 205	
gtc act gac gtg gca gat gaa atg ata ttg aga agg cag atg act gcc	672

Val Thr Asp Val Ala Asp Ala Met Ile Leu Arg Arg Leu Met Thr Ala	
210 215 220	
tta cta tou gat gat tat ggt glc gln ctt ttc gca acc tgg aat aga	720
Leu Leu Ser Asp Asp Tyr Gly Val Val Leu Phe Ala Phe Ser Asn Arg	
225 230 235 240	
cat cca gat gag tgg tat atc aac ggt gtt caa aga caa tca ttt att	768
Glu Pro Asp Glu Leu Tyr Ile Asn Gly Val Gln Arg Gln Ser Phe Ile	
245 250 255	
cct tgt att gaa cgg ata aag cat aga act aag gtt atc ttc ttg aat	816
Pro Cys Ile Glu Leu Ile Lys His Arg Thr Lys Val Ile Phe Leu Asp	
260 265 270	
tcg cca aca gat tac cgt aag att cca aga cct gly lcc tcc gtt tac	864
Ser Pro Thr Asp Tyr Arg Lys Ile Pro Arg Pro Val Ser Ser Val Tyr	
275 280 285	
tat ttc cca tcc gat acg agc ata aaa tac gca tca aag gaa tgt aaa	912
Tyr Phe Pro Ser Asp Thr Ser Ile Lys Tyr Ala Ser Lys Glu Cys Lys	
290 295 300	
acc cgt cga gaa act cat att aag gaa tgg tat aac tat ttc gca cag	960
Thr Arg Arg Glu Thr His Ile Lys Glu Trp Tyr Asn Tyr Phe Ala Glu	
305 310 315 320	
ggt tcc ccc acc gat gat tcc act gat tca cac aag ggg cat aag aca	1008
Ala Ser His Thr Asp Asp Ser Thr Asp Ser His Thr Val His Lys Thr	
325 330 335	
ttt tat gat tat cca tta act att tgg ggg aga gag ttc aaa gtc cct	1056
Phe Tyr Asp Tyr Pro Leu Thr Ile Trp Gly Arg Glu Phe Lys Val Pro	
340 345 350	
aag tgt acc cca cct cga gtc gcg cag ttt act ttc aag cag ttg tgt	1104
Lys Cys Thr Pro Pro Arg Val Ala Gln Phe Thr Phe Lys Gln Leu Cys	
355 360 365	
ggc gag cct ttg gcc gca gga gat tac ttg acg ttg gca aaa aat ttt	1152
Gly Glu Pro Leu Ala Ala Gly Asp Tyr Leu Thr Leu Ala Lys Asn Phe	
370 375 380	

gaa ggc ttt ata gtg acc gat att gaa tat ttg tcc att tac gtt cgt 1260
 Glu Ala Phe Ile Val Thr Asp Ile Pro Tyr Leu Ser Ile Tyr Val Arg
 385 390 395 400

gat gaa gtg cga aga ttt att acg ttt cta gat gct gta tat gac agt 1268
 Asp Glu Val Arg Arg Phe Ile Thr Phe Leu Asp Ala Val Tyr Asp Ser
 405 410 415

ggc ggg aaa ctg gcc act acg ggt gca gcg gaa ttt tct tcc ttg ttt 1276
 Gly Gly Lys Leu Ala Thr Thr Gly Ala Ala Asp Phe Ser Ser Leu Phe
 420 425 430

gtg gaa cct gaa cag ata ctt aat gat ttt gag tta cgc cca aca acc 1284
 Val Glu Pro Glu Gln Ile Leu Asn Asp Thr Glu Leu Arg Pro Thr Thr
 435 440 445

aaa gaa cct gat agc gtc gat act ggt atg gla gat gag atg gtt gag 1292
 Lys Glu Pro Arg Ser Val Asp Thr Gly Met Val Asp Glu Met Val Glu
 450 455 460

cac cac ggt ttt tgg aaa gag att gcc aag aaa tgg cag atg ttt gct 1300
 His His Gly Phe Ser Lys Glu Ile Ala Lys Lys Ser Gln Met Phe Ala
 465 470 475 480

ctt gat gaa gca agc ttt gcc ttt gca cgt gcc tta agc agg ctg tca 1308
 Leu Asp Glu Glu Arg Phe Ala Phe Ala Arg Ala Leu Ser Arg Leu Ser
 485 490 495

cag atg agc tcc aac gat tgg gtt act aag cct aca tcc taa 1316
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 500 505

<210> 49

<211> 509

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 49

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Cys Leu Thr Pro Leu Glu Glu Tyr Asp Arg Leu Val Lys Leu Gly Lys	35	40	45
Leu Arg Asp Asp Thr Tyr Glu Arg Gly Ile Ile Ser Ser Leu Gly Asp	50	55	60
Leu Tyr Asp Ser Leu Val Lys Tyr Val Pro Pro Val Val Lys Thr Pro	65	70	75
Asn Ala Val Asp Glu Val Gly Gly Trp Leu Asn Gly Leu Lys Ser Val	85	90	95
Phe Ser Arg Gly Lys Pro Lys Asn Ile Gly Ala Tyr Val Asp Val Ser	100	105	110
Lys Ile Gly Asn Ser Ile Pro Arg Gly Val Tyr Leu Tyr Gly Asp Val	115	120	125
Gly Cys Gly Lys Thr Met Leu Met Asp Leu Phe Tyr Thr Thr Ile Pro	130	135	140
Asn His Leu Thr Pys Lys Arg Ile His Phe His Glu Phe Met Glu Tyr	145	150	155
Val His Lys Arg Ser His Glu Ile Val Arg Glu Glu Asn Leu Lys Glu	165	170	175

Leu Gly Asp Ala Lys Gly Lys Glu Ile Asp Thr Val Pro Phe Leu Ala
 180 185 190

Ala Glu Ile Ala Asn Asn Ser His Val Leu Cys Phe Asp Glu Phe Glu
 195 200 205

Val Thr Asp Val Ala Asp Ala Met Ile Leu Arg Arg Leu Met Thr Ala
 210 215 220

Leu Leu Ser Asp Asp Tyr Gly Val Val Leu Phe Ala Thr Ser Asn Arg
 225 230 235 240

His Pro Asp Glu Leu Tyr Ile Asn Gly Val Glu Arg Glu Ser Phe Ile
 245 250 255

Pro Cys Ile Glu Leu Ile Lys His Arg Thr Lys Val Ile Phe Leu Asn
 260 265 270

Ser Pro Thr Asp Tyr Arg Lys Ile Pro Arg Pro Val Ser Ser Val Tyr
 275 280 285

Tyr Phe Pro Ser Asp Thr Ser Ile Lys Tyr Ala Ser Lys Glu Cys Lys
 290 295 300

Thr Arg Arg Glu Thr His Ile Lys Glu Trp Tyr Asn Tyr Phe Ala Glu
 305 310 315 320

Ala Ser His Thr Asp Asp Ser Thr Asp Ser His Thr Val His Lys Thr
 325 330 335

Phe Tyr Asp Tyr Pro Leu Thr Ile Trp Gly Arg Glu Phe Lys Val Pro
 343 345 353

Lys Cys Thr Pro Pro Arg Val Ala Glu Phe Thr Phe Lys Glu Leu Cys
 355 360 365

Gly Glu Pro Leu Ala Ala Gly Asp Tyr Leu Thr Leu Ala Lys Asp Phe
 370 375 380

Glu Ala Phe Ile Val Thr Asp Ile Pro Tyr Leu Ser Ile Tyr Val Arg
 385 390 395 400

Asp Glu Val Arg Arg Phe Ile Thr Phe Leu Asp Ala Val Tyr Asp Ser
 405 410 415

Gly Gly Lys Leu Ala Thr Thr Gly Ala Ala Asp Phe Ser Ser Leu Phe
 420 425 430

Val Glu Pro Glu Ala Ile Leu Asp Asp Phe Thr Leu Arg Pro Thr Thr
 435 440 445

Lys Glu Pro Asp Ser Val Asp Thr Gly Met Val Asp Glu Met Val Glu
 450 455 460

Lys His Gly Phe Ser Lys Glu Ile Ala Lys Lys Ser Glu Met Phe Ala
 465 470 475 480

Leu Asp Glu Glu Arg Phe Ala Phe Ala Arg Ala Leu Ser Arg Leu Ser
 485 490 495

Glu Met Ser Ser Thr Asp Trp Val Thr Lys Pro Val Tyr
 500 505


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<210> 50
<211> 1710
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(1710)

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acc agt cac tgg gga ctt acg ggt aag aag lig ggg tat ttc atc acc 96
Thr Ser His Trp Gly Leu Thr Gly Lys Lys Leu Arg Tyr Phe Ile Thr
20 25 30

atc gca tct atg acg ggc ttc tcc ctg ttt gaa tac gac caa ggg ttg 144
Ile Ala Ser Met Thr Gly Phe Ser Leu Phe Gly Tyr Asp Glu Gly Leu
35 40 45

atg gca agt cta att act ggt aaa gag ttc aac tat gaa ttt cca gaa 192
Met Ala Ser Ile Ile Thr Gly Lys Glu Phe Asn Tyr Glu Phe Pro Ala
50 55 60

acc aaa gaa aat ggc gat cat gac aga cac gca aat gta gtg cag ggc 240
Thr Lys Glu Asn Gly Asp His Asp Arg His Ala Thr Val Val Glu Gly
65 70 75 80

gct aca acc tcc tgt tat gaa tta ggt tgt ttc gaa ggt tct ata ttc 288
Ala Thr Thr Ser Cys Tyr Glu Leu Gly Cys Phe Ala Gly Ser Leu Phe
85 90 95

gtt atg ttc tgc ggt gaa aga att ggt aga aaa cca tta atc ctg atg 336
Val Met Phe Cys Gly Glu Arg Ile Gly Arg Lys Pro Leu Ile Leu Met
100 105 110

ggt tcc gta ata acc atc att ggt gcc gtt att tct aca tgc gca ttc 384

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129/762

Gly Ser Val Ile Thr Ile Ile Gly Ala Val Ile Ser Thr Cys Ala Phe	
115 120 125	
cgt ggt tac tgg gea tta ggc cag ttt atc atc gga aga gtc gtc acc	432
Arg Gly Tyr Trp Ala Leu Gly Gln Phe Ile Ile Gly Arg Val Val Thr	
130 135 140	
ggf gtt gga aca ggg ttg sat aca tct act att ccc gtt tgg caa tca	480
Gly Val Gly Thr Gly Leu Asn Thr Ser Thr Ile Pro Val Trp Glu Ser	
145 150 155 160	
gaa atg tca aaa gct gaa aat aga ggg ttg ctg gtc aat tta gaa ggt	528
Glu Met Ser Lys Ala Glu Asn Arg Gly Leu Leu Val Asn Leu Glu Gly	
165 170 175	
tcc aca act gct ttt ggt act atg att gct tat tgg att gat ttt ggg	576
Ser Thr Ile Ala Phe Gly Thr Met Ile Ala Tyr Trp Ile Asp Phe Gly	
180 185 190	
ttg tct tat acc aac agt tct gtt cag tgg aga ttc ccc gtc lca atg	624
Leu Ser Tyr Thr Asn Ser Ser Val Gln Trp Arg Phe Pro Val Ser Met	
195 200 205	
caa atc gtt ttt gct cta ttc atg ctt gct ttc atg att aca cta cct	672
Glu Ile Val Phe Ala Leu Phe Leu Leu Ala Phe Met Ile Lys Leu Pro	
210 215 220	
gac tgg aca cgt tgg ctg att tct caa agt cga aca gaa gaa gct cgg	720
Glu Ser Pro Arg Trp Leu Ile Ser Gln Ser Arg Thr Glu Glu Ala Arg	
225 230 235 240	
tac ttg gta gga aca cta gac gac gog gat cca aat cat gag gaa gtt	768
Tyr Leu Val Gly Thr Leu Asp Asp Ala Asp Pro Asn Asp Glu Glu Val	
245 250 255	
ata aca gaa gtt gct atg ctt cag gat gct gtt aac agg acc aaa cag	816
Ile Thr Glu Val Ala Met Leu His Asp Ala Val Asn Arg Thr Lys His	
260 265 270	
gag aaa cat tca ctg tca agt ttg ttc tcc aga ggc agg tcc caa aat	864
Glu Lys His Ser Leu Ser Ser Leu Phe Ser Arg Gly Arg Ser Glu Asn	
275 280 285	

ctt cag agg gct ttg att gca gct tca acg cca ttt ttc cag cca ttt	874
Leu Gln Arg Ala Leu Ile Ala Ala Ser Thr Gln Phe Phe Gln Gln Phe	
290 295 300	
act ggt tgt aac gct gcc ata tac tac cct act gta tta ttc aac aaa	950
Thr Gly Cys Asn Ala Ala Ile Tyr Tyr Ser Thr Val Leu Phe Asn Lys	
305 310 315 320	
aca att aaa tta gac tat aga tta tca atg atc ata ggt ggg gtc ttc	1008
Thr Ile Lys Leu Asp Tyr Arg Leu Ser Met Ile Ile Gly Gly Val Phe	
325 330 335	
gca aca atc tac gcc tta tct act att ggt tca ttt ttt cta att gaa	1056
Ala Thr Ile Tyr Ala Leu Ser Thr Ile Gly Ser Phe Phe Leu Ile Glu	
340 345 350	
aag cta ggt aga ogt aag ctg ttt tta tta ggt gcc aca ggt caa gca	1104
Lys Leu Gly Arg Arg Lys Leu Phe Ser Leu Gly Ala Thr Gly Gln Ala	
355 360 365	
gll taa ttc aca ail aac lll gac lgv ttg glu aac gaa aal aca gaa	1152
Val Ser Phe Thr Ile Thr Phe Ala Cys Leu Val Lys Glu Asn Lys Glu	
370 375 380	
aac gcc aga ggt gct gcc gtc gcc tta ttt ttg ttc att aca ttc ttt	1200
Asn Ala Arg Gly Ala Ala Val Gly Leu Phe Leu Phe Ile Thr Phe Phe	
385 390 395 400	
ggt ttg tct ttg cta tca tta cca tgg ata tac cca cca gaa att gca	1248
Gly Leu Ser Leu Leu Ser Leu Pro Trp Ile Tyr Pro Pro Glu Ile Ala	
405 410 415	
tca atg aaa gtt ogt gca tca aca aac gct ttc tcc aca tgt act aat	1296
Ser Met Lys Val Arg Ala Ser Thr Asn Ala Phe Ser Thr Cys Thr Asn	
420 425 430	
tgg ttg tgt aac ttt gcg gtt gtc acg ttc aac cca ata ttt att gga	1344
Trp Leu Cys Asn Phe Ala Val Val Met Phe Thr Pro Ile Phe Ile Gly	
435 440 445	
cag tcc ggt tgg ggt tgc tac tta ttt ttt gct gtt atg aat tat tta	1392

Cln Ser Gly Trp Gly Cys.Tyr Leu Phe Phe Ala Val Met Asn Tyr Leu
 450 455 460
 tac att aca gtt atc ttc ttt tcc lac uol gau auu gcc gga aga agt 1440
 Tyr Ile Pro Val Ile Phe Phe Phe Tyr Pro Glu Thr Ala Gly Arg Ser
 465 470 475 480
 ttg gag gaa atc gac atc atc ttt gct aaa gca tac gag gat gcc act 1488
 Leu Glu Glu Ile Asp Ile Ile Phe Ala Lys Ala Tyr Glu Asp Gly 'thr
 485 490 495
 cca cca tgg aga gtt gct aac cat ttg ccc aag tta tcc cta caa gaa 1536
 Glu Pro Trp Arg Val Ala Asn His Leu Pro Lys Leu Ser Leu Glu Glu
 500 505 510
 gcc gaa gat cat gcc aat gca ttg gcc tct tat gac gac gaa atg gaa 1584
 Val Glu Asp His Ala Asn Ala Leu Gly Ser Tyr Asp Asp Glu Met Glu
 515 520 525
 aca gag gac ttt ggt gaa gat aga gta gaa gac acc tat aac caa att 1632
 Lys Glu Asp Phe Gly Glu Asp Arg Val Glu Asp Thr Tyr Asn Cln His
 530 535 540
 aac gcc gat aat tgg tct agt tct tca aac atc aaa aat gaa gat aca 1680
 Asn Gly Arg Asn Ser Ser Ser Ser Ser Asn Ile Lys Asn Glu Asp Thr
 545 550 555 560
 gtg aac gat aaa gca aal ttt gag ggt tga 1710
 Val Asn Asp Lys Ala Asn Phe Glu Gly
 565

<210> 51

<211> 569

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 51

Met Lys Arg Asn Lys Leu Ser Asn Phe Lys Gly Lys Phe Ile Ser Arg
 1 5 10 15

Thr Ser His Trp Gly Leu Thr Gly Lys Lys Leu Arg Tyr Phe Ile Thr
20 25 30

Ile Ala Ser Met Thr Gly Phe Ser Leu Phe Gly Tyr Asp Gln Gly Leu
35 40 45

Met Ala Ser Leu Ile Thr Gly Lys Gln Phe Asn Tyr Glu Phe Pro Ala
50 55 60

Thr Lys Glu Asn Gly Asp His Asp Arg His Ala Thr Val Val Gln Gly
65 70 75 80

Ala Thr Thr Ser Cys Tyr Glu Leu Gly Cys Phe Ala Gly Ser Leu Phe
85 90 95

Val Met Phe Cys Gly Glu Arg Ile Gly Arg Lys Pro Leu Ile Leu Met
100 105 110

Gly Ser Val Ile Thr Ile Ile Gly Ala Val Ile Ser Thr Cys Ala Phe
115 120 125

Arg Gly Tyr Trp Ala Leu Gly Gln Phe Ile Ile Gly Arg Val Val Thr
130 135 140

Gly Val Gly Thr Gly Leu Asn Thr Ser Thr Ile Pro Val Trp Gln Ser
145 150 155 160

Glu Met Ser Lys Ala Glu Asn Arg Gly Leu Leu Val Asn Leu Glu Gly
165 170 175

Ser Thr Ile Ala Phe Gly Thr Met Ile Ala Tyr Trp Ile Asp Phe Gly

180

195

190

Leu Ser Tyr Thr Asn Ser Ser Val Gln Trp Arg Phe Pro Val Ser Met
195 200 205

Gln Ile Val Phe Ala Leu Phe Leu Leu Ala Phe Met Ile Lys Leu Pro
210 215 220

Glu Ser Pro Arg Trp Leu Ile Ser Gln Ser Arg Thr Glu Glu Ala Arg
225 230 235 240

Tyr Leu Val Gly Thr Leu Asp Asp Ala Asp Pro Asn Asp Glu Glu Val
245 250 255

Ile Thr Glu Val Ala Met Leu His Asp Ala Val Asn Arg Thr Lys His
260 265 270

Glu Lys His Ser Leu Ser Ser Leu Phe Ser Arg Gly Arg Ser Gln Asn
275 280 285

Leu Gln Arg Ala Leu Ile Ala Ala Ser Thr Gln Phe Phe Gln Gln Phe
290 295 300

Thr Gly Cys Asn Ala Ala Ile Tyr Tyr Ser Thr Val Leu Phe Asn Lys
305 310 315 320

Thr Ile Lys Leu Asp Tyr Arg Leu Ser Met Ile Ile Gly Gly Val Phe
325 330 335

Ala Thr Ile Tyr Ala Leu Ser Thr Ile Gly Ser Phe Phe Leu Ile Glu
340 345 350

Lys Leu Gly Arg Arg Lys Leu Phe Leu Leu Gly Ala Thr Gly Gln Ala
345 360 385

Val Ser Phe Thr Ile Thr Phe Ala Cys Leu Val Lys Glu Asn Lys Glu
370 375 380

Asn Ala Arg Gly Ala Ala Val Gly Leu Phe Leu Phe Ile Thr Phe Phe
385 390 395 400

Gly Leu Ser Leu Leu Ser Leu Pro Trp Ile Tyr Pro Pro Glu Ile Ala
405 410 415

Ser Met Lys Val Arg Ala Ser Thr Asn Ala Phe Ser Thr Cys Thr Asn
420 425 430

Trp Leu Cys Asn Phe Ala Val Val Met Phe Thr Pro Ile Phe Ile Gly
435 440 445

Gln Ser Gly Trp Gly Cys Tyr Leu Phe Phe Ala Val Met Asn Tyr Leu
450 455 460

Tyr Ile Pro Val Ile Phe Phe Phe Tyr Pro Glu Thr Ala Gly Arg Ser
465 470 475 480

Leu Glu Glu Ile Asp Ile Ile Phe Ala Lys Ala Tyr Glu Asp Gly Thr
485 490 495

Gln Pro Trp Arg Val Ala Asn His Leu Pro Lys Leu Ser Leu Gln Glu
500 505 510

Val Glu Asp His Ala Asn Ala Leu Gly Ser Tyr Asp Asp Glu Met Gly
515 520 525

Lys Glu Asp Phe Gly Gln Asp Arg Val Glu Asp Thr Tyr Asn Gln Ile
530 535 540

Asn Gly Asp Asn Ser Ser Ser Ser Ser Asn Ile Lys Asn Glu Asp Thr
545 550 555 560

Val Asn Asp Lys Ala Asn Phe Glu Gly
565

<210> 52

<211> 432

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(132)

<400> 52

atg gag acc aat ttt tcc ttc gac tcg aat tta att gtt att atc att 40
Met Glu Thr Asn Phe Ser Phe Asp Ser Asn Leu Ile Val Ile Ile Ile
1 5 10 15

atc acg ttg ttt gcc acc aca att att gct aaa aga ttt tta tct aat 96
Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
20 25 30

cca aaa atg gta tcc cag gaa acc gtt gct cac gta aag gat ctg att 144
Pro Lys Met Val Ser Gln Gly Thr Val Ala His Val Lys Asp Leu Ile
35 40 45

ggc caa aag gaa gtg ttt gtt gca gaa aag acc tac tgc cct tac tgt 192
Gly Glu Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
50 55 60

ann gct act ttt tct acc ctc ttc caa gaa ttg aac gtt ccc aaa tcc 240
 tps ala thr leu ser thr leu phe gln glu leu asn val pro lys ser
 65 73 75 80

aag gac att gtg ttg gaa tta gat gaa atg agc aat ggc tca gag att 283
lys ala leu val leu glu leu asp glu met ser asn gly ser glu ile
85 90 95

caa gaag gct tta gaa caa atc tag ggc caa aaa act gta cct aac gta 336
Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
100 103 110

Lac ala val ggu aag cac att ggt ggn aac agn gat ttg gaa not ttg 384
 Tyr ile asn gly lys his ile gly gly asn ser asp leu glu thr leu
 115 120 125

AAC AAA AAT AGC AAG ATT GCT GAA ATA TTG AAG CCG GTA TTT CAA TAG 432
 Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
 130 135 140

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<210> 53
<211> 143
<212> DNA
<213> Saccharomyces cerevisiae
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400 53

Met Glu Thr Asa Phe Ser Phe Asp Ser Asn (asp ile val) ile ile ile
 1 5 10 15

Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
20 25 30

Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
35 40 45

Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys

50

55

60

Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
65 70 75 80

Lys Ala Leu Val Leu Glu Leu Asp Gln Met Ser Asn Gly Ser Glu Ile
85 90 95

Gln Asp Ala Leu Glu Gln Ile Ser Gly Gln Lys Thr Val Pro Asn Val
100 105 110

Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
115 120 125

Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val His Gln
130 135 140

<210> 54

<211> 426

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(426)

<400> 54

atg aaa tgt oac gag caa cgg acc ctt gcc ttt ttg gcg acg gca ctt 48
Met Lys Cys His Ala Lys Arg Thr Leu Ala Phe Leu Ala Thr Ala Leu
1 5 10 15

ccc cta tct gga aaa agc cga gca tgu acc cgt acc cca caa agc ttc 96
Pro Leu Ser Gly Lys Ser Arg Ala Cys Thr Arg Thr Pro Gln Ser Phe
20 25 30

gct tcc ggt ttc cgg gca gca gcg ccg ttt ctt ttt tcc cgc tgc ttc 144
 Ala Ser Gly Phe Arg Ala Ala Ala Pro Phe Leu Phe Ser Arg Cys Phe
 35 40 45

gac ctt tgt att acg cat tgc gca ctt ttt cgc ttg cca tat tgc ttc 192
 Ala Leu Cys Ile Thr His Cys Ala Leu Phe His Leu Pro Tyr Ser Phe
 50 55 60

acc ggt ttt tct ttt tat ttc ttc gtc ttt ttt cgt ctt ttt ctt ccc 240
 Thr Gly Phe Ser Phe Tyr Phe Phe Val Phe Phe Arg Leu Phe Leu His
 65 70 75 80

tgg ata tac gct ttt tgc att tgc aat tgc aca tat gtg tat ata tat 288
 Trp Ile Tyr Ala Phe Cys Ile Cys Asn Ser Thr Tyr Val Tyr Ile Tyr
 85 90 95

aag caa gtg ttg agc ttg cct gtc aac tcc tcc atg tgc cct tat cgt 326
 Lys Glu Val Leu Ser Leu Pro Val Lys Ser Ser Met Cys Pro Ser Arg
 100 105 110

cta tct tgt tct gtc tgg tat aga gta ala ctt aca tac ata tac gta 364
 Leu Ser Cys Ser Val Trp Tyr Arg Val Ile Leu Thr Tyr Ile Tyr Val
 115 120 125

dot tgt ttc cgc tgg cta gtt cgt aac cac ctc ctt tcc tag 426
 His Cys Phe Arg Trp Leu Val Arg Asn His Leu Leu Ser
 130 135 140

<210> 55

<211> 141

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 55

Met Lys Cys His Ala Lys Arg Thr Leu Ala Phe Leu Ala Thr Ala Leu
 1 5 10 15

Pro Leu Ser Gly Lys Ser Arg Ala Cys Thr Arg Thr Pro Glu Ser Phe
 20 25 30

Ala Ser Gly Phe Arg Ala Ala Ala Pro Phe Leu Phe Ser Arg Cys Phe
 25 40 45

Ala Leu Cys Ile Thr His Cys Ala Leu Phe His Leu Pro Tyr Ser Phe
 50 55 60

Thr Gly Phe Ser Phe Tyr Phe Phe Val Phe Phe Arg Leu Phe Leu His
 65 70 75 80

Trp Ile Tyr Ala Phe Cys Ile Cys Asn Ser Thr Tyr Val Tyr Ile Tyr
 85 90 95

Lys Gln Val Leu Ser Leu Pro Val Lys Ser Ser Met Cys Pro Ser Arg
 100 105 110

Leu Ser Cys Ser Val Trp Tyr Arg Val Ile Leu Thr Tyr Ile Tyr Val
 115 120 125

His Cys Phe Arg Trp Leu Val Arg Asn His Leu Leu Ser
 130 135 140

<210> 56
 <211> 1488
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1488)

<400> 56

140/762

atg aaa act gat aga tta ctg att aac gct tcc cgg gag aca tgt acc	48
Met Lys Thr Asp Arg Leu Leu Ile Asn Ala Ser Pro Glu Thr Cys Thr	
2 5 10 15	
aag gga gat gct cag atg gat act atg gat act att gac aga atg aca	96
Lys Gly Asp Ala Glu Met Asp Thr Met Asp Thr Ile Asp Arg Met Thr	
20 25 30	
tca gtt aaa gtt tta cgg gaa ggc aag gta tta agc aac ttc gaa gaa	144
Ser Val Lys Val Leu Ala Gly Gly Lys Val Leu Ser Asn Phe Glu Glu	
35 40 45	
cgg ggc tta atg agg tgc ggt tat cat gat gca aaa aac lyy ylc aga	192
Pro Gly Leu Met Arg Cys Gly Tyr His Asp Ala Lys Asn Trp Val Arg	
50 55 60	
aga tta cgg agc gaa aca att gtc ggt gag gac acg agt aat tta tac	240
Arg Leu Ser Ser Glu Thr Ile Val Gly Glu Asp Thr Ser Asn Leu Tyr	
65 70 75 80	
cca ttt tat gtt gat act gca tac gat gta agg agt tgg aga aag gat	288
Pro Phe Tyr Val Asp Thr Ala Tyr Asp Val Arg Arg Leu Arg Lys Asp	
85 90 95	
utt ata aat gct aag gtt gac ttg cag gtt gaa aac ctg ata ata atc	336
Leu Ile Asn Ala Lys Val Asp Leu Glu Val Glu Asn Leu Ile Ile Ile	
100 105 110	
tcg aat att aat gat att tcc act gta ttt ctc atg aga gaa gcg gtc	384
Cys Asn Ile Asn Asp Ile Ser Thr Val Phe Leu Met Arg Glu Val Val	
115 120 125	
gaa cgg atc tta cgc aat ttc cat tca atc gta tat gta caa gat	432
Glu Trp Ile Leu Arg Asn Phe His Ser Ile Thr Val Tyr Val Glu Asp	
130 135 140	
att ttt aaa aag tca cct cag ttt gct gtt ggt gac ctc tgc aaa gac	480
Ile Phe Lys Lys Ser Thr Glu Phe Ala Val Gly Asp Leu Cys Lys Asp	
145 150 155 160	
agc aat tgc agt aaa aac aga gta aag tat tgg tca aaa gaa ttt gtt	528
Ser Asn Cys Ser Lys Asn Arg Val Lys Tyr Trp Ser Lys Glu Phe Val	

165	170	175	
aaa aaa cac gat tca ttc ttt gac ttg atg att acn cta ggg ggt gat			576
Lys Lys His Asp Ser Phe Phe Asp Leu Met Ile Thr Leu Gly Gly Asp			
180	185	190	
gga act gtc ctt ttt gct tca tct ata ttc acg aaa gat gtt ccg ccg			624
Gly Thr Val Leu Phe Ala Ser Ser Ile Phe Thr Lys Asp Val Pro Pro			
195	200	205	
att gtt cca ttt gcc ctt gga tca tta gga ttt cta acn aat ctt gaa			672
Ile Val Pro Phe Ala Leu Gly Ser Leu Gly Phe Leu Thr Asn Phe Glu			
210	215	220	
ttt caa aat ttc aaa gaa acg ttg aaa cat atc tta acn gat gag gtt			720
Phe Gln Asn Phe Lys Glu Thr Leu Lys His Ile Leu Thr Asp Glu Val			
225	230	235	240
cgt atc aat ttc cga atg agg ttg cca tgc aaa ctc tac cgt aga aat			768
Arg Ile Asn Leu Arg Met Arg Leu Gln Cys Lys Leu Tyr Arg Arg Asn			
245	250	255	
aaa cca gaa att gat gcc gca aat ggg aga aaa ata tgt tac atn gat			816
Lys Pro Glu Ala Asp Ala Ala Thr Gly Arg Lys Ile Cys Tyr Ile Asp			
260	265	270	
ttc atc tcc gaa cat cac gta ttg aac gaa gta acc ata gat aga ggt			864
Phe Ile Ser Glu His His Val Leu Asn Glu Val Thr Ile Asp Arg Gly			
275	280	285	
cca gct cct tgt tta tcc cta tta gaa ctc tat gga aac gac tca cta			912
Pro Ala Pro Cys Leu Ser Leu Leu Glu Leu Tyr Gly Asn Asp Ser Leu			
290	295	300	
atg acn aag gtt cag gga gat gga ttg att gtt gcc acg cct acg gga			960
Met Thr Lys Val Gln Gly Asp Gly Leu Ile Val Ala Thr Pro Thr Gly			
305	310	315	320
tcc acg gca tac tca ttg agt gca gga ggc tct tta ata tog cca agc			1008
Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser Leu Ile Ser Pro Ser			
325	330	335	

gta aat gcc ata gag gbg acg oot ata tgt cct cat act tgg agc ttt	1056
Val Asn Ala Ile Ala Val Thr Pro Ile Cys Pro His Thr Leu Ser Phe	
340 345 350	
agg cct ata att tta cca gat agc atg gaa tta aaa gtt aga gta gat	1104
Arg Pro Ile Ile Leu Pro Asp Ser Met Glu Leu Lys Val Arg Val Asp	
355 360 365	
atg aac tca aga ggg acg tgg tgg gbg aal ttt gac gga aaa gat aga	1152
Met Asn Ser Arg Gly Thr Ser Trp Val Asn Phe Asp Gly Lys Asp Arg	
370 375 380	
gtt gac ttg aaa cag ggt gac tat gtt ggg ata act gca agc ccc tat	1200
Val Glu Leu Lys Gln Gly Asp Tyr Val Val Ile Thr Ala Ser Pro Tyr	
385 390 395 400	
tcg gta ccg act atn gag tca tct gcc agt gaa ttt ttt gaa agt atc	1248
Ser Val Pro Thr Ile Glu Ser Ser Ala Ser Glu Phe Phe Glu Ser Ile	
405 410 415	
agt aaa aat ott aat tgg aat gac cgc gaa gag cag aag cca ttt gca	1296
Ser Lys Asn Leu Asn Trp Asn Asp Arg Glu Glu Gln Lys Pro Phe Ala	
420 425 430	
cat att ctg ccg uua aat cca gaa aaa tat aga ttc gcc tca tgg	1344
His Ile Leu Ser Pro Lys Asn Gln Glu Lys Tyr Arg Leu Asp Ser Ser	
435 440 445	
aaa aat gga aac gac acc ata agt aat ccc ctg gag agt tca tgc ata	1392
Lys Asn Gly Asn Asp Thr Ile Ser Asn Pro Leu Glu Ser Ser Cys Ile	
450 455 460	
agc tca gat gca caa gat gag gag agg aaa tcc gta acg gaa cca gaa	1440
Ser Ser Asp Ala Gln Asp Glu Gln Arg Lys Ser Val Thr Glu Thr Glu	
465 470 475 480	
aca gaa ala gtt gtt gaa cgg act cgt ccg gct cat ttt gca atc taa	1488
Thr Glu Ile Val Val Glu Arg Thr Arg Gln Ala His Phe Ala Ile	
485 490 495	

<211> 498
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 57

Met	Lys	Thr	Asp	Arg	Leu	Leu	Ile	Asn	Ala	Ser	Pro	Glu	Thr	Cys	Thr
1				5						10				15	

Lys	Gly	Asp	Ala	Glu	Met	Asp	Thr	Met	Asp	Thr	Ile	Asp	Arg	Met	Thr
			20					25					30		

Ser	Val	Lys	Val	Leu	Ala	Glu	Gly	Lys	Val	Leu	Ser	Asn	Phe	Glu	Glu
			35					40					45		

Pro	Gly	Leu	Met	Arg	Cys	Gly	Tyr	His	Asp	Ala	Lys	Asn	Trp	Val	Arg
			50				55					60			

Arg	Leu	Ser	Ser	Glu	Thr	Ile	Val	Gly	Glu	Asp	Thr	Ser	Asn	Leu	Tyr
65					70						75				80

Pro	Phe	Tyr	Val	Asp	Thr	Ala	Tyr	Asp	Val	Arg	Arg	Leu	Arg	Lys	Asp
				85					90					95	

Leu	Ile	Asn	Ala	Lys	Val	Asp	Leu	Gln	Val	Glu	Asn	Leu	Ile	Ile	Ile
				100					105					110	

Cys	Asn	Ile	Asn	Asp	Ile	Ser	Thr	Val	Phe	Leu	Met	Arg	Glu	Val	Val
			115					120					125		

Glu	Trp	Ile	Leu	Arg	Asn	Phe	His	Ser	Ile	Thr	Val	Tyr	Val	Gln	Asp
	130						135						140		

Ile Phe Lys Lys Ser Thr Gln Phe Ala Val Gly Asp Leu Cys Lys Asp
 145 150 155 160

Ser Asn Cys Ser Iys Asn Arg Val Lys Tyr Trp Ser Lys Glu Phe Val
 165 170 175

Lys Lys His Asp Ser Phe Phe Asp Leu Met Ile Thr Leu Gly Gly Asp
 180 185 190

Gly Thr Val Leu Phe Ala Ser Ser Ile Phe Thr Lys Asp Val Pro Pro
 195 200 205

Ile Val Pro Phe Ala Leu Gly Ser Ser Gly Phe Leu Thr Asn Phe Glu
 210 215 220

Phe Gln Asn Phe Lys Glu Thr Leu Lys His Ile Leu Thr Asp Glu Val
 225 230 235 240

Arg Ile Asn Leu Arg Met Arg Leu Gln Cys Lys Leu Tyr Arg Arg Asn
 245 250 255

Lys Pro Glu Ile Asp Ala Ala Thr Gly Arg Lys Ile Cys Tyr Ile Asp
 260 265 270

Phe Ile Ser Glu His His Val Leu Asn Glu Val Thr Ile Asp Arg Gly
 275 280 285

Pro Ala Pro Cys Leu Ser Leu Leu Glu Leu Tyr Gly Asn Asp Ser Leu
 290 295 300

Met Thr Lys Val Gln Gly Asp Gly Leu Ile Val Ala Thr Pro Thr Gly
 305 310 315 320

Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser Leu Ile Ser Pro Ser
325 330 335

Val Asn Ala Ile Ala Val Thr Pro Ile Cys Pro His Thr Leu Ser Phe
340 345 350

Arg Pro Ile Ile Leu Pro Asp Ser Met Glu Leu Lys Val Arg Val Asp
355 360 365

Met Asn Ser Arg Gly Thr Ser Trp Val Asn Phe Asp Gly Lys Asp Arg
370 375 380

Val Glu Leu Lys Gln Gly Asp Tyr Val Val Ile Thr Ala Ser Pro Tyr
385 390 395 400

Ser Val Pro Thr Ile Glu Ser Ser Ala Ser Glu Phe Phe Glu Ser Ile
405 410 415

Ser Lys Asn Leu Asn Trp Asn Asp Arg Glu Glu Gln Lys Pro Phe Ala
420 425 430

His Ile Leu Ser Pro Lys Asn Gln Glu Lys Tyr Arg Leu Asp Ser Ser
435 440 445

Lys Asn Gly Asn Asp Thr Ile Ser Asn Pro Leu Glu Ser Ser Cys Ile
450 455 460

Ser Ser Asp Ala Gln Asp Glu Glu Arg Lys Ser Val Thr Glu Thr Glu
465 470 475 480

Thr Glu Ile Val Val Glu Arg Thr Arg Gln Ala His Phe Ala Ile
 495 490 495

<210> 58

<211> 1125

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1125)

<400> 58

atg agg ata cag tcg ctt ttt gtt tta ttt aat gtt gcc atc atc gca 48
 Met Arg ile Gln Ser Leu Phe Val Leu Phe Asn val Ala ile ile Ala
 1 5 10 15

tgg tca tat cca tat gag cct tta agg gtt tta cca gta gga gag aa- 96
 Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
 20 25 30

gag gta atg gag gtt ccc gaa tca gaa aag cta aac tta cga aga aga 144
 Glu Val Met Glu Val Pro Glu Ser Glu Lys Leu Asn Leu Arg Arg Arg
 35 40 45

ggc gtc aaa ttc ttt gat gtc acc aaa cac act tct ttc tta ccc ttc 192
 Gly Val Lys Phe Phe Arg Val Thr Lys His Thr Ser Phe Leu pro phe
 50 55 60

ttt aac aag gag gaa gag cca aca gta cca aag tat aac tat cct cct 240
 Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
 65 70 75 80

gag ata tcg aac aac gaa gta gtc gat gat tcg att aag aat ata gac 288
 Glu ilo Ser Asn Lys Glu Val Val Asp Asp Ser ile Lys Asn ile Asp
 85 90 95

aag ggc tct atg cac aag aac ttg gca aag ttc aca aat ttt tac aac 336
 Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr

147/762

100	105	110	
cgt tac tac aag tcc gat cac ggc ttt gaa tct gcc gag tgg tta gct			384
Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Tyr Leu Ala			
115	120	125	
gca act atc gct aat att aca aaa gal att ccg caa gat acg ttg act			432
Ala Thr Tie Ala Asn Ile Thr Lys Asp Ile Pro Gln Asp Thr Leu Thr			
130	135	140	
att gaa cat ttt gat cac aaa gaa tgg aag caa tai lua att ata gtc			480
Ile Glu His Phe Asp His Lys Glu Trp Lys Gln Tyr Ser Ile Ile Val			
145	150	155	160
cgt gtc acg gga tct act acg cca gaa gat att ata ata att ggt tct			528
Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser			
165	170	175	
cat caa gat tct atc aat ctg cta ctg cca leu ata atg gca gct cca			576
His Glu Asp Ser Ile Asn Leu Leu Leu Pro Ser Ile Met Ala Ala Pro			
180	185	190	
ggc gcc gac gac aat gcc tca gcc acg gtg act aat atg gag gct ctg			624
Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu			
195	200	205	
aga tta tat acg gaa aat ttt ctg atg aga gga att aga tct aac aac			672
Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn			
210	215	220	
act gtg gaa ttt caa ttt tat tcc gcc gaa gag ggg gga ttg ttg ggt			720
Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly			
225	230	235	240
tct ctg gat gtt ttt aca gcc tat gcc aaa cag aaa aag cat gtg aga			768
Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Gln Lys Lys His Val Arg			
245	250	255	
gcc atg ctt cag caa gac atg acg gga tat gtt tct gat cca gaa gat			816
Ala Met Leu Gln Gln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp			
260	265	270	

gaa cat ggg ggg att gtc acc gac tac act act ccc gaa tta act gat 864
 Glu His Val Gly Ile Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
 275 280 285

ttt ata aaa cta att atc aac tct tat cta tcc att cct tac agg gat 912
 Phe Ile Lys Leu Ile Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
 290 295 300

aca caa tgt ggc tat gct tgt agc gat cat ggg agt gcc acc aga aac 960
 Thr Gln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
 305 310 315 320

ggg ttt cca ggc tcc ttc gtg att gaa agt gaa ttc aaa aag act aac 1008
 Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
 325 330 335

aag tat att ccc agc acc atg gat act ttg gac aga tta agt ctc got 1056
 Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
 340 345 350

cat atg gcg gaa ccc aca aca att gta cta ggg gta atc att gaa ctc 1104
 His Met Ala Glu His Thr Arg Ile Val Leu Gly Val Ile Ile Glu Leu
 355 360 365

ggg tca tgg tcc gct tgg taa 1125
 Gly Ser Trp Ser Ala Trp
 370

<210> 59

<211> 373

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 59

Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
 1 5 10 15

Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Gln Asn
 20 25 30

Glu Val Met Glu Val Pro Glu Ser Glc Lys Leu Asn Leu Arg Arg Arg
35 40 45

Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe
50 55 60

Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
65 70 75 80

Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp
85 90 95

Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr
100 105 110

Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Thr Leu Ala
115 120 125

Ala Thr Ile Ala Asn Ile Thr Lys Asp Le Pro Gln Asp Thr Leu Thr
130 135 140

Ile Glu His Phe Asp His Lys Glu Tyr Lys Gln Tyr Ser Ile Ile Val
145 150 155 160

Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser
165 170 175

His Gln Asp Ser Ile Asn Leu Leu Leu Pro Ser Ile Met Ala Ala Pro
180 185 190

Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu
 195 200 205

Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn
 210 215 220

Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly
 225 230 235 240

Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Glu Lys Lys His Val Arg
 245 250 255

Ala Met Leu Cln Cln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp
 260 265 270

Glu His Val Gly Lys Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
 275 280 285

Phe Ile Tyr Leu Phe Lys Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
 290 295 300

Thr Cln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
 305 310 315 320

Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
 325 330 335

Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
 340 345 350

His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu

355

360

365

Gly Ser Trp Ser Ala Trp

370

<210> 60

<211> 1470

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1470)

<400> 60

atg aca aaa agt gat tta tta ttt gat aaa ttc aac gac aaa cat gga 48

Met Thr Lys Ser Asp Leu Leu Phe Asp Lys Phe Asn Asp Lys His Gly

1 5 10 15

aag ttt cta gtt ttt ttt ggt acc ttt gta gat acc cct aaa tta gga 96

Lys His Leu Val Phe Phe Gly Thr Phe Val Asp Thr Pro Lys Leu Gly

20 25 30

gag ctg aga att agn gag aas aca tct gtt gga gtt ctc aac gga atc 144

Gln Leu Arg His Arg Glu Lys Thr Ser Val Gly Val Leu Asn Gly Ile

35 40 45

atc agg ttt gtg aac agn aat tca ctc gat cct gtc aaa gat tgc tta 102

Ile Arg Phe Val Asn Arg Asn Ser Leu Asp Pro Val Lys Asp Cys Leu

50 55 60

gat cac gat agt agc tta tca cca gag gat gtc aag gtg gtt gac ata 240

Asp His Asp Ser Ser Leu Ser Pro Glu Asp Val Thr Val Val Asp His

65 70 75 80

att gga aaa gat aag act cga aat aac agc ttt tat ttt cca ggt ttt 288

Ile Gly Lys Asp Lys Thr Arg Asn Asn Ser Phe Tyr Phe Pro Gly Phe

85 90 95

gtt gac acg cat aac cat gtc tgg caa tat cca aat gtc ggc gta ttt	336
Val Asp Thr His Asn His Val Ser Gln Tyr Pro Asn Val Gly Val Phe	
100 105 110	
ggg aat tat acc ctg ctg gat tgg cta gag aag tat acc ltu ccc ata	384
Gly Asn Ser Thr Leu Leu Arg Trp Leu Glu Lys Tyr Thr Phe Pro Ile	
115 120 125	
gat gcc gca cta gca aac gaa aat act gct aga gaa gtt tac aat aag	432
Glu Ala Ala Leu Ala Asn Glu Asn Ile Ala Arg Glu Val Tyr Asn Lys	
130 135 140	
gta ata agt aag acg att tcc ccc ggt acc acg acc gtc gct tac tat	480
Val Ile Ser Iys Thr Leu Ser His Gly Thr Thr Val Ala Tyr Tyr	
145 150 155 160	
aat acc att gat ccc aag tcc act aag ctc ttg gct caa cta ago tcc	528
Asp Thr Ile Asp Leu Lys Ser Thr Lys Leu Leu Ala Gln Leu Ser Ser	
165 170 175	
tta ttg ggg aag cgt gtt ctt gtt gga aaa gtc cgc atg gat acc aat	576
Leu Leu Gly Gln Arg Val Leu Val Gly Lys Val Cys Met Asp Thr Asn	
180 185 190	
ggt ccc gag Lal Lal all gaa gat act aaa act tcc ttt gca agc act	624
Gly Pro Gln Tyr Tyr Ile Glu Asp Thr Lys Thr Ser Phe Gln Ser Thr	
195 200 205	
gtg aaa gtt gtt aag tac ata cgg gaa acc att tgt gat ccc ctc gta	672
Val Lys Val Val Lys Tyr Ile Arg Glu Thr Ile Cys Asp Pro Leu Val	
210 215 220	
aat ccc ata gtg aaa cca agg ttc gag ccc tct tgt tct aga gaa cta	720
Asn Pro Ile Val Thr Pro Arg Phe Ala Pro Ser Cys Ser Arg Glu Leu	
225 230 235 240	
atg caa caa ttg tcc aag cta gtc aag gat gaa aac ata cac gtt caa	768
Met Gln Gln Leu Ser Tyr Leu Val Lys Asp Glu Asn Ile His Val Gln	
245 250 255	
acc cac ttg tgg gaa aat aag gag gag ata cag tgg gtt caa gat tta	816
Thr His Leu Ser Glu Asn Lys Glu Gln Ile Gln Trp Val Gln Asp Leu	

153/762

260	285	370	
ttt ccc gaa tgt gag agc tat act gat gta tan gac aaa tat ggg ctg			864
Phe Pro Glu Cys Glu Ser Tyr Thr Asp Val Tyr Asp Lys Tyr Gly Leu			
275	280	285	
ctc aca gaa aaa aca gta ttg gaa cat tgt att cat cta aca gat gcc			912
Leu Thr Glu Lys Thr Val Leu Ala His Cys Ile His Leu Thr Asp Ala			
290	295	300	
gaa gcg cgt gtg att aaa cag cgt ugu tgl ggt ata tct cat tgt ccc			360
Glu Ala Arg Val Ile Lys Glu Arg Arg Cys Gly Ile Ser His Cys Pro			
305	310	315	320
att tcc aac tcc tct ctg act tct gga gag tgt agg gtt cga tgg tgg			1008
Ile Ser Asn Ser Ser Leu Thr Ser Gly Glu Cys Arg Val Arg Trp Leu			
325	330	335	
ctg gac cag ggc ata aag gtt ggt cta gac aac gac gtt tca gcc ggt			1056
Leu Asp Glu Gly Ile Lys Val Gly Leu Gly Thr Asp Val Ser Ala Gly			
340	345	350	
cat tcc tgt acc ata ctc acc acc gga agg cag gcc ttt gaa gtt tca			1104
His Ser Cys Ser Ile Leu Thr Thr Gly Arg Glu Ala Phe Ala Val Ser			
355	360	365	
agg cat ttg gca atg aga guu act gat cat gcc aaa ctg tca gtc tcc			1152
Arg His Leu Ala Met Arg Glu Thr Asp His Ala Lys Leu Ser Val Ser			
370	375	380	
gag tgc cta ttt ctg gct aca atg ggc gga gca cca gtc ttg cgt atg			1200
Glu Cys Leu Phe Leu Ala Thr Met Gly Gly Ala Glu Val Leu Arg Met			
385	390	395	400
gat gag acc ctg ggg act ttt gac gtc ggt aag cag ttt gac gct cca			1248
Asp Glu Thr Ser Gly Thr Phe Asp Val Gly Lys Glu Phe Asp Ala Glu			
405	410	415	
atg atc gat acc nat gct ccc ggc tca aac ggg gat atg ttt cat tgg			1296
Met Ile Asp Thr Asn Ala Pro Gly Ser Asn Val Asp Met Phe His Trp			
420	425	430	

cag cta aag gag aag gat caa atg cac gag cca gag cca gag cac ggg 1344
 Gln Leu Lys Glu Lys Asp Gln Met Gln Glu Gln Glu Gln Glu Gly
 435 440 445

caa gac cct tat aag aac cca cag ctg ctt act aat gaa gac ata atc 1392
 Gln Asp Pro Tyr Lys Asn Pro Pro Leu Leu Thr Asn Glu Asp Ile Ile
 450 455 460

gca aaa tgg ttc ttt aac ggt gat gat cgc aac acc aat nan gtt tgg 1440
 Ala Lys Trp Phe Phe Asn Gly Asp Asp Asn Thr Thr Lys Val Trp
 465 470 475 480

gta gcc ggc cag caa gta taa cag att tag 1470
 Val Ala Gly Gln Gln Val Tyr Gln Ile
 485

<210> 51

<211> 489

<212> PRT

<213> Saccharomyces cerevisiae

<400> 51

Met Thr Lys Ser Asp Leu Leu Phe Asp Lys Phe Asn Asp Lys His Gly
 1 5 10 15

Lys Phe Leu Val Phe Phe Gly Thr Phe Val Asp Thr Pro Lys Leu Gly
 20 25 30

Glu Leu Arg Ile Arg Glu Lys Thr Ser Val Gly Val Leu Asn Gly Ile
 35 40 45

Ile Arg Phe Val Asn Arg Asn Ser Leu Asp Pro Val Lys Asp Cys Leu
 50 55 60

Asp His Asp Ser Ser Leu Ser Pro Glu Asp Val Thr Val Val Asp Ile
 65 70 75 80

Ile Gly Lys Asp Lys Thr Arg Asn Asn Ser Phe Tyr Phe Pro Gly Phe
85 90 95

Val Asp Thr His Asn His Val Ser Glu Tyr Pro Asn Val Gly Val Phe
100 105 110

Gly Asn Ser Thr Leu Leu Asp Trp Leu Glu Tyr Tyr Thr Phe Pro Ile
115 120 125

Glu Ala Ala Leu Ala Asn Glu Asn Ile Ala Arg Glu Val Tyr Asn Lys
130 135 140

Val Ile Ser Lys Thr Leu Ser His Gly Thr Thr Thr Val Ala Tyr Tyr
145 150 155 160

Asn Thr Ile Asp Leu Lys Ser Thr Lys Leu Leu Ala Glu Leu Ser Ser
165 170 175

Leu Leu Gly Glu Arg Val Leu Val Gly Tyr Val Cys Met Asp Thr Asn
180 185 190

Gly Pro Glu Tyr Tyr Ile Glu Asp Thr Lys Thr Ser Phe Glu Ser Thr
195 200 205

Val Lys Val Val Lys Tyr Ile Arg Glu Thr Ile Cys Asp Pro Leu Val
210 215 220

Asn Pro Ile Val Thr Pro Arg Phe Ala Pro Ser Cys Ser Arg Glu Leu
225 230 235 240

Met Gln Gln Leu Ser Lys Leu Val Lys Asp Glu Asn Ile His Val Gln
 245 250 255

Thr His Leu Ser Glu Asn Lys Glu Glu Ile Gln Trp Val Gln Asp Leu
 260 265 270

Phe Pro Glu Cys Glu Ser Tyr Thr Asp Val Tyr Asp Lys Tyr Gly Leu
 275 280 285

Leu Thr Gln Lys Thr Val Leu Ala His Cys Phe His Leu Thr Asp Ala
 290 295 300

Glu Ala Arg Val Ile Lys Gln Arg Arg Cys Gly Ile Ser His Cys Pro
 305 310 315 320

Ile Ser Asn Ser Ser Leu Thr Ser Gly Glu Cys Arg Val Arg Trp Leu
 325 330 335

Leu Asp Gln Gly Phe Lys Val Gly Leu Gly Thr Asp Val Ser Ala Gly
 340 345 350

His Ser Cys Ser Ile Leu Thr Thr Gly Arg Gln Ala Phe Ala Val Ser
 355 360 365

Arg His Leu Ala Met Arg Gln Thr Asp His Ala Lys Leu Ser Val Ser
 370 375 380

Glu Cys Leu Phe Leu Ala Thr Met Gly Gly Ala Glu Val Leu Arg Met
 385 390 395 400

Asp Glu Thr Leu Gly Thr Phe Asp Val Gly Lys Gln Phe Asp Ala Glu

405

410

435

Met Ile Asp Thr Asn Ala Pro Gly Ser Asn Val Asp Met Phe His Trp
 420 425 430

Gln Leu Lys Glu Lys Asp Gln Met Gln Glu Gln Glu Gln Glu Gly
 435 440 445

Gln Asp Pro Tyr Lys Asn Pro Pro Leu Leu Thr Asn Glu Asp Ile Ile
 450 455 460

Ala Lys Trp Phe Phe Asn Gly Asp Asn Arg Asn Thr Thr Lys Val Trp
 465 470 475 480

Val Ala Gly Gln Gln Val Tyr Gln Ile
 485

<210> 62

<211> 4x1

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<231> CDS

<222> (1) .. (441)

<400> 62

atg aaa ggc tca ccc att tot cca ttt agt aag acc tct att aat gct 40
 Met Lys Gly Ser Pro Ile Ser Cln Phe Ser Lys Thr Ser Ile Asn Ala
 1 5 10 15

ctt acc agc cct tgg aag aaa tac aga gat ggt gaa tta ttt tat ggg 96
 Leu Thr Arg Pro Trp Lys Lys Tyr Arg Asp Gly Glu Leu Phe Tyr Gly
 20 25 30

ttt tca aaa gtt ggg aat aaa aga gtg cgg ttg acc acg aag caa ggt 144
 Leu Ser Lys Val Gly Asn Lys Arg Val Pro Leu Thr Thr Lys Gln Gly
 35 40 45

aac aag acg atg tac aaa ggg aca aga gct tca ggg aat ggt aga cat 192
 Asn Lys Thr Met Tyr Lys Gly Thr Arg Ala Ser Gly Ile Gly Arg His
 50 55 60

aca aaa ttc ggt ggt tat gtg ata aac tgg aag aaa gtc aga acc tat 240
 Thr Lys Phe Gly Gly Tyr Val Ile Asn Trp Lys Lys Val Arg Thr Tyr
 65 70 75 80

gtr acc tca gat atg gtt aat ttc gaa tta aag ccc tac gtt aac gca 288
 Val Thr Pro Asp Met Val Asn Phe Gln Leu Tyr Pro Tyr Val Asn Ala
 95 90 95

aat gta cca cct cta aaa ccc gac ttt aaa gga ttt agt ggc ggc cca 336
 Asn Val Pro Pro Leu Lys His Glu Phe Lys Gly Phe Ser Gly Gly Pro
 100 105 110

tta gat cct cgt tta cag tta tta aag ata aaa gaa tac ata gta aac 384
 Leu Asp Pro Arg Leu Gln Leu Leu Lys Ile Lys Glu Tyr Ile Val Asn
 115 120 125

ggg agg gta cca ggc gaa ggg gcc acc gac act tca tgt tat aag gag 432
 Gly Arg Val Gln Ser Glu Gly Ala Thr Asp Thr Ser Cys Tyr Lys Glu
 130 135 140

cgt gga taa 441
 Arg Gly
 145

<210> 63

<211> 146

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 63

Met Lys Gly Ser Pro Ile Ser Gln Phe Ser Lys Thr Ser Ile Asn Ala
 1 5 10 15

Leu Thr Arg Pro Trp Lys Lys Tyr Arg Asp Gly Glu Leu Phe Tyr Gly
 20 25 30

Leu Ser Lys Val Gly Asn Lys Arg Val Pro Leu Thr Thr Lys Glu Gly
 35 40 45

Asn Lys Thr Met Tyr Lys Gly Thr Arg Ala Ser Gly Ile Gly Arg His
 50 55 60

Thr Lys Phe Gly Gly Tyr Val Ile Asn Trp Lys Lys Val Arg Thr Tyr
 65 70 75 80

Val Thr Pro Asp Met Val Asn Phe Glu Asn Lys Pro Tyr Val Asn Ala
 85 90 95

Asn Val Pro Pro Leu Lys His Glu Phe Lys Gly Phe Ser Gly Gly Pro
 100 105 110

Leu Asp Pro Arg Leu Cln Leu Leu Lys Ile Lys Glu Tyr Ile Val Asn
 115 120 125

Gly Arg Val Gln Ser Gln Gly Ala Thr Asp Thr Ser Cys Tyr Lys Glu
 130 135 140

Arg Gly
 145

<210> 64

<211> 429

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(429)

<400> 54

atg gcg tat aat caa gaa gat agt aaa aga cta tca gac aag tat aag 43

Met Ala Tyr Asn Gln Glu Asp Ser Lys Arg Leu Ser Asp Lys Tyr Lys

1 5 10 15

aag gag gga cat ttt gac aag ttg aaa aga gaa ata ttg tct aac cca 96

Lys Glu Gly His Phe Asp Lys Ileu Lys Arg Glu Ile Leu Ser Asn Pro

20 25 30

tgg aat aal aca gaa gag aat agc gaa tct ttt aca caa gcg ctt ogg 144

Trp Asn Asn Thr Gln Glu Asn Ser Glu Ser Phe Glu Gln Ala Leu Arg

35 40 45

aaa aga gtt gcc agt aca gtt aas gaa atg gtt aac gaa gat gaa gaa 192

Lys Arg Val Ala Ser Thr Val Tyr Glu Met Val Asn Glu Asp Glu Gln

50 55 60

tta ata ttt aaa aac aga ggg cta acc agt gca ttg att gaa tca caa 240

Leu Ile Phe Lys Asn Arg Gly Leu Thr Ser Ala Leu Ile Gln Ser Gln

65 70 75 80

ttg gtc aag gac aac tac cta aag ctg ggt agt aaa atg gag gcg gat 288

Leu Val Lys Asp Asn Tyr Leu Lys Leu Gly Ser Lys Met Glu Gly Asp

85 90 95

aat ggt gat ggt gag aag aaa ttt gac ttg gat gtc tat cta cgg tcc 336

Asn Gly Asp Gly Glu Lys Lys Phe Asp Leu Asp Val Tyr Val Arg Ser

100 105 110

aag tta cag gat ccc aaa cta ttg gaa atg ata aag gga caa ctt cag 384

Lys Leu Glu Asp Pro Lys Leu Leu Glu Met Ile Tyr Gly Glu Leu Gln

115 120 125

gaa aca ctg aac tct tat gaa gag gaa gaa aat gga agt acg taa 429

Glu Thr Ileu Asn Ser Tyr Glu Glu Glu Ala Asn Gly Ser Thr

130 135 140

<210> 63
 <211> 142
 <212> PRT
 <213> Saccharomyces cerevisiae

<430> 65

Met Ala Tyr Asn Gln Glu Asp Ser Lys Arg Leu Ser Asp Lys Tyr Lys
 1 5 10 15

Lys Glu Gly His Phe Asp Lys Leu Lys Arg Glu Ile Leu Ser Asn Pro
 20 25 30

Tyr Asn Asn Thr Glu Glu Asn Ser Glu Ser Phe Glu Glu Ala Leu Arg
 35 40 45

Lys Arg Val Ala Ser Thr Val Lys Glu Met Val Asn Glu Asp Glu Glu
 50 55 60

Leu Ile Phe Lys Asn Arg Gly Leu Thr Ser Ala Leu Phe Glu Ser Gln
 65 70 75 80

Leu Val Lys Asp Asn Tyr Leu Lys Leu Gly Ser Lys Met Glu Gly Asp
 85 90 95

Asn Gly Asp Gly Glu Lys Lys Phe Asp Leu Asp Val Tyr Val Arg Ser
 100 105 110

Lys Leu Gln Asp Pro Lys Leu Leu Glu Met Ile Lys Gly Gln Leu Gln
 115 120 125

Gln Thr Leu Asn Ser Tyr Glu Glu Glu Ala Asn Gly Ser Thr

120	135	140	
<210> 66			
<211> 462			
<212> DNA			
<213> <i>Saccharomyces cerevisiae</i>			
<220>			
<221> CDS			
<222> {1}..{462}			
<400> 66			
atg acc ttt tta cca ttt atc aat aat aga cca gaa gga cca ggt			40
Met Thr Phe Leu Gln Phe Ile Asn Asn Asn Arg Gln Glu Gly Gln Gly			
1 5 10 15			
tat att tca gaa aaa tta ttc aaa acc cag aag aat gag atg ata aga			56
Tyr Ile Ser Glu Lys Leu Phe Lys Thr Lys Lys Asn Glu Met Ile Arg			
20 25 30			
aaa aca gtt acc aat tta gta gct gta aga tta aaa aac tta tcc aac			144
Lys Thr Val Thr Asn Leu Val Ala Val Arg Leu Lys Asn Leu Ser His			
35 40 45			
gaa tat gat gta aca gag aat tat ctg cgc tat ata gct agc acc agt			192
Glu Phe Asp Val Ile Glu Asn Tyr Leu Arg Tyr Ile Ala Ser Thr Ser			
50 55 60			
gaa cat ata ttt aat gct att aag cgc cac ttt aac aaa tgt gcc aga			240
Glu His Leu Phe Thr Ala Ile Lys Arg His Phe Asn Lys Cys Ala Arg			
65 70 75 80			
aaa ctt ttg aca gaa gca atc gac tcc aaa tca aac tca gaa aat gct			288
Lys Leu Leu Lys Glu Ala Ile Asp Ser Lys Ser Asn Ser Glu Thr Ala			
85 90 95			
acg gcg gtt ctg aca gaa gga ttt tct ggc att tgc tta ttg aaa gcg			336
Thr Val Val Leu Gln Glu Gly Phe Ser Gly Ile Cys Leu Leu Tyr Ala			
100 105 110			

163/762

tct tca att ata tta aaa ata aaa ttg aag ttt cca aaa aag aaa gat 381
 Ser Ser Ile Ile Leu Lys Leu Lys Leu Lys Phe Pro Lys Lys Lys Asp
 115 120 125

aga act gat att agc aaa ttg tgt gac aag aac gaa cgg atg aca cag 432
 Arg Thr Asp Ile Ser Lys Leu Cys Asp Lys Lys Glu Arg Met Thr Glu
 130 135 140

tgg tta gaa att tca att ttg atg aac tga 462
 Trp Trp Glu Ile Ser Ile Leu Met Asn
 145 150

<210> 67

<211> 153

<212> 2BT

<213> *Saccharomyces cerevisiae*

<400> 67

Met Thr Phe Leu Gln Phe Ile Asn Asn Asn Arg Gln Glu Gly Gln Gly
 1 5 10 15

Tyr Ile Ser Glu Lys Leu Phe Lys Thr Lys Lys Asn Glu Met Ile Arg
 20 25 30

Lys Thr Val Thr Asn Leu Val Ala Val Arg Leu Lys Asn Leu Ser His
 35 40 45

Glu Phe Asp Val Ile Glu Asn Tyr Leu Arg Tyr Ile Ala Ser Thr Ser
 50 55 60

Glu His Leu Phe Thr Ala Ile Lys Arg His Phe Asn Lys Cys Ala Arg
 65 70 75 80

Lys Leu Leu Lys Glu Ala Ile Asp Ser Lys Ser Asn Ser Glu Thr Ala

85

90

95

Thr Val Val Leu Gln Glu Gly Phe Ser Gly Ile Cys Leu Leu Lys Ala
 100 105 110

Ser Ser Ile Ile Leu Lys Leu Lys Leu Lys Phe Pro Lys Lys Lys Asp
 115 120 125

Arg Thr Asp Ile Ser Lys Leu Cys Asp Lys Lys Gln Arg Met Thr Gln
 130 135 140

Trp Leu Glu Ile Ser Ile Leu Met Asn
 145 150

<210> 58

<211> 1584

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1584)

<400> 68

atg agt ctc tgg cag ggg tca cct tta ccc cat atc aag gat gtt gtt 40

Met Ser Leu Ser Gln Val Ser Pro Leu Pro His Ile Lys Asp Val Val

1 5 10 15

tta gga gat aca gta ggc caa ggc gca ttc gcc tgc gtt aaa aat gct 80

Leu Gly Asp Thr Val Gly Gln Gly Ala Phe Ala Cys Val Lys Asn Ala

20 25 30

cat ctt cna atg gat ccc tcc att att cta gct gtt aaa ttc att cat 114

His Leu Trp Met Asp Pro Ser Ile Ile Leu Ala Val Lys Phe Ile His

35 40 45

gtt ccc aot tgc aaa aaa atg gga ctc agt gac aag gat atc acu aaa	192
Val Pro Thr Cys Lys Lys Met Gly Leu Ser Asp Lys Asp Ile Thr Lys	
50 55 60	
gag gtt gtt ttg caa tcg aag tqt tct aag cat cct aat gtt ttg aga	240
Glu Val Val Ileu Glu Ser Lys Cys Ser Lys His Pro Asn Val Leu Arg	
65 70 75 80	
ctt atc gat tgt aat gtc tct aaa gaa tat atg tgg ata att ctg gag	288
Leu Ile Asp Cys Asn Val Ser Lys Glu Tyr Met Trp Ile Ile Ileu Glu	
85 90 95	
atg gca gat ggt ggt gat cta ttt gat aag att gag cct gaa yll gga	336
Met Ala Asp Gly Arg Asp Leu Phe Asp Lys Ile Glu Pro Asp Val Gly	
100 105 110	
gtt gat lou gac gtg gcc caa ttt taa ttt caa cag ctc gtt agt gct	384
Val Asp Ser Asp Val Ala Glu Phe Tyr Phe Glu Glu Leu Val Ser Ala	
115 120 125	
att aat tat ctg cat gta gaa tgt gga gtt gct cac aqa gac atc aag	432
Ile Asn Tyr Leu His Val Glu Cys Gly Val Ala His Arg Asp Ile Lys	
130 135 140	
cct gaa aac atc lla ulu yat aag aac gga aat ctg aag cta gct gat	480
Pro Glu Asn Ile Leu Ileu Asp Lys Asn Gly Asn Ileu Lys Leu Ala Asp	
145 150 155 160	
ttt ggg ctc gac tct caa ttt agg agg aas gat ggt aca tta ugt gta	528
Phe Gly Leu Ala Ser Glu Phe Arg Arg Lys Asp Gly Thr Leu Arg Val	
165 170 175	
too atg gat caa agg ggt tct cea ccc tac atg gct cct gaa gta tta	576
Ser Met Asp Glu Arg Gly Ser Pro Pro Tyr Met Ala Pro Glu Val Leu	
180 185 190	
tat tct gaa gag ggt tat taa gca gat cga aca gat ata tgg tct att	624
Tyr Ser Glu Glu Gly Tyr Tyr Ala Asp Arg Thr Asp Ile Trp Ser Ile	
195 200 205	
ggc atc ctc ttg ttc gta lly ttg act ggt caa aag cct taa gaa tta	672
Gly Ile Leu Leu Phe Val Leu Leu Thr Gly Glu Thr Pro Trp Glu Leu	

210	215	220	
cct tca tta gag aac gaa gat ttc gtc ttt ttt att gaa aat gat gga			720
Pro Ser Leu Glu Asn Glu Asp Phe Val Phe Phe Ile Glu Asn Asp Gly			
225	230	235	240
aat tta aac tgg gga ccc tgg tca aag ata gaa ttt act cac tlg aac			768
Asn Leu Asn Trp Gly Pro Trp Ser Lys Ile Glu Phe Thr His Leu Asn			
245	250	255	
cta ctc cga aaa att tta cca cct gac cca aat aag agg ctg aca ttg			816
Leu Leu Arg Lys Ile Leu Ser Pro Asp Pro Asn Lys Arg Val Thr Leu			
260	265	270	
aag gct tta aag tta cat cct tgg gta tta cgt cga gct tca ttt tct			864
Lys Ala Leu Lys Leu His Pro Trp val Leu Arg Arg Ala Ser Phe Ser			
275	280	285	
ggg gct gat ggt ctg tgt aat gac cct gaa ctc ttg gct aag aac ctg			912
Gly Asp Asp Gly Leu Cys Asn Asp Pro Glu Leu Leu Ala Lys Lys Leu			
290	295	300	
ttt tct cac tta aaa gtc tca ctg agt aac gaa aat tat ttg acn ttc			960
Phe Ser His Leu Lys Val Ser Leu Ser Asn Gln Asn Tyr Leu Lys Phe			
305	310	315	320
act caa gat aca aac tct aat aat aag tac att tct act cag cca att			1008
Thr Gln Asp Thr Asn Ser Asn Ser Arg Tyr Ile Ser Thr Gln Pro Ile			
325	330	335	
ggc aac gaa ttg gct gag ctt gaa cac gac tca atg cat ttc cag aca			1056
Gly Asn Glu Leu Ala Glu Leu Glu His Asp Ser Met His Phe Gln Thr			
340	345	350	
gtt tgg aat aca caa cgt gaa ttt acc ctg tat gat tca aat aag aac			1104
Val Ser Asn Thr Gln Arg Ala Phe Thr Ser Tyr Asp Ser Asn Thr Asn			
355	360	365	
tat aat aac cga aca ggt aly aca caa gag gct aag tgg aag caa ttc			1152
Tyr Asn Ser Gly Thr Gly Met Thr Gln Glu Ala Lys Trp Thr Gln Phe			
370	375	380	

ata agc tat gat atc gct gcc tta cag ttt cat tct gat gaa aat gat	1200
Ile Ser Tyr Asp Ile Ala Ala Leu Gln Phe His Ser Asp Glu Asn Asp	
385 390 395 400	
tgk aat gaa tta gta aaa cga cat tta caa ttt aat ccg aat aaa ctt	1248
Cys Asn Glu Leu Val Lys Arg His Leu Gln Phe Asn Pro Asn Lys Leu	
405 410 415	
acc aag ttc tac acg ttg aaa cct atg gat gtt ttg tta ccg att ctg	1296
Thr Lys Phe Tyr Thr Leu Gln Pro Met Asp Val Leu Leu Pro Ile Leu	
420 425 430	
gag aaa gcc ttg aat tta tta caa att agn gta aaa ccc gac ctc ttt	1344
Glu Lys Ala Leu Asn Leu Ser Gln Ile Arg Val Lys Pro Asp Leu Phe	
435 440 445	
gag aat ttt gaa aga ttg tgc gaa tta ttg ggt tat gat aac gtt ttc	1392
Ala Asn Phe Glu Arg Leu Cys Glu Leu Leu Gly Tyr Asp Asn Val Phe	
450 455 460	
cca ctt att ata aat att aca ccc aac agt aat ggg ggt tat caa tta	1440
Pro Leu Ile Ile Asn Ile Lys Thr Lys Ser Asn Gly Gly Tyr Gln Leu	
465 470 475 480	
tcg ggt agc att tcc atc aia aag att gaa gaa gag ttg aac agt gtc	1488
Cys Gly Ser Ile Ser Ile Ile Lys Ile Glu Glu Glu Leu Lys Ser Val	
485 490 495	
gga ttt gaa aga aaa act ggt gat cct tta gaa tgg aga aga ttg ltc	1536
Gly Phe Glu Asn Lys Thr Gly Asp Pro Leu Glu Trp Arg Arg Leu Phe	
500 505 510	
aag aaa att tca act atc tgt agg gat att atc cta att ccc aac tga	1584
Lys Lys Ile Ser Thr Ile Cys Arg Asp Ile Ile Leu Ile Pro Asn	
515 520 525	

<210> 69

<211> 327

<212> PPT

<213> *Saccharomyces cerevisiae*

<400> 50

Met Ser Leu Ser Gln Val Ser Pro Leu Pro His Ile Lys Asp Val Val

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Leu Gly Asp Thr Val Gly Gln Gly Ala Phe Ala Cys Val Lys Asn Ala

20 25 30

His Leu Gln Met Asp Pro Ser Ile Ile Leu Ala Val Lys Phe Ile His

35 40 45

Val Pro Thr Cys Lys Lys Met Gly Leu Ser Asp Lys Asp Ile Thr Lys

50 55 60

Glu Val Val Leu Gln Ser Lys Cys Ser Lys His Pro Asn Val Leu Arg

65 70 75 80

Leu Ile Asp Cys Asn Val Ser Lys Glu Tyr Met Trp Ile Ile Leu Glu

85 90 95

Met Ala Asp Gly Gly Asp Leu Phe Asp Tyr Phe Glu Pro Asp Val Gly

100 105 110

Val Asp Ser Asp Val Ala Gln Phe Tyr Phe Gln Gln Leu Val Ser Ala

115 120 125

Ile Asn Tyr Leu His Val Glu Cys Gly Val Ala His Arg Asp Ile Lys

130 135 140

Pro Glu Asn Ile Leu Leu Asp Lys Asn Gly Asn Leu Lys Leu Ala Asp

145 150 155 160

Phe Gly Leu Ala Ser Gln Phe Arg Arg Lys Asp Gly Thr Asn Arg Val
 165 173 175

Ser Met Asp Gln Arg Gly Ser Pro Pro Tyr Met Ala Pro Glu Val Leu
 180 185 190

Tyr Ser Glu Glu Gly Tyr Tyr Ala Asp Arg Thr Asp Ile Trp Ser Ile
 195 200 205

Gly Ile Leu Leu Phe Val Leu Leu Thr Gly Gln Thr Pro Trp Glu Leu
 210 215 220

Pro Ser Leu Glu Asn Glu Asp Phe Val Phe Phe Ile Glu Asn Asp Gly
 225 230 235 240

Asn Leu Asn Trp Gly Pro Trp Ser Lys Ile Glu Phe Thr His Leu Asn
 245 250 255

Leu Leu Arg Lys Ile Leu Gln Pro Asp Pro Asn Lys Arg Val Thr Leu
 260 265 270

Lys Ala Leu Lys Leu His Pro Trp Val Leu Arg Arg Ala Ser Phe Ser
 275 280 285

Gly Asp Asp Gly Leu Cys Asn Asp Pro Glu Leu Leu Ala Lys Lys Leu
 290 295 300

Phe Ser His Leu Lys Val Ser Leu Ser Asn Glu Asn Tyr Leu Lys Phe
 305 310 315 320

Thr Gln Asp Thr Asn Ser Asn Asn Arg Tyr Ile Ser Thr Gln Pro Ile

325

330

335

Gly Asn Glu Leu Ala Glu Leu Glu His Asp Ser Met His Phe Gln Thr
 340 345 350

Val Ser Asn Thr Gln Arg Ala Phe Thr Ser Tyr Asp Ser Asn Thr Asn
 355 360 365

Tyr Asn Ser Gly Thr Gly Met Thr Gln Glu Ala Lys Trp Thr Gln Phe
 370 375 380

Ile Ser Tyr Asp Ile Ala Ala Leu Gln Phe His Ser Asp Glu Asn Asp
 385 390 395 400

Cys Asn Glu Leu Val Lys Arg His Leu Gln Phe Asn Pro Asn Lys Leu
 405 410 415

Thr Lys Phe Tyr Thr Leu Gln Pro Met Asp Val Leu Leu Pro Ile Leu
 420 425 430

Glu Lys Ala Leu Asn Leu Ser Gln Ile Arg Val Lys Pro Asp Leu Phe
 435 440 445

Ala Asn Phe Glu Arg Leu Cys Glu Leu Leu Gly Tyr Asp Asn Val Phe
 450 455 460

Pro Leu Ile Ile Asn Ile Lys Thr Lys Ser Asn Gly Gly Tyr Gln Leu
 465 470 475 480

Cys Gly Ser Ile Ser Ile Ile Lys Ile Glu Glu Glu Leu Lys Ser Val
 485 490 495

Gly Phe Glu Arg Lys Thr Gly Asp Pro Leu Glu Trp Arg Arg Leu Phe
500 505 510

Lys Lys Ile Ser Thr Ile Cys Arg Asp Ile Ile Leu Ile Pro Asn
515 520 525

<210> 70

<211> 849

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(849)

<400> 70

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Met Asp Pro Ser Leu Val Leu Glu Gln Thr Ile Gln Asp Val Ser Asn
1 K -C 15

ctc cca tca gaa ttt cgt tac ctc tta gag gag atc ggt tca acc gat 96
Leu Pro Ser Glu Phe Arg Tyr Leu Leu Glu Glu Ile Gly Ser Ser Asp
20 25 30

ttg aag ctu atc gaa gaa aaa aag aaa tac gag caa aaa gaa tca caa 144
Leu Lys Leu Ile Glu Glu Lys Lys Lys Tyr Glu Gln Lys Glu Ser Gln
35 40 45

ata cac aaa ttt ata aga cag caa ggc tca ata cag aaa cat cca cag 192
Ile His Lys Phe Ile Arg Gln Gln Gly Ser Ile Pro Lys His Pro Gln
50 55 60

gaa gat ggg ctt gac aaa gaa ata aaa gaa caa att ttg aaa tgt cag 240
Glu Asp Gly Leu Asp Lys Glu Ile Lys Glu Ser Leu Leu Lys Cys Gln
65 70 75 80

tct ttg caa aga gaa aaa tgc gtt ctg gog aac acc gcc ttg ttt cta 288
Ser Leu Gln Arg Glu Lys Cys Val Leu Ala Asn Thr Ala Leu Phe Leu

	85	90	95	
att gct aga cag ttg aat aap ttg gaa aaa aac atc gct tta ttg gag				336
Ile Ala Arg His Leu Asn Lys Leu Glu Lys Asn Ile Ala Leu Ser Glu				
	100	105	110	
gaa gat ggt gtc cta gcc ccc gtg gaa gaa gat gga gac atg gat agc				384
Glu Asp Gly Val Leu Ala Pro Val Glu Glu Asp Gly Asp Met Asp Ser				
	115	120	125	
gct gct gaa ggc tct aga gaa agt tca gtt gtg agt aac agt agc gtg				432
Ala Ala Glu Ala Ser Arg Glu Ser Ser Val Val Ser Asn Ser Ser Val				
	130	135	140	
aaa aag aga aga gct gca tca agc tca gga tcc gtt cca ccc act ttg				480
Lys Lys Arg Arg Ala Ala Ser Ser Ser Gly Ser Val Pro Pro Thr Leu				
	145	150	155	160
aaa aag aaa aaa act agt cga acc tct aac ctg cca aat gaa att gcc				528
Lys Lys Lys Lys Thr Ser Arg Thr Ser Lys Leu Gln Asn Glu Ile Asp				
	165	170	175	
gtt tct tca aga gaa aag tct gtt acg cca gtg agc cca agc att gaa				576
Val Ser Ser Arg Glu Lys Ser Val Thr Pro Val Ser Pro Ser Ile Glu				
	180	185	190	
aaa aag att gca aga acc aac gaa ttc aaa aac agt aga aat ggt aaa				624
Lys Lys Ile Ala Arg Thr Lys Glu Phe Cys Asn Ser Arg Asn Gly Lys				
	195	200	205	
ggc aca aac ggt tcc cct gaa aac gag gaa gag gac aaa act tta tac				672
Gly Gln Asn Gly Ser Pro Glu Asn Glu Glu Glu Asp Lys Thr Leu Tyr				
	210	215	220	
tgc ttc tgt caa aga gtt tgc ttt gga gaa atg gtt gca tgt gat gga				720
Cys Phe Cys Gln Arg Val Ser Phe Gly Glu Met Val Ala Cys Asp Gly				
	225	230	235	240
ccc aac tgt aaa taa gaa tgg ttt cat tat gat tgt gta aat tta aaa				768
Pro Asn Cys Lys Tyr Glu Trp Phe His Tyr Asp Cys Val Asn Leu Lys				
	245	250	255	

gaa cot cgg aaa gga aca tgg lac tgt ccc gaa tgt aaa att gag atg 816
 glu pro pro lys gly thr trp tyr cys pro glu cys lys ile glu met
 260 265 270

gan aaa aac aaa ctg aaa aga aaa cgt aac tga 849
 glu lys asn lys leu lys arg lys arg asn
 275 280

<210> 71

<211> 282

<212> PRT

<213> Saccharomyces cerevisiae

<400> 71

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 1 5 10 15

Leu Pro Ser Glu Phe Arg Tyr Leu Leu Glu Glu Ile Gly Ser Asn Asp
 20 25 30

Leu Lys Leu Ile Glu Glu Lys Lys Lys Tyr Glu Gln Lys Glu Ser Gln
 35 40 45

Ile His Lys Phe Ile Arg Gln Gln Gly Ser Ile Pro Lys His Pro Gln
 50 55 60

Glu Asp Gly Leu Asp Lys Glu Ile Lys Glu Ser Leu Leu Lys Cys Gln
 65 70 75 80

Ser Leu Gln Arg Glu Lys Cys Val Leu Ala Asn Thr Ala Leu Phe Leu
 85 90 95

Ile Ala Arg His Leu Asn Lys Leu Glu Lys Asn Ile Ala Leu Leu Glu
 100 105 110

Glu Asp Gly Val Leu Ala Pro Val Glu Glu Asp Gly Asp Met Asp Ser
115 120 125

Ala Ala Glu Ala Ser Arg Glu Ser Ser Val Val Ser Asn Ser Ser Val
130 135 140

Lys Lys Arg Arg Ala Ala Ser Ser Ser Gly Ser Val Pro Pro Thr Leu
145 150 155 160

Lys Lys Lys Lys Thr Ser Arg Thr Ser Lys Leu Gln Asn Glu Ile Asp
165 170 175

Val Ser Ser Arg Glu Lys Ser Val Thr Pro Val Ser Pro Ser Ile Glu
180 185 190

Lys Lys Ile Ala Arg Thr Lys Glu Phe Lys Asn Ser Arg Asn Gly Lys
195 200 205

Gly Glu Asn Gly Ser Pro Glu Asn Glu Glu Glu Asp Lys Thr Leu Tyr
210 215 220

Cys Phe Cys Gln Arg Val Ser Phe Gly Glu Met Val Ala Cys Asp Gly
225 230 235 240

Pro Asn Cys Lys Tyr Glu Trp Phe His Tyr Asp Cys Val Asn Leu Lys
245 250 255

Glu Pro Pro Lys Gly Thr Trp Tyr Cys Pro Glu Cys Lys Ile Glu Met
260 265 270

Glu Lys Asn Lys Leu Lys Arg Lys Arg Asn

275

280

<210> 72

<211> 1479

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> {1}..{1479}

<400> 72

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Met	Glu	Ser	Arg	Thr	Thr	Gly	Pro	Leu	Thr	Thr	Glu	Thr	Tyr	Asp	Gly	
1			5				10				15					

ccc	act	gtg	gcc	ttc	atg	ata	tta	ggg	gcc	gcc	cta	gta	ttt	ttt	atg	36
Pro	Thr	Val	Ala	Phe	Met	Ile	Leu	Gly	Ala	Ala	Leu	Val	Phe	Phe	Met	
		20					25				30					

gtg	ccc	ggg	ttg	gga	ttc	ttg	tac	tcc	ggg	ttg	gca	aga	agg	aag	tct	144
Val	Pro	Gly	Leu	Gly	Phe	Leu	Tyr	Ser	Gly	Leu	Ala	Arg	Arg	Lys	Ser	
		35					40				45					

gca	cta	gca	cta	atc	tgg	gtt	gta	tta	atg	ggg	act	tig	gca	ggg	aaa	192
Ala	Leu	Ala	Leu	Ile	Trp	Val	Val	Leu	Met	Ala	Thr	Leu	Val	Gly	Phe	
		50					55				60					

ctg	caa	tgg	tat	ttc	tgg	ggg	tac	tct	cta	gct	ttt	tca	aag	tcc	gct	240
Leu	Gln	Trp	Tyr	Phe	Trp	Gly	Tyr	Ser	Leu	Ala	Phe	Ser	Lys	Ser	Ala	
65					70				75				80			

ccg	aat	aat	aaa	tcc	att	ggg	aac	cta	gat	tgg	ttt	ggc	ttt	aga	aaa	288
Pro	Asn	Asn	Lys	Phe	Ile	Gly	Asn	Leu	Asp	Ser	Phe	Gly	Phe	Arg	Asn	
			85				90					95				

gag	tac	ggg	aaa	aaa	ttc	ggt	gaa	gat	gcc	tac	cct	ggg	ccc	ggg	tat	336
Val	Tyr	Gly	Lys	Lys	Phe	Asp	Glu	Asp	Ala	Tyr	Pro	Glu	Leu	Ala	Tyr	

176/762

100	105	110	
gca acc ttc cca atg atg ttt tgg tgc gtc aac tta agt att atc gct			394
Ala Thr Phe Glu Met Met Phe Ser Cys Val Asn Leu Ser Ile Ile Ala			
115	123	125	
ggc gcc act gcc gaa aga ggc agg ctg cta cag aac atg gtt ttt ctg			432
Gly Ala Thr Ala Glu Arg Gly Arg Leu Leu Pro His Met Val Phe Leu			
130	135	140	
lll all cll gct acc att gga tat tgt cca gtg acg tat tgg att tgg			480
Phe Ile Leu Ala Thr Ile Gly Tyr Cys Pro Val Thr Tyr Trp Ile Trp			
145	150	155	160
toa cca ggt ggt tgg gca tac cca tgg ggn gcc ctg gat tgg gca ggc			528
Ser Pro Gly Gly Trp Ala Tyr Glu Trp Gly Val Leu Arg Trp Ala Gly			
165	170	175	
ggc gcc aac att gaa ata tta agc gct gtt tcc ggg ttt gtt tac tct			576
Gly Gly Asn Ile Glu Ile Leu Ser Ala Val Ser Gly Trp Val Tyr Ser			
180	185	190	
tgg ttt ttg ggc aaa aga aat gaa aag tta ctg ata aat ttt agg act			624
Trp Phe Leu Gly Lys Arg Asn Glu Lys Leu Asn Ile Asn Phe Arg Pro			
195	200	205	
cat aac gtt toa ttg gtc acc cta ggc aca tcc ata ctg tgg ttt ggc			672
His Asn Val Ser Leu Val Thr Leu Gly Thr Ser Ile Leu Trp Phe Gly			
210	215	220	
tgg ctg cta ttt aat tct gca tcc tca tta tcc cca aat ttg agg toa			720
Trp Leu Leu Phe Asn Ser Ala Ser Ser Leu Ser Pro Asn Leu Arg Ser			
225	230	235	240
ggt tat gca ttc atg aat aca tgc ctg agt gcc att act ggt ggg atg			768
Val Tyr Ala Phe Met Asn Thr Cys Leu Ser Ala Ile Thr Gly Gly Met			
245	250	255	
acg tgg tgt att ctg ggt tac aga tgg gag aag aaa tgg tgg aca gtt			816
Thr Trp Cys Leu Leu Asp Tyr Arg Ser Glu Lys Lys Trp Ser Thr Val			
260	265	270	

ggg ctg tgc tcc ggt atc att tct ggg ctg gbg gct gca acg cca agc	864
Gly Leu Cys Ser Gly Ile Ile Ser Gly Leu Val Ala Ala Thr Pro Ser	
275 280 285	
cca ggc tgt ata acc ctt tac ggt tca ctt att caa ggc att gtg ggc	912
Ser Gly Cys Ile Thr Leu Tyr Gly Ser Leu Ile Gln Gly Ile Val Ala	
290 295 300	
ggg gta gtg tgt aac ttt ggc acg aag ttg aaa tac tac gca aaa gta	960
Gly Val Val Cys Asn Phe Ala Thr Lys Leu Lys Tyr Tyr Ala Tyr Val	
305 310 315 320	
gat gat gcc atg gat att cta got gag cac ggg gtt gca ggc gta ata	1008
Asp Asp Ala Met Asp Ile Leu Ala Glu His Gly Val Ala Gly Val Ile	
325 330 335	
gga cta att ttc act gcc ctt ttt gga gcc gac tgg gtc att ggt atg	1056
Gly Leu Ile Phe Asn Ala Leu Phe Gly Ala Asp Trp Val Ile Gly Met	
340 345 350	
gat ggc cct cca gag cac gag ggc ggc tgg gta act cac aat cac aag	1104
Asp Gly Thr Thr Glu His Glu Gly Gly Trp Val Thr His Asn Tyr Lys	
355 360 365	
caa atg lcl aag cag atc got tac att gcc gca tcc att ggg tac acc	1152
Glu Met Tyr Lys Gln Ile Ala Tyr Ile Ala Ala Ser Ile Gly Tyr Thr	
370 375 380	
gct gct gta acc gca ata atc tgc ttt gtg ctc ggc tuc ata ccc ggt	1200
Ala Ala Val Thr Ala Ile Ile Cys Phe Val Leu Gly Tyr Ile Pro Gly	
385 390 395 400	
atg agg cta aga ata tca gaa gag gca gag gag ggc ggt atg gac gaa	1248
Met Arg Leu Arg Ile Ser Glu Glu Ala Glu Glu Ala Gly Met Asp Glu	
405 410 415	
gac caa att ggc gaa ttt gcg tac gat tat gtg gaa gtg aga aga gat	1296
Asp Gln Ile Gly Glu Phe Ala Tyr Asp Tyr Val Glu Val Arg Arg Asp	
420 425 430	
tac tat cta lyy ggt gta gac gaa gat tca caa cgc tct gat gta aat	1344
Tyr Tyr Leu Trp Gly Val Asp Glu Asp Ser Gln Arg Ser Asp Val Asn	

178/762

435	440	445	
cac egg gts aac aac gct cat ttg gcc gct gaa cgt agc agt agc ggt			1392
His Arg Val Asn Asn Ala His Leu Ala Ala Glu Arg Ser Ser Ser Gly			
450	455	460	
act aat agt tcc tgg gat ggg aat gga gaa atg att cda tcc gaa aag			1440
Thr Asn Ser Ser Ser Asp Gly Asn Gly Glu Met Ile Gln Ser Gln Lys			
465	470	475	480
atc cta cda att cat caa gaa gat cct gcc aat agg taa			1479
Ile Leu Pro Ile His Gln Glu Asp Pro Ala Asn Arg			
485	490		
<210>	73		
<211>	492		
<212>	PRT		
<213>	Saccharomyces cerevisiae		
<400>	73		
Met Glu Ser Arg Thr Thr Gly Pro Leu Thr Thr Glu Thr Tyr Asp Gly			
1	5	10	15
Pro Thr Val Ala Phe Met Ile Leu Gly Ala Ala Leu Val Phe Phe Met			
20	25	30	
Val Pro Gly Leu Gly Phe Leu Tyr Ser Gly Leu Ala Arg Arg Tyr Ser			
35	40	45	
Ala Leu Ala Leu Ile Trp Val Val Leu Met Ala Thr Leu Val Gly Ile			
50	55	60	
Leu Gln Trp Tyr Phe Trp Gly Tyr Ser Leu Ala Phe Ser Lys Ser Ala			
65	70	75	80

Pro Asn Asn Lys Phe Ile Gly Asn Leu Asp Ser Phe Gly Phe Arg Asn
85 50 95

Val Tyr Gly Lys Lys Phe Asp Glu Asp Ala Tyr Pro Glu Leu Ala Tyr
100 105 110

Ala Thr Phe Gln Met Met Phe Ser Cys Val Asn Leu Ser Ile Ile Ala
115 120 125

Gly Ala Thr Ala Glu Arg Gly Arg Leu Leu Pro His Met Val Phe Leu
130 135 140

Phe Ile Leu Ala Thr Ile Gly Tyr Cys Pro Val Thr Tyr Trp Ile Trp
145 150 155 160

Ser Pro Gly Gly Trp Ala Tyr Gln Trp Gly Val Leu Asp Trp Ala Gly
165 170 175

Gly Gly Asn Ile Glu Ile Leu Ser Ala Val Ser Gly Phe Val Tyr Ser
180 185 190

Trp Phe Leu Gly Lys Arg Asn Glu Lys Leu Leu Ile Asn Phe Arg Pro
195 200 205

His Asn Val Ser Leu Val Thr Leu Gly Thr Ser Ile Leu Trp Thr Gly
210 215 220

Trp Leu Leu Phe Asn Ser Ala Ser Ser Leu Ser Pro Asn Leu Arg Ser
225 230 235 240

Val Tyr Ala Phe Met Asn Tyr Cys Leu Ser Ala Ile Thr Gly Gly Met
245 250 255

Thr Trp Cys Leu Leu Asp Tyr Arg Ser Glu Lys Lys Trp Ser Thr Val
 250 255 270

Gly Leu Cys Ser Gly Ile Ile Ser Gly Leu Val Ala Ala Thr Pro Ser
 275 280 285

Ser Gly Cys Ile Thr Leu Tyr Gly Ser Leu Ile Gln Gly Ile Val Ala
 290 295 300

Gly Val Val Cys Asn Phe Ala Thr Lys Leu Lys Tyr Tyr Ala Lys Val
 305 310 315 320

Asp Asp Ala Met Asp Ile Leu Glu Glu Gly Val Ala Gly Val Ile
 325 330 335

Gly Leu Ile Phe Asn Ala Leu Phe Gly Ala Asp Trp Val Ile Gly Met
 340 345 350

Asp Gly Thr Thr Glu His Glu Gly Gly Trp Val Thr His Asn Tyr Lys
 355 360 365

Glu Met Tyr Lys Gln Ile Ala Tyr Ile Ala Ala Ser Ile Gly Tyr Thr
 370 375 380

Ala Ala Val Thr Ala Ile Ile Cys Phe Val Leu Gly Tyr Ile Pro Gly
 385 390 395 400

Met Arg Leu Arg Ile Ser Glu Glu Ala Glu Glu Ala Gly Met Asp Glu
 405 410 415

Asp Gln Ile Gly Glu Phe Ala Tyr Asp Tyr Val Glu Val Arg Arg Asp
 420 425 430

Tyr Tyr Leu Trp Gly Val Asp Glu Asp Ser Gln Arg Ser Asp Val Asn
 435 440 445

His Arg Val Asn Asn Ala His Leu Ala Ala Glu Arg Ser Ser Ser Gly
 450 455 460

Thr Asn Ser Ser Ser Asp Gly Asn Gly Glu Met Ile Gln Ser Glu Lys
 465 470 475 480

Ile Leu Pro Ile His Gln Glu Asp Pro Ala Asn Arg
 485 490

<210> 74
 <211> 939
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(939)

<400> 74
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 Met Cys Ile Leu Met Ala Thr Arg Ala His Pro Asp Tyr Glu Leu Ile
 1 5 10 15

tta ata tct aac aga gac gaa ttc ttg gcc aga aac sca cat gct aca 96
 Leu Ile Ser Asn Arg Asp Glu Phe Leu Ala Arg Lys Thr His Ala Thr
 20 25 30

lgc lgg cat aac aal gat ttt atc ctt tca ccc taa gat ctg gcc aaa 144
 Cys Trp His Asn Asn Asp Phe Ile Leu Ser Pro Tyr Asp Leu Ala Lys

182/762

35	40	45	
acc lea gca gaa aaa caa ata ttt ggc act tgg tot ggc ata aat aaa			192
Thr Ser Ala Glu Lys Glu Ile Phe Gly Thr Trp Ser Gly Ile Asn Lys			
50	55	60	
gaa gga aaa tta gcc act att ctt aat tta aaa ctt gac aat gag caa			240
Glu Gly Lys Leu Ala Thr Ile Leu Asn Leu Lys Leu Asp Asn Glu Glu			
65	70	75	80
aat aat aag aaa tca aga leu cgt ggt ctg tta cca ttt ata ttt ttg			288
Asn Asn Thr Lys Ser Arg Ser Arg Gly Leu Leu Pro Phe Ile Phe Leu			
85	90	95	
tgg atc cat aaa gca gat ttt gaa gat tgg gac aat tac aaa aag ttt			336
Ser Ile His Lys Ala Asp Phe Glu Asp Trp Asp Asn Tyr Lys Lys Phe			
100	105	110	
gaa ggt cag tat gal ggg ttg aag tcc acc ggt gat tct cat ttt ttt			384
Glu Gly His Tyr Asp Gly Leu Lys Ser Thr Gly Asp Phe Asn Phe Phe			
115	120	125	
tan cgc gac gtt atc aaa aag caa tat aaa gtt act gat tct cta gga			432
Tyr Gly Asp Val Ile Lys Lys Glu Tyr Lys Val Ile Asp Ser Leu Gly			
130	135	140	
aga act ttt gal gty ttg agt tct acc tgt aag aaa gat ctt gat tct			480
Arg Thr Phe Asp Val Leu Ser Ser Thr Cys Arg Lys Asp Leu Asp Ser			
145	150	155	160
tac aly gtt gtt tct aat ggt caa ttt tat gac agc tcc agt ata cca			528
Tyr Met Val Val Ser Asn Gly Lys Phe Tyr Asp Ser Ser Ser Ile Pro			
165	170	175	
ggg cag gct tgg gaa aca gta aag gta gca cgt gat agt tta gaa aat			576
Gly Glu Ala Trp Glu Lys Val Lys Val Ala Arg Asp Ser Leu Glu Asn			
180	185	190	
cta gtt tta gaa aat att gaa leu gat gag gag aaa ata ata cca agc			624
Leu Val Ser Glu Asn Ile Glu Ser Asp Glu Glu Lys Ile Ile Ser Ser			
195	200	205	

tgc ttt caa ctg ggc tgg aag tct tcc ctt cca agc act att tca aac 672
 Cys Phe Gln Leu Ala Ser Lys Ser Ser Leu Pro Ser Thr Ile Ser Asn
 210 215 220

cca gat gtc ttg cag atg gta gat cca aat gta acc atg aat acc ata 720
 Pro Asp Val Leu Gln Met Val Asp Pro Asn Val Thr Met Asn Thr Ile
 225 230 235 240

tac gta cca cct tta cgg agg cct ccc agg gat gac tta ggt gcc tca 768
 Tyr Val Pro Pro Leu Arg Arg Pro Pro Arg Asp Asp Leu Gly Ala Ser
 245 250 255

att cct gat ggt gat tac tac gga acg cgc tct cca ala gtt tta ctc 816
 Ile Pro Asp Gly Asp Tyr Tyr Gly Thr Arg Ser Gln Ile Val Leu Leu
 260 265 270

gtg agt aag gat tca ccg aga gtt acc ttt ata gaa agg gtc ctt lai 864
 Val Ser Lys Asp Ser Thr Arg Val Thr Phe Ile Glu Arg Val Leu Tyr
 275 280 285

agc tca gat gaa gac gtc cgc aag tat tgg gta acc tca cct aag gag 912
 Ser Ser Asp Glu Asp Val Arg Lys Tyr Ser Val Thr Ser Pro Lys Glu
 290 295 300

gaa aaa agg ttt aaa ctc aac ttg taa 939
 Glu Lys Arg Phe Lys Phe Lys Leu
 305 310

<210> 75

<211> 312

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 75

Met Cys Ile Leu Met Ala Thr Arg Ala His Pro Asp Tyr Glu Leu Ile
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Leu Ile Ser Asn Arg Asp Glu Phe Leu Ala Arg Lys Thr His Ala Thr
 20 25 30

Cys Trp His Asn Asn Asp Phe Ile Leu Ser Pro Tyr Asp Leu Ala Lys
35 40 45

Thr Ser Ala Glu Lys Gln Ile Phe Gly Thr Trp Ser Gly Ile Asn Lys
50 55 60

Glu Gly Lys Leu Ala Thr Ile Leu Asn Leu Lys Leu Asp Asn Glu Gln
65 70 75 80

Asn Asn Thr Lys Ser Arg Ser Arg Gly Leu Leu Pro Phe Ile Phe Leu
85 90 95

Ser Ile His Lys Ala Asp Phe Glu Asp Trp Asp Asn Tyr Lys Lys Phe
100 105 110

Glu Gly His Tyr Asp Gly Leu Lys Ser Thr Gly Asp Phe Asn Phe Phe
115 120 125

Tyr Gly Asp Val Ile Lys Lys Gln Tyr Lys Val Ile Asp Ser Leu Gly
130 135 140

Arg Thr Phe Asp Val Leu Ser Ser Thr Cys Arg Lys Asp Leu Asp Ser
145 150 155 160

Tyr Met Val Val Ser Asn Gly Lys Phe Tyr Asp Ser Ser Ser Ile Pro
165 170 175

Gly Gln Ala Trp Glu Lys Val Lys Val Ala Arg Asp Ser Leu Glu Asn
180 185 190

Leu Val Leu Glu Asn Ile Gln Ser Asp Glu Glu Lys Ile Ile Ser Ser
 195 200 205

Cys Phe Gln Leu Ala Ser Lys Ser Ser Leu Pro Ser Thr Ile Ser Asn
 210 215 220

Pro Asp Val Leu Gln Met Val Asp Pro Asn Val Thr Met Asn Thr Ile
 225 230 235 240

Tyr Val Pro Pro Leu Arg Arg Pro Pro Arg Asp Asp Leu Gly Ala Ser
 245 250 255

Ile Pro Asp Gly Asp Tyr Tyr Gly Thr Arg Ser Gln Ile Val Leu Leu
 260 265 270

Val Ser Lys Asp Ser Thr Arg Val Thr Phe Ile Glu Arg Val Leu Tyr
 275 280 285

Gly Ser Asp Glu Asp Val Arg Lys Tyr Ser Val Thr Ser Pro Lys Glu
 290 295 300

Glu Lys Arg Phe Lys Phe Lys Leu
 305 310

<210> 76

<211> 2595

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2595)

<400> 76

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Met	Tyr	Met	Ala	Arg	Cys	Gly	Pro	Lys	Asn	Asn	Val	Leu	Cys	Phe	Pro	
1				5						10				15		

ttt	caa	ctt	tcg	ttt	cta	ttt	tca	aaa	cga	cta	ata	aat	aag	cgt	ttc	96
Phe	Gln	Leu	Ser	Phe	Leu	Phe	Ser	Lys	Arg	Leu	Ile	Asn	Lys	Arg	Phe	
		20						25				30				

aag	tat	acc	cta	caa	act	gaa	gat	gaa	aag	aat	atg	atg	ggg	agt	ttc	144
Lys	Tyr	Thr	Leu	Gln	Thr	Glu	Asp	Glu	Lys	Asn	Met	Met	Gly	Ser	Leu	
		35					40					45				

agt	aaa	aat	aaa	ata	ata	aca	ccc	gaa	gac	gtt	gag	ttc	aaa	ttc	gaa	192
Ser	Lys	Asn	Lys	Ile	Ile	Thr	Pro	Glu	Asp	Val	Glu	Phe	Lys	Leu	Ala	
		50				55				60						

aaa	ttc	cga	gaa	ttt	tcg	aat	ccc	ttc	aaa	gaa	cgc	att	aac	aac	act	240
Gln	Leu	Arg	Glu	Phe	Ser	Asn	Thr	Leu	Lys	Glu	arg	ile	His	Asn	Thr	
65					70					75				80		

aaa	tcg	gtg	aat	tca	gat	ggc	ccc	caa	agc	aat	agt	atc	gca	cca	atc	288
Lys	Ser	Val	Asn	Ser	Asp	Gly	His	Gln	Ser	Asn	Ser	Ile	Ala	Pro	Ile	
			85					90					95			

tca	gaa	gac	tca	agg	aat	gtt	aat	gtc	acc	aaa	aca	tca	tcg	gtt	ccc	336
Ser	Glu	Asp	Ser	Arg	Asn	Val	Asn	Val	Thr	Lys	Thr	Ser	Ser	Val	Pro	
		100						105					110			

aat	gaa	gaa	aaa	tcg	aaa	aat	cta	tca	gat	ttc	att	cat	tcg	tcg	ttt	384
Asn	Glu	Glu	Lys	Ser	Lys	Asn	Leu	Ser	Asp	Leu	Ile	His	Ser	Ser	Phe	
		115					120					125				

ttc	gaa	aaa	atg	gat	ccc	ctc	gtc	cca	aaa	gtt	ata	aga	gaa	aga	gta	432
Leu	Glu	Lys	Met	Asp	His	Leu	Val	Pro	Lys	Val	Ile	Arg	Glu	Arg	Val	
	130					135						140				

gca	gac	gac	gac	ata	ctt	gca	aaa	aac	ctt	ttt	gat	aga	tca	cac	agt	480
Ala	Asp	Asp	Asp	Ile	Leu	Ala	Lys	Asn	Leu	Phe	Asp	Arg	Ser	His	Ser	
145				150						155				160		

aat	tcg	gca	ccc	gtc	ata	gat	agg	ctt	tat	gtc	agt	gag	aaa	cgg	ttc	528
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Asn	Trp	Ala	Pro	Val	Ile	Asp	Arg	Leu	Tyr	Val	Ser	Glu	Lys	Arg	Phe	
				165					170					175		
atg	gat	att	gat	tcc	aga	gaa	ttt	tct	gtt	tgg	tta	aat	ggc	aca	gtc	573
Met	Asp	Ile	Asp	Ser	Arg	Glu	Phe	Ser	Val	Trp	Leu	Asn	Gly	Thr	Val	
				180				185					190			
aaa	tat	ttg	cca	ttt	cat	agt	ata	cta	cac	ttg	gat	gaa	atg	gla	llu	624
Lys	Tyr	Leu	Pro	Phe	His	Ser	Ile	Leu	His	Leu	Asp	Glu	Met	Leu	Leu	
				195				200					205			
gaa	caa	atc	aat	gga	gat	gtt	cta	aaa	ttt	aat	acc	caa	atg	tac	gaa	672
Glu	Gln	Ile	Asn	Gly	Asp	Val	Val	Lys	Phe	Asn	Thr	His	Met	Tyr	Glu	
		210				215						220				
tgt	atc	ttt	aac	aac	tta	gga	aat	tta	aaa	cca	act	aat	ttt	aat	cag	720
Cys	Ile	Phe	Asn	Asn	Leu	Gly	Asn	Leu	Lys	Pro	Thr	Asn	Phe	Asn	Gln	
		225			230					235				240		
gat	ggc	aot	aac	gal	aaa	gtt	atc	ccc	aaa	atg	aaa	gag	ttg	tta	gag	768
Asp	Gly	Thr	Asn	Asp	Lys	Val	Ile	Leu	Lys	Met	Lys	Glu	Leu	Leu	Glu	
				245					250					255		
agg	tat	gat	acg	gca	ttt	aaa	ata	act	gaa	gaa	aga	att	aac	aaa	aaa	816
Arg	Tyr	Asp	Lys	Ala	Leu	Lys	Ile	Thr	Glu	Glu	Arg	Ile	Asn	Lys	Lys	
				260					265					270		
gaa	gga	ttc	cct	tcc	aaa	gla	caa	aag	atg	acg	caa	gaa	ata	ctt	aat	864
Glu	Gly	Phe	Pro	Ser	Lys	Val	Pro	Lys	Met	Thr	Gln	Ala	Ile	Leu	Asn	
				275				280					285			
aat	tgt	tta	aaa	tac	tcc	acc	aag	tgt	tca	agg	ttt	acc	gac	atg	gat	912
Asn	Cys	Leu	Lys	Tyr	Ser	Thr	Lys	Cys	Ser	Ser	Phe	His	Asp	Met	Asp	
				290				295					300			
tat	thr	att	aca	aaa	tcc	aga	gat	gat	tat	ggc	ata	act	cct	aat	aag	960
Tyr	Phe	Ile	Thr	Lys	Phe	Arg	Asp	Asp	Tyr	Gly	Ile	Thr	Pro	Asn	Lys	
		305				310					315			320		
caa	aac	cta	act	act	gta	ata	caa	tcc	tac	tct	agg	aag	gaa	acc	act	1008
Gln	Asn	Leu	Thr	Thr	Val	Ile	Gln	Phe	Tyr	Ser	Arg	Lys	Glu	Met	Thr	
					325					330				335		

aag caa gcc tgg aat act ttt gaa acn atg aaa ttt tta tct aca aaq	1056
Lys Gln Ala Trp Asn Thr Phe Asp Thr Met Lys Phe Leu Ser Thr Lys	
340 345 350	
cat ttc cct gat atc tgc aca tat aac aca atg ctg cga ata tgc gag	1104
His Phe Pro Asp Ile Cys Thr Tyr Asn Thr Met Leu Arg Ile Cys Glu	
355 360 365	
aag gaa cgg aat ttt cct aag gcl ttg gat tta ttt caa gaa att caa	1152
Lys Glu Arg Asn Phe Pro Lys Ala Leu Asp Leu Phe Gln Glu Ile Gln	
370 375 380	
gac cac aat ata aag cct aca aca aac act lac ata atg atg gca aga	1200
Asp His Asn Ile Lys Pro Thr Thr Asn Thr Tyr Ile Met Met Ala Arg	
385 390 395 400	
gug lig got tct tgg agc agt aat gaa gtt gtc agt gag ggt aaa taa	1248
Val Leu Ala Ser Ser Ser Asn Ala Val Val Ser Glu Gly Lys Ser	
405 410 415	
gac tct cta aga tta ctg gga tgg aca tac ctt cat gag ttg gag gac	1296
Asn Ser Leu Arg Leu Leu Gly Trp Lys Tyr Leu His Gln Leu Glu Asp	
420 425 430	
aaq aat ctt tac aga cat aaa aac gat gac tta aat tta ttt ttg got	1344
Lys Asn Leu Tyr Arg His Lys Lys Asp Asp Leu Asn Leu Phe Leu Ala	
435 440 445	
atg atg gca tta gcc gcg ttt gat ggt gat att gaa tra agt aga gct	1392
Met Met Ala Leu Ala Ala Phe Asp Gly Asp Ile Glu Leu Ser Arg Ala	
450 455 460	
cta tar tac ttg ttc atc gag aaa aag tar aaa act ttg tgc gca aat	1440
Leu Tyr Tyr Leu Phe Ile Ala Lys Lys Tyr Lys Tyr Leu Cys Ala Asn	
465 470 475 480	
tgg aac gga aac att ctc gta gat caa gat aca att tgg aag leu act	1488
Trp Lys Gly Asn Ile Leu Val Asp Glu Asp Thr Ile Trp Lys Ser Thr	
485 490 495	
tta atg cca gaa atg ctg aat tat ttg atg ctt gct tat gca aga ttt	1536

Leu Met Pro Glu Met Leu Asn Tyr Leu Met Ile Ala Tyr Ala Arg Phe	
500	510
gat ccc aga aat ttg cca gtc tta tcc ggt tat gaa aaa ggc att gaa	1584
Asp Pro Arg Asn Leu Pro Val Leu Ser Gly Tyr Glu Lys Gly Ile Glu	
515	520
ttg aga aga aaa ttt ctt cgc gaa ttt gat tcc tcc atg agg tta gat	1632
Leu Arg Arg Lys Phe Leu Arg Glu Phe Asp Ser Ser Met Arg Leu Asp	
530	535
gat aca gac aaa ttg gtc aaa ttt aza tta cca ttt ctt cca att agt	1680
Asp Thr Asp Lys Leu Val Lys Phe Lys Leu Pro Phe Leu Pro Ile Ser	
545	550
gac cta aat tcg gag cca caa gta ttg gcg gaa tct aac gca atc tgg	1728
Asp Leu Asn Ser Glu Ala Gln Val Leu Ala Glu Ser Asn Ala Ile Trp	
565	570
agt ttc aat atg gaa aat gga gga acg cgc aat aca ttg aca tct tca	1776
Ser Phe Asn Met Glu Asn Gly Gly Thr Arg Asn Thr Leu Thr Ser Ser	
580	585
aat gaa gcg gcg ttg gag gat atc aaa aaa tat agg caa tta ctt gat	1824
Asn Glu Ala Ala Leu Glu Asp Ile Lys Lys Tyr Arg Gln Leu Leu Asp	
595	600
tcg ttt gcg caa gaa gaa gag gat ttc aac gag ttt aag ttt aaa gtt	1872
Ser Phe Ala Gln Glu Ala Glu Asp Phe Asn Glu Phe Lys Phe Lys Val	
610	615
atg tac gaa gtg acg aaa atg caa aga gaa agt att aat gtg aac gtc	1920
Met Tyr Glu Val Thr Lys Met Gln Arg Glu Ser Ile Asn Val Asn Val	
625	630
ttc aat aaa att tca cta cac aca tat ttg tca att ccc att aac tta	1968
Phe Asn Lys Ile Ser Leu His Thr Tyr Leu Ser Ile Pro Ile Asn Leu	
645	650
aaa caa cag aag gaa ttc ttg cga agg ttg acg ttc ttc act ttc caa	2016
Lys Gln Gln Lys Glu Phe Leu Arg Arg Leu Thr Phe Phe Thr Phe Gln	
660	665
	670

cna cnc gaa ttt gaa gct gtc ata aag agt ttg tat gaa gga tac cgt	2044
Gln His Glu Phe Glu Ala Val Ile Lys Arg Leu Tyr Glu Gly Tyr Arg	
675 680 685	
aat att cct tgg tcc gat aag cgt gac caa aat tca ata tca acc gaa	2048
Asn Ile Pro Ser Ser His Thr Arg Asp Gln Asn Ser Ile Ser Thr Glu	
690 695 700	
gac atc tca gta tcc aaa cct gag acc aag gaa gac ctc aac tta ata	2052
Ala Ile Ser Val Ser Lys Pro Glu Thr Thr Glu Asp Leu Asn Leu Ile	
705 710 715 720	
atg cak gat ata tgg tat att aca tgt ttg agg cac aac atc arg atg	2208
Met His Asp Ile Trp Tyr Ile Thr Cys Leu Arg His Lys Ile Met Met	
725 730 735	
gac acc aag tta tat gag ctg gtg atg aaa gcc gat ata gaa ttt cna	2256
Asp Thr Thr Leu Tyr Glu Leu Val Met Lys Ala Ala Ile Glu Phe Gln	
740 745 750	
aat gag gac tta gca aag aac gta tga aat gat agg ggc aac ttt agg	2304
Asn Gln Asp Leu Ala Lys Lys Val Trp Asn Asp Arg Gly Lys Phe Arg	
755 760 765	
acg aak gln cag ttt ctg aca atg gac caa aga ata aga ata gca aag	2352
Thr Thr Val Pro Phe Leu Lys Met Asp Gln Arg Ile Arg Ile Ala Lys	
770 775 780	
gat caa aaa ttt gcc cak cta atg gtc gaa ttc ttc aac aag caa gga	2400
Asp Gln Lys Phe Ala His Leu Met Val Glu Phe Phe Thr Lys Gln Gly	
785 790 795 800	
aag tat tgg gac gcc ata gct atc ala tly tct tca aaa aat cgc ttc	2448
Lys Tyr Ser Asp Ala Ile Ala Ile Ile Leu Ser Ser Lys Asn Arg Phe	
805 810 815	
aat tgg act tat tcc atg gtt agg aat ttg cat aac gca tta gaa gaa	2496
Asn Trp Thr Tyr Ser Met Val Arg Asn Leu His Lys Ala Leu Glu Gln	
820 825 830	
atc gag gal aga aat agc ggt gaa atc tta ctg gat gta gta aac aaa	2544

Ile Glu Asp Arg Asn Ser Val Glu Ile Leu Leu Asp Val Val Asn Lys
 835 840 845

aag tca cac gca aag gcc ctg aag tgg gag gaa caa gaa ctt aac atg 2592
 Lys Ser His Ala Lys Ala Leu Lys Trp Glu Glu Gln Glu Leu Asn Met
 850 855 860

tag 2595

<210> 77
 <211> 854
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 77

Met Tyr Met Ala Arg Cys Gly Pro Lys Asn Asn Val Leu Cys Phe Pro
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Phe Gln Leu Ser Phe Leu Phe Ser Lys Arg Leu Ile Asn Lys Arg Phe
 20 25 30

Lys Tyr Thr Leu Gln Thr Glu Asp Glu Lys Asn Met Met Gly Ser Leu
 35 40 45

Ser Lys Asn Lys Ile Ile Thr Pro Glu Asp Val Glu Phe Lys Leu Ala
 50 55 60

Glu Leu Arg Glu Phe Ser Asn Thr Leu Lys Glu Arg Ile His Asn Thr
 65 70 75 80

Lys Ser Val Asn Ser Asp Gly His Gln Ser Asn Ser Ile Ala Pro Ile
 85 90 95

Ser Glu Asp Ser Arg Asn Val Asn Val Thr Lys Thr Ser Ser Val Pro

103

105

110

Asn Glu Glu Lys Ser Lys Asn Icu Ser Asp Leu Ile His Ser Ser Phe
 115 120 125

Leu Glu Lys Met Asp His Leu Val Pro Lys Val Ile Arg Glu Arg Val
 130 135 140

Ala Asp Asp Asp Ile Leu Ala Lys Asn Leu Phe Asp Arg Ser Phe Ser
 145 150 155 160

Asn Trp Ala Pro Val Ile Asp Arg Leu Tyr Val Ser Glu Lys Arg Phe
 165 170 175

Met Asp Ile Asp Ser Arg Glu Phe Ser Val Trp Leu Asn Gly Thr Val
 180 185 190

Lys Tyr Leu Pro Phe His Ser Ile Leu His Leu Asp Glu Met Leu Leu
 195 200 205

Glu Glu Ile Asn Gly Asp Val Val Lys Phe Asn Thr His Met Tyr Glu
 210 215 220

Cys Ile Phe Asn Asn Leu Gly Asn Leu Lys Pro Thr Asn Phe Asn Glu
 225 230 235 240

Asp Gly Thr Asn Asp Lys Val Ile Leu Lys Met Lys Glu Leu Leu Glu
 245 250 255

Arg Tyr Asp Lys Ala Leu Lys Ile Thr Glu Glu Arg Ile Asn Lys Lys
 260 265 270

Glu Gly Phe Pro Ser Lys Val	Pro Lys Met Thr Glu Ala Ile Leu Asn
275	280 285

Asn Cys Leu Lys Tyr Ser Thr Lys Cys Ser Ser Phe His Asp Met Asp
290 295 300

Tyr Phe Ile Thr Lys Phe Arg Asp Asp Tyr Gly Ile Thr Pro Asn Lys
305 310 315 320

Glu Asn Leu Thr Thr Val Ile Glu Phe Tyr Ser Arg Lys Glu Met Thr
325 330 335

Lys Glu Ala Trp Asn Thr Phe Asp Tyr Met Lys Phe Leu Ser Thr Lys
340 345 350

His Phe Pro Asp Ile Cys Thr Tyr Asn Thr Met Leu Arg Ile Cys Glu
355 360 365

Lys Glu Arg Asn Phe Pro Lys Ala Leu Asp Leu Phe Glu Glu Ile Glu
370 375 380

Asp His Asn Ile Lys Pro Thr Thr Asn Thr Tyr Ile Met Met Ala Arg
385 390 395 400

Val Leu Ala Ser Ser Ser Ser Asn Ala Val Val Ser Glu Gly Lys Ser
405 410 415

Asp Ser Leu Arg Leu Leu Gly Trp Lys Tyr Leu His Glu Leu Glu Asp
420 425 430

Lys Asn Leu Tyr Arg His Lys Lys Asp Asp Leu Asn Leu Phe Leu Ala
 435 440 445

Met Met Ala Leu Ala Ala Phe Asp Gly Asp Ile Glu Leu Ser Arg Ala
 450 455 460

Leu Tyr Tyr Leu Phe Ile Ala Lys Lys Tyr Lys Thr Leu Cys Ala Asn
 465 470 475 480

Tyr Lys Gly Asn Ile Leu Val Asp Gln Asp Thr Ile Trp Lys Ser Thr
 485 490 495

Leu Met Pro Glu Met Leu Asn Tyr Leu Met Leu Ala Tyr Ala Arg Phe
 500 505 510

Asp Pro Arg Asn Leu Pro Val Leu Ser Gly Tyr Glu Lys Gly Ile Gln
 515 520 525

Leu Arg Arg Lys Phe Leu Arg Glu Phe Asp Ser Ser Met Arg Leu Asp
 530 535 540

Asp Thr Asp Lys Leu Val Lys Phe Lys Leu Pro Phe Leu Pro Ile Ser
 545 550 555 560

Asp Leu Asn Ser Glu Ala Gln Val Leu Ala Glu Ser Asn Ala Ile Trp
 565 570 575

Ser Phe Asn Met Gln Asn Gly Gly Thr Arg Asn Thr Leu Thr Ser Ser
 580 585 590

Asn Glu Ala Ala Leu Glu Asp Ile Lys Lys Tyr Arg Gln Leu Leu Asp
 595 600 605

Ser Phe Ala Gln Glu Ala Gln Asp Phe Asn Glu Phe Lys Phe Lys Val
610 615 620

Met Tyr Glu Val Thr Lys Met Gln Arg Glu Ser Ile Asn Val Asn Val
625 630 635 640

Phe Asn Lys Ile Ser Leu His Thr Tyr Leu Ser Ile Pro Ile Asn Leu
645 650 655

Lys Gln Gln Lys Glu Phe Leu Arg Arg Leu Thr Phe Phe Thr Phe Glu
660 665 670

Glu His Glu Phe Glu Ala Val Ile Lys Arg Leu Tyr Glu Gly Tyr Arg
675 680 685

Asn Ile Pro Ser Ser His Thr Arg Asp Glu Asn Ser Ile Ser Thr Glu
690 695 700

Ala Ile Ser Val Ser Lys Pro Glu Thr Thr Glu Asp Leu Asn Leu Ile
705 710 715 720

Met His Asp Ile Trp Tyr Ile Thr Cys Leu Arg His Lys Ile Met Met
725 730 735

Asp Thr Thr Leu Tyr Glu Leu Val Met Lys Ala Ala Ile Glu Phe Gln
740 745 750

Asn Glu Asp Leu Ala Lys Lys Val Trp Asn Asp Arg Gly Lys Phe Arg
755 760 765

Thr Thr Val Pro Phe Leu Lys Met Asp Gln Arg Ile Arg Ile Ala Lys
 770 775 780

Asp Gln Lys Phe Ala His Leu Met Val Gln Phe Phe Thr Lys Gln Gly
 785 790 795 800

Lys Tyr Ser Asp Ala Ile Ala Ile Ile Leu Ser Ser Lys Asn Arg Phe
 805 810 815

Asn Trp Thr Tyr Ser Met Val Arg Asn Leu His Lys Ala Leu Gln Gly
 820 825 830

Ile Glu Asp Arg Asn Ser Val Glu Ile Leu Leu Asp Val Val Asn Lys
 835 840 845

Lys Ser His Ala Lys Ala Leu Lys Trp Glu Glu Gln Glu Leu Asn Met
 850 855 860

<210> 78

<211> 357

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(357)

<400> 78

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 1 5 10 15

tct ttc ttt ctc cta ctt ttg gca tac ttt ttc agg ggc aga agt cat 96
 Ser Phe Phe Leu Leu Leu Leu Ala Tyr Phe Phe Arg Gly Arg Ser Pro
 20 25 30

tat tac gea cgt tga taa cgc cgg ctt gct gtt aca cct ggt gcc atc 144
 Tyr Tyr Ala Arg Cys Tyr Arg Arg Leu Ala Val Thr Pro Gly Ala Ile
 35 40 45

act att gcc att gcc att gct acc gat tca att cgg gcg ctt gca aag 192
 Thr Ile Ala Ile Ala Ile Ala Thr Asp Ser Ile Pro Ala Leu Ala Lys
 50 55 60

tec aaa gtt ctg gly tgg gtt tgt tct caa aca gat ccc tgt aca gcg 240
 Ser Lys Val Leu Val Ser Val Cys Ser His Thr Asp Pro Cys Thr Ala
 65 70 75 80

tct tgt aac ctg atu ccu ttc ccc cgc ccc ttc tgg aac agc ctg aag 288
 Ser Cys Asn Leu Ile Pro Phe Pro Arg Pro Phe Ser Asn Ser Leu Thr
 85 90 95

cgc ttc cld ttt tgt ttg ggc tgg gcc cgt ttt tgc att tcc ttt ccc 336
 Arg Phe Leu Phe Cys Leu Gly Ser Ala Arg Phe Cys Ile Ser Phe Pro
 100 105 110

tgt ttc gga ttg agt ata laa 357
 Cys Phe Gly Leu Ser Ile
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<210> 79

<211> 118

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 79

Met Gln Thr Met Gly Gly Gln His Leu Leu Leu Ser Gln Leu Lys Gly
 1 5 10 15

Ser Phe Phe Leu Leu Leu Leu Ala Tyr Phe Phe Arg Gly Arg Ser Pro
 20 25 30

Tyr Tyr Ala Arg Cys Tyr Arg Arg Leu Ala Val Thr Pro Gly Ala Ile

35

40

45

Thr Ile Ala Ile Ala Ile Ala Thr Asp Ser Ile Pro Ala Leu Ala Lys
 50 55 60

Ser Lys Val Leu Val Ser Val Cys Ser His Thr Asp Pro Cys Thr Ala
 65 70 75 80

Ser Cys Asn Leu Ile Pro Phe Pro Arg Pro Phe Ser Asn Ser Leu Thr
 85 90 95

Arg Phe Leu Phe Cys Leu Gly Ser Ala Arg Phe Cys Ile Ser Phe Pro
 100 105 110

Cys Phe Gly Leu Ser Ile
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<210> 80

<211> 1062

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1062)

<400> 80

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 Met Ile Gln Phe Lys Ser Pro Gly Asn Trp Leu Phe Ile Val Pro Trp
 1 5 10 15

att gcc ttc att cca tgg tat ggt atg ctg ata gcc atg att att tgg 96
 Ile Ala Phe Ile Pro Trp Tyr Gly Met Leu Ile Ala Met Leu Ile Cys
 20 25 30

199/762

egg gcc agt gaa ggc cat ccc ata tat tgg ttc atg cac tgg gag gaa	144
Tyr Ala Ser Gln Gly His Pro Ile Tyr Tyr Phe Met His Ser Glu Gln	
35 40 45	
ttc cct gtg tcc att tca gaa ala ggc gcc act aat tta agg cca ctg	192
Phe Pro Val Tyr Ile Ser Asp Ile Gly Ala Thr Asn Leu Arg Pro Leu	
50 55 60	
ttt ata tgg tgc gcc ggc tgg cag ggc cta ggc tat gta atc act gtt	240
Phe Ile Ser Cys Ala Gly Tyr Gln Gly Leu Gly Tyr Val Ile Thr Val	
65 70 75 80	
ggc ctt gag ttt ttt cca aga tcc ggc tat ctg cct tta gaa ctg aaa	288
Ala Leu Glu Phe Phe Gln Arg Ser Gly Tyr Leu Pro Phe Gln Leu Tyr	
85 90 95	
aaa aaa gac cct tct atc tct gat tcc acc tct tat gct gag aaa tgg	336
Lys Lys Asp Pro Ser Ile Ser Asp Ser Thr Ser Tyr Ala Glu Lys Leu	
100 105 110	
caa agc ggt aaa tcc tta atg cct cca tat tcc aca arg gat gaa ggg	384
His Ser Gly Lys Tyr Leu Met Pro Pro Tyr Tyr Thr Lys Asp Glu Arg	
115 120 125	
acc ctg att ttc gca gct ttt gtt ctg ggc agc atc ggt gaa cta gcc	432
Asn Leu Ile Phe Phe Ala Phe Val Leu Gly Ser Ile Gly Glu Leu Ala	
130 135 140	
ctt tta ttc agt tcc atc ttc tca acc gcc ctg leu aat ggc gtt caa	480
Leu Leu Phe Ser Ser Ile Phe Ser Thr Ala Leu Tyr His Arg Val His	
145 150 155 160	
att gct atg gtc tct gtt ttc gtc gtc ttc atg ttc cta tcc act tgc	528
Ile Ala Met Val Ser Val Phe Val Val Phe Met Phe Leu Ser Thr Cys	
165 170 175	
tgg ttg att gca gag tat ttc ctg atg gca agg cac tat gcc tca gtc	576
Cys Leu Ile Ala Glu Tyr Phe Leu Met Gly Arg His Tyr Ala Ser Val	
180 185 190	
cac ccc cta gcc agc cct cat ttc aat cct cca tca tct gaa aaa agc	624
His Pro Leu Ala Ser Pro His Phe Asn Pro Gln Ser Ser Glu Lys Ser	

200/762

195	200	205	
ttt aac caa gat tat aac acc gtg gat gag ctg cct tgg tat aac tgg			672
Phe Asn Glu Asp Tyr Asn Thr Val Asp Glu Leu Pro Trp Tyr Lys Trp			
210	215	220	
aaa ggc cat gta tgg aat aaa ttt acc atc agt gca acg cta aaa gtt			720
Lys Gly His Val Trp Asn Lys Phe Thr Ile Ser Ala Thr Leu Lys Val			
225	230	235	240
ata tgg tta act ctc gca gtc gta tgg gcc att tgt ttt ggt gct atc			768
Ile Trp Leu Thr Leu Ala Val Val Trp Ala Ile Cys Phe Gly Ala Ile			
245	250	255	
aat gat aga tct aag agt gat tgt ttc gaa tgg ttg cta gca ttt tgg			816
Asn Asp Arg Ser Lys Ser Ala Cys Phe Glu Trp Leu Leu Ala Phe Trp			
260	265	270	
ttt ggt atc ata ttt atg att ctt tcc gcc gac ttt tat tta ggt ggc			864
Phe Gly Ile Ile Phe Met Ile Leu Ser Ala Asp Phe Tyr Leu Gly Gly			
275	280	285	
aga tac aga caa tcc cgc tat ttc aac cac gtg gaa tca ttt tgg ggt			912
Arg Tyr Arg Glu Ser Arg Tyr Phe Asn His Val Glu Ser Phe Ser Gly			
290	295	300	
tat tac aag tat gac aag gag cta ggc ctg tac cac agt gaa gac gtt			960
Tyr Tyr Lys Tyr Asp Lys Ala Leu Gly Leu Tyr His Ser Glu Asp Val			
305	310	315	320
ttg cct tgg gac gat aac gcc ggc gtg att gcc aca gaa aca gaa tct			1008
Leu Pro Ser Asp Asp Asn Ala Gly Val Ile Ala Thr Glu Thr Ala Ser			
325	330	335	
tca aat att tac aat aat tcc tct tcc aac gaa tct att caa gta gtc			1056
Ser Asn Ile Tyr Asn Asn Ser Ser Ser Asn Glu Ser Ile Glu Val Val			
340	345	350	
gta tga			1062
Val			

<210> 81

<211> 353

<212> MET

<213> *Saccharomyces cerevisiae*

<400> 81

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Ile	Ala	Phe	Ile	Pro	Trp	Tyr	Gly	Met	Leu	Ile	Ala	Met	Leu	Ile	Cys
			20				25						30		

Trp	Ala	Ser	Gln	Gly	His	Pro	Ile	Tyr	Trp	Phe	Met	His	Ser	Glu	Gln
		35				40						45			

Phe	Pro	Val	Tyr	Ile	Ser	Asp	Ile	Gly	Ala	Thr	Asn	Leu	Arg	Pro	Leu
	50					55					60				

Phe	Ile	Ser	Cys	Ala	Gly	Trp	Gln	Gly	Leu	Gly	Tyr	Val	Ile	Thr	Val
65					70				75				80		

Ala	Leu	Glu	Phe	Phe	Gln	Arg	Ser	Gly	Tyr	Ile	Pro	Phe	Gln	Leu	Lys
			85						90					95	

Lys	Lys	Asp	Pro	Ser	Ile	Ser	Asp	Ser	Thr	Ser	Tyr	Ala	Glu	Lys	Leu
			100						105					110	

His	Ser	Gly	Lys	Tyr	Leu	Met	Pro	Pro	Tyr	Tyr	Thr	Lys	Asp	Glu	Arg
		115							120					125	

Asn	Leu	Ile	Phe	Ala	Ala	Phe	Val	Leu	Gly	Ser	Ile	Gly	Glu	Leu	Ala
		130							135					140	

Leu Leu Phe Ser Ser Ile Phe Ser Thr Ala Leu Tyr His Arg Val His
145 150 155 160

Ile Ala Met Val Ser Val Phe Val Val Phe Met Phe Leu Ser Thr Cys
165 170 175

Cys Leu Ile Ala Glu Tyr Phe Leu Met Gly Arg His Tyr Ala Ser Val
180 185 190

His Pro Leu Ala Ser Pro His Phe Asn Pro Gln Ser Ser Glu Lys Ser
195 200 205

Phe Asn Gln Asp Tyr Asn Thr Val Asp Glu Leu Pro Trp Tyr Lys Trp
210 215 220

Lys Gly His Val Trp Asn Lys Phe Thr Ile Ser Ala Thr Leu Lys Val
225 230 235 240

Ile Trp Leu Thr Leu Ala Val Val Trp Ala Ile Cys Phe Gly Ala Ile
245 250 255

Asn Asp Arg Ser Lys Ser Ala Cys Phe Glu Trp Leu Leu Ala Phe Trp
260 265 270

Phe Gly Ile Ile Phe Met Ile Leu Ser Ala Asp Phe Tyr Leu Gly Gly
275 280 285

Arg Tyr Arg Gln Ser Arg Tyr Phe Asn His Val Glu Ser Phe Ser Gly
290 295 300

Tyr Tyr Lys Tyr Asp Lys Ala Leu Gly Leu Tyr His Ser Glu Asp Val
 305 310 315 320

Leu Pro Ser Asp Asp Asn Ala Gly Val Ile Ala Thr Glu Thr Ala Ser
 325 330 335

Ser Asn Ile Tyr Asn Asn Ser Ser Ser Asn Glu Ser Ile Gln Val Val
 340 345 350

Val

<210> 82

<211> 975

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> (DS)

<222> (1)..(975)

<400> 82

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1 5 10 15

gcc cag aag ata tgg aag ttt ggt tgg ttt gtg gct ggt ggg cta gca 96

Ala Gln Lys Ile Ser Lys Phe Gly Ser Phe Val Ala Gly Gly Leu Ala

20 25 30

gca tgt ata gct gtt aca gtt act aat cag atc gaa ttg att caa atc 144

Ala Cys Ile Ala Val Thr Val Thr Asn Pro Ile Glu Leu Ile Lys Ile

35 40 45

aga atg cag ctt caa ggt gaa atg tca gcc taa gct gaa aat gtt tac 192

Arg Met Gln Leu Gln Gly Glu Met Ser Ala Ser Ala Ala Lys Val Tyr			
50	55	60	
aaa aat cca atc caa ggt atg gcg gta att ttc aaa aac gaa ggt ata	240		
Lys Asn Pro Ile Gln Gly Met Ala Val Ile Phe Lys Asn Glu Gly Ile			
65	70	75	80
aaa ggt ctg caa aaa ggg tta aat gct gct tat atc tat caa att ggg	288		
Lys Gly Leu Gln Lys Gly Leu Asn Ala Ala Tyr Ile Tyr Glu Ile Gly			
85	90	95	
ulu aat ggt tcc aga tta ggg ttt tat gag cca atc aga tca tca tta	336		
Leu Asn Gly Ser Arg Leu Gly Phe Tyr Glu Pro Ile Arg Ser Ser Leu			
100	105	110	
aat cag ctt ttc ttc cca gat caa gag cca cat aag gta cag agc gtc	384		
Asn Gln Leu Phe Phe Pro Asp Gln Glu Pro His Lys Val Gln Ser Val			
115	120	125	
ggg gtt aag gtc ttt tct ggt gcc gca tct ggt ata att agt gca gtc	432		
Gly Val Asn Val Phe Ser Gly Ala Ala Ser Gly Ile Ile Gly Ala Val			
130	135	140	
att ggc tat cca tta ttc ttg gtg aaa aca aga ctt cca tca tat tcc	480		
Ile Gly Ser Pro Leu Phe Leu Val Lys Thr Arg Leu Gln Ser Tyr Ser			
145	150	155	160
gag ttt ata aaa att ggt gaa caa acg cac cac acc ggt gtt tgg aac	528		
Glu Phe Ile Lys Ile Gly Glu Gln Thr His Tyr Thr Gly Val Trp Asn			
165	170	175	
ggg tta gta acc att tta aaa acc gaa ggt gtt aag ggt cta ttc aga	576		
Gly Leu Val Thr Ile Phe Lys Thr Gln Gly Val Lys Gly Leu Phe Arg			
180	185	190	
ggg att gat gcg gca att tta agg aca ggt gct ggt tcc tct gct caa	624		
Gly Ile Asp Ala Ala Ile Leu Arg Thr Gly Ala Gly Ser Ser Val Gln			
195	200	205	
cca cct atc tac aac aca gca aag aac att tgg gtc aaa aat gat ctg	672		
Leu Pro Ile Tyr Asn Thr Ala Lys Asn Ile Leu Val Lys Asn Asp Leu			
210	215	220	

atg aag gat ggc cca gca tta cct tta act gct agt act atc tct ggg 720
 Met Tyr Asp Gly Pro Ala Leu His Leu Thr Ala Ser Thr Ile Ser Gly
 225 230 235 240

tta ggt gtt gcc gtc gtt atg aac cca tgg gat gtc att ttg aca aga 760
 Leu Gly Val Ala Val Val Met Asn Pro Trp Asp Val Ile Leu Thr Arg
 245 250 255

atc tac aat caa aaa ggt gac ttg tac aag gga cct ata gat tgt ttg 800
 Ile Tyr Asn Gln Lys Gly Asp Leu Tyr Lys Gly Pro Ile Asp Cys Leu
 260 265 270

gld aaa act gtt aga atc gaa ggt gta acc gct ttg tat aag ggt ttt 840
 Val Lys Thr Val Arg Ile Gln Gly Val Thr Ala Leu Tyr Lys Gly Phe
 275 280 285

gcc gct caa gtg ttc aga atc gca cct cat aca atc atg tgt ttg acc 912
 Ala Ala Gln Val Phe Arg Ile Ala Pro His Thr Ile Met Cys Leu Thr
 290 295 300

ttc atg gaa cag aca atg aaa ata gtt tat tgg ata gag tgg aag gtt 960
 Phe Met Gln Gln Thr Met Lys Leu Val Tyr Ser Ile Gln Ser Arg Val
 305 310 315 320

tta ggc cat aat taa 975
 Leu Gly His Asn

<210> 83

<211> 324

<212> CBT

<213> *Saccharomyces cerevisiae*

<400> 83

Met Ser Ser Asp Asn Ser Lys Gln Asp Lys Gln Ile Gln Lys Thr Ala
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Ala Gln Lys Ile Ser Lys Phe Gly Ser Phe Val Ala Gly Gly Leu Ala

20

25

30

Ala Cys Ile Ala Val Thr Val Thr Asn Pro Ile Glu Leu Ile Lys Ile
35 40 45

Arg Met Cln Leu Gln Gly Glu Met Ser Ala Ser Ala Ala Lys Val Tyr
50 55 60

Lys Asn Pro Ile Gln Gly Met Ala Val Ile Phe Lys Asn Glu Gly Ile
65 70 75 80

Lys Gly Leu Gln Lys Gly Leu Asn Ala Ala Tyr Ile Tyr Gln Ile Gly
85 90 95

Leu Asn Gly Ser Arg Leu Gly Phe Tyr Glu Pro Ile Arg Ser Ser Leu
100 105 110

Asn Gln Leu Phe Phe Pro Asp Glu Glu Pro His Lys Val Glu Ser Val
115 120 125

Gly Val Ser Val Phe Ser Gly Ala Ala Ser Gly Ile Ile Gly Ala Val
130 135 140

Ile Gly Ser Pro Leu Phe Leu Val Lys Thr Arg Leu Gln Ser Tyr Ser
145 150 155 160

Glu Phe Ile Lys Ile Gly Glu Gln Thr His Tyr Thr Gly Val Trp Asn
165 170 175

Gly Leu Val Thr Ile Phe Lys Thr Glu Gly Val Lys Gly Leu Phe Arg
180 185 190

Gly Ile Asp Ala Ala Ile Leu Arg Thr Gly Ala Gly Ser Ser Val Cln
 195 200 205

Leu Pro Ile Tyr Asn Thr Ala Lys Asn Ile Leu Val Lys Asn Asp Leu
 210 215 220

Met Lys Asp Gly Pro Ala Leu His Leu Thr Ala Ser Thr Ile Ser Gly
 225 230 235 240

Leu Gly Val Ala Val Val Met Asn Pro Trp Asp Val Ile Leu Thr Arg
 245 250 255

Ile Tyr Asn Glu Lys Gly Asp Leu Tyr Lys Gly Pro Ile Asp Cys Leu
 260 265 270

Val Lys Thr Val Arg Ile Glu Gly Val Thr Ala Leu Tyr Lys Gly Phe
 275 280 285

Ala Ala Glu Val Phe Arg Ile Ala Pro His Thr Ile Met Cys Leu Thr
 290 295 300

Phe Met Glu Glu Thr Met Lys Leu Val Tyr Ser Ile Glu Ser Arg Val
 305 310 315 320

Leu Gly His Asn

<210> 34

<211> 1062

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1062)

<400> 84

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Met	Ser	Thr	Ala	Gln	Lys	Ala	Lys	Ile	Leu	Gln	Leu	Ile	Asp	Ser	Cys	
1			5					10					15			

tgc	caa	aat	gca	aaa	agc	aca	caa	ctg	aaa	tct	tta	tca	ttt	gtt	att	95
Cys	Gln	Asn	Ala	Lys	Ser	Thr	Ala	Leu	Lys	Ser	Leu	Ser	Phe	Val	Ile	
			20					25					30			

gga	gca	gta	aat	ggc	acg	aag	aaa	gaa	gct	aaa	aga	acc	tac	att	caa	141
Gly	Ala	Val	Asn	Gly	Thr	Thr	Lys	Glu	Ala	Lys	Arg	Thr	Tyr	Ile	Gln	
			35					40					45			

gaa	cag	tgt	gaa	ttt	ttg	gag	aag	tta	aga	caa	caa	aag	ala	aga	gag	192
Glu	Glu	Cys	Glu	Phe	Leu	Glu	Lys	Leu	Arg	Gln	Gln	Lys	Ile	Arg	Glu	
			50				55						60			

gga	aga	att	aac	ata	ttg	tct	atg	gat	gct	ggt	gtt	tct	aac	ttt	gct	240
Gly	Arg	Ile	Asn	Ile	Leu	Ser	Met	Asp	Ala	Gly	Val	Ser	Asn	Phe	Ala	
65					70					75				80		

ttc	tct	aag	atg	caa	ttg	ctc	aat	aat	gat	cag	ctc	cct	aaa	gta	cta	288
Phe	Ser	Tyr	Met	Gln	Ile	Leu	Asn	Asn	Asp	Pro	Leu	Pro	Lys	Val	Leu	
					85					90				95		

gac	tgg	caa	aag	ata	aat	cta	gag	gag	aaa	tct	ttt	caa	aac	ctc	aaa	336
Asp	Trp	Gln	Lys	Ile	Asn	Leu	Glu	Glu	Lys	Phe	Phe	Gln	Asn	Leu	Lys	
			100					105					110			

aag	tta	agc	ttg	aat	cct	gct	gaa	act	tct	gag	cct	gta	ttc	aac	ctc	384
Lys	Leu	Ser	Leu	Asn	Pro	Ala	Glu	Thr	Ser	Glu	Leu	Val	Phe	Asn	Leu	
			115					120					125			

acg	gag	tat	tta	ttt	gaa	tct	atg	cag	ata	cca	gat	atg	ttt	aca	att	432
Thr	Glu	Tyr	Leu	Phe	Glu	Ser	Met	Pro	Ile	Pro	Asp	Met	Phe	Thr	Ile	
			130				135						140			

gaa agy gaa cgt acc aga acg atg tct tog agy cat att tta gaa cca	480
Glu Arg Gln Arg Thr Arg Thr Met Ser Ser Arg His Ile Leu Asp Pro	
145 150 155 160	
att tta aaa gtg aat att ctc gaa cag att ctt ttc tct aac ttg gaa	528
Ile Leu Lys Val Asn Ile Leu Glu Gln Ile Leu Phe Ser Asn Ien Gln	
165 170 175	
aat aaa atg aag tat acg aat aaa ata cag aat acg tcc aag ttg agy	576
Asn Lys Met Lys Tyr Thr Asn Lys Ile Pro Asn Thr Ser Lys Ieu Arg	
180 185 190	
tat atg gta tgt tgg tcc gat cca cat cgg atg act tca tat lyy lyy	624
Tyr Met Val Cys Ser Ser Asp Pro His Arg Met Thr Ser Tyr Trp Cys	
195 200 205	
att cca aga gaa gag aca cag acc agt tca aaa aag tta aaa tct aac	672
Ile Pro Arg Glu Gln Thr Pro Thr Ser Ser Lys Lys Leu Lys Ser Asn	
210 215 220	
aaa cat agc aaa gat tct cga ata aag cta gtg aaa aaa ata att tca	720
Lys His Ser Lys Asp Ser Arg Ile Lys Leu Val Lys Lys Ile Leu Ser	
225 230 235 240	
acc tca ata cta gaa ggt cat tcc aat agt tct aca aaa ctg gtc gag	768
Thr Ser Ile Leu Glu Gly Asn Ser Thr Ser Ser Thr Lys Leu Val Glu	
245 250 255	
ttc ala gga gtt tgg aat aat agy ata aga aat gac ctt acc aca aaa	816
Phe Ile Gly Val Trp Asn Asn Arg Ile Arg Asn Ala Leu Thr Lys Lys	
260 265 270	
aaa agt ttc aag cta tgt gat ata cta gag atc caa gat aat tgg ggg	864
Lys Ser Phe Lys Leu Cys Asp Ile Leu Glu Ile Gln Asp Asn Ser Gly	
275 280 285	
gtg aga cca gnt gat ggt ttg gca gat tca ttc ctc cat tgt ttg tct	912
Val Arg Lys Asp Asp Asp Leu Ala Asp Ser Phe Leu His Cys Leu Ser	
290 295 300	
tgy atg gag tgg tta aaa aat tat gaa agt att act aca ctc ttg aat	960
Trp Met Glu Trp Leu Lys Asn Tyr Glu Ser Ile Thr Glu Leu Leu Asn	

305	320	315	320	
tca aaa aca ctg gtt aaa aca cag ttc gga cag gbg ttt gaa ttt tgt				1008
Ser Lys Thr Leu Val Lys Thr Gln Phe Gly Gln Val Phe Glu Phe Cys				
325	330	335		
gaa aat aag gta cna aag ctg aaa ttt ttg cag aac act tac aac aat				1058
Glu Asn Lys Val Gln Lys Leu Lys Phe Leu Gln Asn Thr Tyr Asn Asn				
340	345	350		
gac taa				1062
Asp				

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<210> 85
<211> 353
<212> PRT
<213> Saccharomyces cerevisiae
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Met Ser Thr Ala Gln Lys Ala Lys Ile Leu Gln Leu Ile Asp Ser Cys

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Cys Gln Asn Ala Lys Ser Thr Gln Leu Lys Ser Leu Ser Phe Val Ile
20 25 30

Gly Ala Val Asn Gly Thr Thr Lys Glu Ala Lys Arg Thr Tyr Ile Glu
35 40 45

Glu Gln Cys Glu Phe Leu Gln Lys Leu Arg Gln Gln Lys Ile Arg Glu
50 35 60

Gly Arg Ile Asn Ile Leu Ser Met Asp Ala Gly Val Ser Asn Phe Ala
65 70 75 80

Phe Ser Lys Met Gln Leu Leu Asn Asn Asp Pro Leu Pro Lys Val Leu
85 90 95

Asp Trp Gln Lys Ile Asn Leu Glu Glu Lys Phe Phe Gln Asn Leu Lys
100 105 110

Lys Leu Ser Leu Asn Pro Ala Glu Thr Ser Gln Leu Val Thr Asn Leu
115 120 125

Thr Glu Tyr Leu Phe Glu Ser Met Pro Ile Pro Asp Met Phe Thr Ile
130 135 140

Glu Arg Gln Arg Thr Arg Thr Met Ser Ser Arg His Ile Leu Asp Pro
145 150 155 160

Ile Leu Lys Val Asn Ile Leu Glu Glu Ile Leu Phe Ser Asn Leu Glu
165 170 175

Asn Lys Met Lys Tyr Thr Asn Lys Ile Pro Asn Thr Ser Lys Leu Arg
180 185 190

Tyr Met Val Cys Ser Ser Asp Pro His Arg Met Thr Ser Tyr Trp Cys
195 200 205

Ile Pro Arg Glu Glu Thr Pro Thr Ser Ser Lys Lys Leu Lys Ser Asn
210 215 220

Lys His Ser Lys Asp Ser Arg Ile Lys Leu Val Lys Lys Ile Leu Ser
225 230 235 240

Thr Ser Ile Leu Glu Gly Asn Ser Thr Ser Ser Thr Lys Leu Val Glu

245

250

255

Phe Ile Gly Val Trp Asn Asn Arg Ile Arg Asn Ala Leu Thr Lys Lys
 260 265 270

Lys Ser Phe Lys Leu Cys Asp Ile Leu Glu Ile Gln Asp Asn Ser Gly
 275 280 285

Val Arg Lys Asp Asp Asp Leu Ala Arg Ser Phe Leu His Cys Leu Ser
 290 295 300

Trp Met Glu Trp Leu Lys Asn Tyr Glu Ser Ile Thr Glu Leu Leu Asn
 305 310 315 320

Ser Lys Thr Leu Val Lys Thr Gln Phe Gly Glu Val Phe Glu Phe Cys
 325 330 335

Glu Asn Lys Val Gln Lys Leu Lys Phe Leu Gln Asn Thr Tyr Asn Asn
 340 345 350

Asp

<210> 86

<211> 2052

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(2052)

<400> 86

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cct gaa caa gac att caa aca act tct agg cta tta aca aag cta tct	96
Arg Glu Gln Asp Ile Gln Thr Thr Ser Arg Leu Leu Thr Thr Leu Ser	
20 25 30	
atc caa caa ttg gtg caa aat ggc ttg gca ata aac aac ata cat cta	144
Ile Gln Gln Leu Val Glu Asn Gly Leu Ala Ile Asn Asn Phe His Leu	
35 40 45	
gaa aac ata aga tcc ggt ctg att ggc aaa tta tat atg gaa ctg gga	192
Glu Asn Ile Arg Ser Gly Leu Ile Gly Lys Leu Tyr Met Glu Lys Gly	
50 55 60	
cct aac ttg gcg gtt aac gac aac att caa agg ggt gat att aag gll	240
Pro Asn Leu Ala Val Asn Asn Lys Ile Gln Arg Gly Asp Ile Lys Val	
65 70 75 80	
ggc gat att gtt ttg gta cgc cct gca aaa acc aaa gta aat aac aag	288
Gly Asp Ile Val Leu Val Arg Pro Ala Lys Thr Lys Val Asn Thr Lys	
85 90 95	
acg aag ccc aac gtc aca aag gtg tct gaa gac tcc aat ggc gag caa	336
Thr Lys Pro Lys Val Lys Lys Val Ser Glu Asp Ser Asn Gly Glu Glu	
100 105 110	
ggc gaa tgc tca ggc gtt gtc taa aaa atg agt gat aca caa acc acc	384
Ala Glu Cys Ser Gly Val Val Tyr Lys Met Ser Asp Thr Gln Ala Thr	
115 120 125	
ata gct cta gaa gaa tct caa gac gtt att gct acc aca ttt tat tct	432
Ile Ala Leu Glu Glu Ser Gln Asp Val Ile Ala Thr Thr Phe Tyr Ser	
130 135 140	
tat agc aca ctt tac att tta aag act acc aat gtc gtc aag tat aat	480
Tyr Ser Lys Leu Tyr Ile Leu Lys Thr Thr Asn Val Val Thr Tyr Asn	
145 150 155 160	
aga atg gaa tcc acc atg aga aaa ctg tct gaa att agt tca ccc ata	528
Arg Met Glu Ser Thr Met Arg Lys Leu Ser Glu Ile Ser Ser Pro Ile	

214/762

	165	170	175	
caa gac aaa att ata caa tac ttg gta aac gaa cgc ccc ttc atc ccc				575
Gln Asp Lys Ile Ile Gln Tyr Leu Val Asn Glu Arg Pro Phe Ile Pro				
	180	185	190	
aat aca aac agc ttt csa aac att aaa tct ttt tta aac ccg aat ctg				624
Asn Thr Asn Ser Phe Gln Asn Ile Lys Ser Phe Leu Asn Pro Asn Leu				
	195	200	205	
aat gac tcc cag aaa act gcc att aat ttt gcc att aac aat gac ttg				572
Asn Asp Ser Gln Lys Thr Ala Ile Asn Phe Ala Ile Asn Asn Asp Leu				
	210	215	220	
acc att ata cat ggt cct cct ggt acg ggt aaa aca ttc aca tta att				720
Thr Ile Ile His Gly Pro Pro Gly Thr Gly Lys Thr Phe Thr Leu Ile				
	225	230	235	240
gaa ttg atc cag caa ttg cta att aac aat cct gag gag aga atc tta				760
Glu Leu Ile Gln Gln Leu Leu Ile Lys Asn Pro Glu Glu Arg Ile Leu				
	245	250	255	
att tgt ggg cct tcc aat att tct gtg gat aag att ctg gag agg cta				816
Ile Cys Gly Pro Ser Asn Ile Ser Val Asp Thr Ile Leu Glu Arg Leu				
	260	265	270	
acg cct ctt gtg ccg aat aat tta tta tta aga atc ggt cat cct gct				864
Thr Pro Leu Val Pro Asn Asn Leu Leu Leu Arg Ile Gly His Pro Ala				
	275	280	285	
agg cta tta gac tct aat aaa aga cac tct ctt gat ata ctt agt aaa				912
Arg Leu Leu Asp Ser Asn Lys Arg His Ser Leu Asp Ile Leu Ser Lys				
	290	295	300	
aag aat act att gtg aag gac att tcc cag gag att gac aaa tta att				960
Lys Asn Thr Ile Val Lys Asp Ile Ser Gln Glu Ile Asp Lys Leu Ile				
	305	310	315	320
cag gag aat aca aaa cta aaa aac tat aag caa ggt aca gaa aac tgg				1008
Gln Glu Asn Lys Lys Leu Lys Asn Tyr Lys Gln Arg Lys Glu Asn Trp				
	325	330	335	

aac gaa att aaa ctg ctg cgc aac gat tca aag aaa aga gag ttc aaa asn glu ile lys leu leu arg lys asp leu lys lys arg glu phe lys 340 345 350	1056
acc att aag gac tta ata atn caa tcc aga ata gtc gtc acc act ata thr ile lys asp leu ile ile sin ser arg ile val val thr thr leu 355 360 365	1104
cac ggt tca tca tcy aga gaa cta tgc tcc ctt tat aga gat gat cca his gly ser ser ser arg glu leu cys ser leu tyr arg asp asp pro 370 375 380	1152
aat ttc cag ctt ttc gat acc ttg atc atc gat gaa gtc tca cag gac asn phe glu leu phe asp thr leu ile ile asp glu val ser gln ala 385 390 395 400	1200
atg gac aca caa tgc hgg atc cca ata att gca cat caa act cag ttc met glu pro gln cys trp ile pro leu ile ala his gln asn gln phe 405 410 415	1248
aac aaa cta gtc ctt gct ggt gac nat aaa caa ttg cca ccc aca atc his lys leu val leu ala gly asp asn lys gln leu pro pro thr ile 420 425 430	1296
aaa acs yaa gcc gac aca aat glu att cac nat ctg gac acc aca glu lys thr glu asp asp lys asn val ile his asn leu glu thr thr leu 435 440 445	1344
ttt gac aga ata atc aaa ata ttc ccg aaa agg gat atg gra aaa ttt phe asp arg ile ile lys ile phe pro lys arg asp met val lys phe 450 455 460	1392
ctt aac gtt caa tac agg atg aat caa aaa att atg gaa ttt cca tcc leu asn val gln tyr arg met asn gln lys ile met glu phe pro ser 465 470 475 480	1440
cac taa atg tat aat ggg aaa ata ttg gcc gat gca acg gtc ycg aan his ser met tyr asn gly lys leu leu ala asp ala thr val ala asn 485 490 495	1488
aga ctt ttg ata gac cta ccg acc gtc gat gct acg cca tct cag gat arg leu leu ile asp leu pro thr val asp ala thr pro ser glu asp 500 505 510 515	1536

216/762

500	505	510	
gat gac gat aca aac att cct tta atk tgg tat gat cag csa ggt gat Asp Asp Asp Thr Lys Ile Pro Leu Ile Trp Tyr Asp Thr Gln Gly Asp 515	520	525	1584
gaa ttt caa gag aat gaa gat gaa got act atc att aga tct aag tat Glu Phe Gln Gln Thr Ala Asp Glu Ala Thr Ile Leu Gly Ser Lys Tyr 530	535	540	1632
aal gag ggu gaa aat gaa all gaa aaa gaa aat all gag aat tta agg Asn Glu Gly Gln Ile Ala Ile Val Lys Glu His Ile Glu Asn Leu Arg 545	550	555	1680
tca ttc aac gtc cag gag aac tct ata ggt gtt att tct oca tac aat Ser Phe Asn Val Pro Glu Asn Ser Ile Gly Val Ile Ser Pro Tyr Asn 565	570	575	1728
gaa caa gtt tct cat ctg aac aaa ttg atc cat gat gaa tta aaa tta Ala Gln Val Ser His Leu Lys Lys Leu Ile His Asp Glu Leu Lys Leu 580	585	590	1776
act gat att gaa ata tca act gta gat ggg ttc cag gcc cgt gaa aaa Thr Asp Ile Glu Ile Ser Thr Val Asp Gly Phe Gln Gly Arg Glu Lys 595	600	605	1824
gat gtt atc ata ttg agt tta gtt cgt agc aat gaa aaa ttt gaa gtt Asp Val Ile Ile Leu Ser Leu Val Arg Ser Asn Glu Lys Phe Glu Val 610	615	620	1872
ggg ttc att aag gac gaa aga aga ctg aac gtc gcc atg aca aga ccc Gly Phe Leu Lys Glu Glu Arg Arg Leu Asn Val Ala Met Thr Arg Pro 625	630	635	1920
aga agg oaa cta gtt gtt gtt ggc aat ata gaa gtt ctg caa agg tgc Arg Arg Gln Leu Val Val Val Gly Asn Ile Gln Val Leu Gln Arg Cys 645	650	655	1968
ggg aac aag tac cta aaa agt tgg tca gaa tgg lyl gaa gag aac got Gly Asn Lys Tyr Leu Lys Ser Trp Ser Glu Trp Cys Glu Glu Asn Ala 660	665	670	2016

gac gta agg tac gcc aac att gac gat tat ttg taa 2052
 Asp Val Arg Tyr Pro Asn Ile Asp Asp Tyr Leu
 675 689

<210> 87
 <211> 683
 <212> FET
 <213> *Saccharomyces cerevisiae*

<400> 87

Met Asn Lys Glu Leu Ala Ser Lys Phe Leu Ser Ser Ile Lys His Glu
 1 5 10 15

Arg Glu Gln Asp Ile Gln Thr Thr Ser Arg Leu Leu Thr Thr Leu Ser
 20 25 30

Ile Gln Gln Leu Val Gln Asn Gly Leu Ala Thr Asn Asn Ile His Leu
 35 40 45

Glu Asn Ile Arg Ser Gly Leu Ile Gly Lys Leu Tyr Met Glu Leu Gly
 50 55 60

Phe Asn Leu Ala Val Asn Asp Lys Ile Gln Arg Gly Asp Ile Lys Val
 65 70 75 80

Gly Asp Ile Val Leu Val Arg Phe Ala Lys Thr Lys Val Asn Thr Lys
 85 90 95

Thr Lys Pro Lys Val Lys Lys Val Ser Glu Asp Ser Asn Gly Glu Gln
 100 105 110

Ala Glu Cys Ser Gly Val Val Tyr Lys Met Ser Asp Thr Gln Ile Thr

115

120

125

Phe Ala Leu Glu Gln Ser Gln Asp Val Ile Ala Thr Thr Phe Tyr Ser
130 135 140

Tyr Ser Lys Leu Tyr Ile Leu Lys Thr Thr Asn Val Val Thr Tyr Asn
145 150 155 160

Arg Met Glu Ser Thr Met Arg Lys Leu Ser Glu Ile Ser Ser Pro His
165 170 175

Gln Asp Lys Ile Ile Gln Tyr Leu Val Asn Glu Arg Pro Phe Ile Pro
180 185 190

Asn Thr Asn Ser Phe Gln Asn Ile Lys Ser Phe Leu Asn Pro Asn Leu
195 200 205

Asn Asp Ser Glu Lys Thr Ala Ile Asn Phe Ala Ile Asn Asn Asp Leu
210 215 220

Thr Ile Ile His Gly Pro Pro Gly Thr Gly Lys Thr Phe Thr Leu Ile
225 230 235 240

Glu Leu Ile Gln Gln Leu Leu Ile Lys Asn Pro Glu Glu Arg Ile Leu
245 250 255

Ile Cys Gly Pro Ser Asn Ile Ser Val Asp Thr Ile Leu Glu Arg Leu
260 265 270

Thr Pro Leu Val Pro Asn Asn Leu Leu Leu Arg Ile Gly His Pro Ala
275 280 285

Arg Leu Leu Asp Ser Asn Lys Arg His Ser Leu Asp Ile Leu Ser Lys
 290 295 300

Lys Asn Thr Ile Val Lys Asp Ile Ser Gln Glu Ile Asp Lys Leu Ile
 305 310 315 320

Gln Glu Asn Lys Lys Leu Lys Asn Tyr Lys Gln Arg Lys Glu Asn Trp
 325 330 335

Asn Glu Ile Lys Leu Leu Arg Lys Asp Leu Lys Lys Arg Glu Phe Lys
 340 345 350

Thr Ile Lys Asp Ser Ile Ile His Ser Arg Ile Val Val Thr Thr Leu
 355 360 365

His Gly Ser Ser Ser Arg Glu Lys Cys Ser Leu Tyr Arg Asp Asp Pro
 370 375 380

Asn Phe Gln Leu Phe Asp Thr Leu Ile Ile Asp Glu Val Ser Gln Ala
 385 390 395 400

Met Glu Pro Gln Cys Trp Ile Pro Leu Ile Ala His Gln Asn Gln Phe
 405 410 415

His Lys Leu Val Leu Ala Gly Asp Asn Lys Gln Leu Pro Pro Thr Ile
 420 425 430

Lys Thr Glu Asp Asp Lys Asn Val Ile His Asn Leu Glu Thr Thr Leu
 435 440 445

Phe Asp Arg Ile Ile Lys Ile Phe Pro Lys Arg Asp Met Val Lys Phe
 450 455 460

Leu Asn Val Gln Tyr Arg Met Asn Gln Lys Ile Met Gln Phe Pro Ser
 465 470 475 480

His Ser Met Tyr Asn Gly Lys Leu Leu Ala Asp Ala Thr Val Ala Asn
 485 490 495

Arg Leu Leu Ile Asp Leu Pro Thr Val Asp Ala Thr Pro Ser Glu Asp
 500 505 510

Asp Asp Asp Thr Lys Ile Pro Leu Ile Tyr Tyr Asp Thr Gln Gly Asp
 515 520 525

Glu Phe Glu Glu Thr Ala Asp Glu Ala Thr Ile Leu Gly Ser Lys Tyr
 530 535 540

Asn Glu Gly Glu Ile Ala Ile Val Lys Glu His Ile Glu Asn Leu Arg
 545 550 555 560

Ser Phe Asn Val Pro Glu Asn Ser Ile Gly Val Ile Ser Pro Tyr Asn
 565 570 575

Ala Gln Val Ser His Leu Lys Lys Leu Ile His Asp Glu Leu Lys Leu
 580 585 590

Thr Asp Ile Glu Ile Ser Thr Val Asp Gly Phe Glu Gly Arg Glu Lys
 595 600 605

Asp Val Ile Ile Leu Ser Leu Val Arg Ser Asn Glu Lys Phe Glu Val
 610 615 620

Gly Phe Leu Lys Glu Glu Arg Arg Leu Asn Val Ala Met Thr Arg Pro
 625 630 635 640

Arg Arg Gln Leu Val Val Val Gly Asn Ile Glu Val Leu Gln Arg Cys
 645 650 655

Gly Asn Lys Tyr Leu Lys Ser Trp Ser Glu Trp Cys Glu Glu Asn Ala
 660 665 670

Asp Val Arg Tyr Pro Asn Ile Asp Asp Tyr Leu
 675 680

<210> 88

<211> 474

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(414)

<400> 88

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Met Glu Thr Glu Val Pro Ala Pro Val Arg Thr His Ser Tyr Ala Leu

1 5 10 15

gac aga tat gtt aga cag aaa agg agg gaa aaa caa aga aag cag agc 96

Asp Arg Tyr Val Arg Gln Lys Arg Arg Glu Lys Glu Arg Lys Gln Ser

20 25 30

tta aag cgc gtc gaa aag aaa tat act cct agt gaa tta gct ctg tac 144

Leu Lys Arg Val Glu Lys Lys Tyr Thr Pro Ser Glu Leu Ala Leu Tyr

35 40 45

gaa att cga aac tac caa cgt tcc aag gat tta tta atc tcc aaa att 192
 Glu Ile Arg Lys Tyr Glu Arg Ser Thr Asp Leu Leu Ile Ser Lys Ile
 50 55 60

cca ttt gca agg cta gtg aaa gaa att aca gac gag ttt aca act aaa 240
 Pro Phe Ala Arg Leu Val Lys Glu Val Thr Asp Glu Phe Thr Thr Lys
 65 70 75 80

gat cag gat tta cgt tgg cag tca atg gcg att atg gcg tta cag gaa 288
 Asp Gln Asp Leu Arg Trp Gln Ser Met Ala Ile Met Ala Leu Gln Glu
 85 90 95

gaa agc gaa gcg tat ctg gta gga tta ttg gaa cat aca aac ctc ttg 336
 Ala Ser Glu Ala Tyr Leu Val Gly Leu Leu Glu His Thr Asn Leu Leu
 100 105 110

gcg ctg cat gaa aaa aga att act ata atg aag aca gac atg caa cca 384
 Ala Leu His Ala Lys Arg Ile Thr Ile Met Lys Lys Asp Met Gln Leu
 115 120 125

gaa aga aga atc agg gga cag ttt att tgg 414
 Ala Arg Arg Ile Arg Gly Glu Phe Ile
 130 135

<210> 89

<211> 137

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 89

Met Glu Thr Glu Val Pro Ala Pro Val Arg Thr His Ser Tyr Ala Leu
 1 5 10 15

Asp Arg Tyr Val Arg Glu Lys Arg Arg Glu Lys Glu Arg Lys Glu Ser
 20 25 30

Leu Lys Arg Val Glu Lys Lys Tyr Thr Pro Ser Glu Leu Ala Leu Tyr
 35 40 45

Glu Ile Arg Lys Tyr Gln Arg Ser Thr Asp Leu Leu Ile Ser Lys Ile
 50 55 60

Pro Phe Ala Arg Leu Val Lys Glu Val Thr Asp Glu Phe Thr Thr Lys
 65 70 75 80

Asp Glu Asp Leu Arg Trp Gln Ser Met Ala Ile Met Ala Leu Gln Glu
 85 90 95

Ala Ser Glu Ala Tyr Leu Val Gly Leu Leu Glu His Thr Asn Leu Leu
 100 105 110

Ala Leu His Ala Lys Arg Ile Thr Ile Met Lys Lys Asp Met Glu Leu
 115 120 125

Ala Arg Arg Ile Arg Gly Gln Phe Ile
 130 135

<210> 90
 <211> 1293
 <212> JNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (1)..(1293)

<400> 90
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 Met Asp Asp Ile Ser Gly Arg Gln Thr Leu Pro Arg Ile Asn Arg Leu
 1 5 10 15
 ttg gag cac gtg gga aat ccc caa gat agt ttg tca atc cta cat ata 96

224/762

Leu Glu His Val Gly Asn Pro Gln Asp Ser Leu Ser Ile Leu His Ile	
20 25 30	
ggg gga acc aac ggt aag gag acc gta tct aca ttt ttg acc tcc ata	142
Ala Gly Thr Asn Gly Lys Glu Thr Val Ser Lys Phe Leu Thr Ser Ile	
35 40 45	
ttg cag cat cag ggg cca cag cgg aca agg gtc ttg att ggt agg tat	192
Leu Gln His Pro Gly Gln Gln Arg Gln Arg Val Leu Ile Gly Arg Tyr	
50 55 60	
act aca tct tcc ttg cta aac gcc aac gaa gag gat att agc att aat	240
Thr Thr Ser Ser Leu Leu Asn Ala Lys Glu Glu Asp Ile Ser Ile Asn	
65 70 75 80	
aat gaa gcc aat tcc ttg ata gag tat tct agg atc gaq aag gaa ctt	288
Asn Glu Ala Ile Ser Asn Val Glu Tyr Ser Arg Ile Glu Lys Glu Leu	
85 90 95	
ata gaa gca gat agt tct ttg aac tta cag tgc aac aac atc gaa cag	336
Ile Glu Ala Asp Ser Ser Leu Lys Thr Gln Cys Asn Asn Leu Glu Leu	
100 105 110	
cta aca agc gta ggt ctc gta tac ttc gct aag aac aat tgc caa tgg	384
Leu Thr Ser Val Ala Leu Val Tyr Phe Ala Lys Lys Asn Cys Gln Trp	
115 120 125	
tgc ata ata gaa act ggt tta gct gga aac cag gac cct gga agt ata	432
Cys Ile Ile Glu Thr Gly Leu Ala Gly Lys Gln Asp Pro Gly Ser Ile	
130 135 140	
att gct ggt caa agt aga gtc tgt tgc gcc att act aac atg ggc att	480
Ile Ala Gly Gln Ser Arg Val Cys Cys Ala Ile Thr Asn Val Gly Ile	
145 150 155 160	
agc gat gaa gct ttt tta tgc aag ttt ttg tct caa att act gaa agt	528
Ser Asp Glu Ala Phe Leu Cys Lys Phe Leu Ser Gln Ile Thr Glu Ser	
165 170 175	
acc aca aat aaa gca att ttt cta tca gac ggt tct aat gac gaa ttt	576
Ser Thr Asn Lys Ala Ile Phe Leu Leu Asp Gly Ser Asn Asp Glu Phe	
180 185 190	

gta cga aat acg ata acg aaa cgg tgc cat gat gtt gga tgt cca tta	624
Val Arg Asn Thr Ile Thr Lys Arg Cys His Asp Val Gly Cys Pro Leu	
195 200 205	
gaa atc acc gac oot tot ctt agg gat tac aat gta cnc aca gac acc	672
Glu Ile Thr Asp Pro Ser Leu Arg Asp Tyr Asn Val His Thr Asp Thr	
210 215 220	
tgg ggc act ctt gaa gtt cgc ctg cca tac agt gaa gaa gaa tat caa	720
Trp Gly Thr Leu Glu Val Arg Leu Pro Tyr Ser Glu Glu Glu Tyr Gln	
225 230 235 310	
ata ttt aat ttg aga gtt ggc ata ggc gtt tta gac ttt ttg agc aag	768
Ile Phe Asn Leu Arg Val Ala Ile Ala Val Leu Asp Phe Leu Ser Lys	
245 250 255	
gaa aaa aag gtt tgt att tca aag gat caa cta tcc caa ggt tta ata	816
Glu Lys Lys Val Cys Ile Ser Lys Asp Gln Leu Ser Gln Gly Leu Phe	
260 265 270	
tct gtg gat tgg aca aga cgt ttc cca cgt ttg gat tcc tgt tat gaa	864
Ser Val Asp Trp Pro Arg Ser Leu His Arg Leu Asn Tyr Cys Tyr Gln	
275 280 285	
tct act agt gga aag aaa atc gca tta cta tta gac aac gca act aat	912
Ser Thr Ser Gly Lys Lys Ile Ala Leu Leu Leu Asp Asn Ala Asn Asn	
290 295 300	
ggg aag gca gct cga aat tta gcc tgc cat tta agg acc acg ttc ggt	960
Ala Lys Ala Ala Arg Asn Leu Ala Cys His Leu Arg Thr Thr Tyr Gly	
305 310 315 320	
gat arg cca tta aca ttt gtc att got ats aca act ggg aaa aag gtg	1008
Asp Thr Pro Leu Thr Phe Val Ile Ala Ile Thr Thr Gly Lys Lys Val	
325 330 335	
tct ccc tta ctt gat cgg cta ata cgt cca caa gal tat gtt att gly	1056
Ser Pro Leu Leu Asp Pro Leu Ile Arg Pro Gln Asp Tyr Val Ile Val	
340 345 350	
act aga ttt ggg tca gtg gtt gga atg cgg tgg atc caa tcc cta gaa	1104

Thr Arg Phe Gly Ser Val Val Gly Met Pro Trp Ile Gln Ser Leu Glu
 355 360 365

cgg gtg aat att ctc gca ttt atc aaa aac cgg tat acg aga aat gtt 1151
 Pro Val Asn Leu Leu Ala Phe Ile Lys Asn Arg Tyr Thr Arg Asn Val
 370 375 380

aac atg cag cgg gat att caa agt gtc tgg acc ttc ctt gaa aca agt 1200
 Asn Met Gln Pro Asp Leu Gln Ser Val Trp Thr Phe Leu Glu Thr Ser
 385 390 395 400

ggg tta aag acg att gtt cct gtt atc gta tgt gga tca ctg tat atc 1248
 Gly Leu Lys Thr Ile Val Pro Val Ile Val Cys Gly Ser Leu Tyr Ile
 405 410 415

tgc aaa gag cta ttg cgc tta cac aac tgt cac ttg cca gta tag 1293
 Cys Lys Glu Leu Leu Arg Leu His Asn Cys His Leu Pro Val
 420 425 430

<210> 91
 <211> 430
 <212> FRF
 <213> *Saccharomyces cerevisiae*
 <400> 91

Met Asp Asp Ile Ser Gly Arg Gln Thr Leu Pro Arg Ile Asn Arg Leu
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Leu Glu His Val Gly Asn Pro Gln Asp Ser Leu Ser Ile Leu His Ile
 20 25 30

Ala Gly Thr Asn Gly Lys Glu Thr Val Ser Lys Phe Leu Thr Ser Ile
 35 40 45

Leu Gln His Pro Gly Gln Gln Arg Gln Arg Val Leu Ile Gly Arg Tyr
 50 55 60

Thr Thr Ser Ser Leu Leu Asn Ala Lys Glu Glu Asp Ile Ser Ile Asn
 65 70 75 80

Asn Glu Ala Ile Ser Leu Ile Glu Tyr Ser Arg Ile Glu Lys Glu Leu
 85 90 95

Ile Glu Ala Asp Ser Ser Leu Lys Leu Glu Cys Asn Asn Leu Glu Leu
 100 105 110

Leu Thr Ser Val Ala Leu Val Tyr Phe Ala Lys Lys Asn Cys Glu Trp
 115 120 125

Cys Ile Ile Glu Thr Gly Leu Ala Gly Lys Gln Asp Pro Gly Ser Ile
 130 135 140

Ile Ala Gly Gln Ser Arg Val Cys Cys Ala Ile Thr Asn Val Gly Ile
 145 150 155 160

Ser Asp Glu Ala Phe Leu Cys Lys Phe Leu Ser Gln Ile Thr Glu Ser
 165 170 175

Ser Thr Asn Lys Ala Ile Phe Leu Leu Asp Gly Ser Asn Asp Glu Phe
 180 185 190

Val Arg Asn Thr Ile Thr Cys Arg Cys His Asp Val Gly Cys Pro Leu
 195 200 205

Glu Ile Thr Asp Pro Ser Leu Arg Asp Tyr Asn Val His Thr Asp Thr
 210 215 220

Trp Gly Thr Leu Glu Val Arg Leu Pro Tyr Ser Glu Glu Glu Tyr Gln
 225 230 235 240

Ile Phe Asn Leu Arg Val Ala Ile Ala Val Leu Asp Phe Leu Ser Lys
 245 250 255

Glu Lys Lys Val Cys Ile Ser Lys Asp Gln Leu Ser Gln Gly Leu Ile
 260 265 270

Ser Val Asp Trp Pro Arg Ser Leu His Arg Leu Asp Tyr Cys Tyr Glu
 275 280 285

Ser Thr Ser Gly Lys Lys Ile Ala Leu Leu Leu Asp Asn Ala Asn Asn
 290 295 300

Ala Lys Ala Ala Arg Asn Leu Ala Cys His Leu Arg Thr Thr Tyr Gly
 305 310 315 320

Asp Thr Pro Leu Thr Phe Val Ile Ala Ile Thr Thr Gly Lys Lys Val
 325 330 335

Ser Pro Leu Leu Asp Pro Leu Ile Arg Pro Gln Asp Tyr Val Ile Val
 340 345 350

Thr Arg Phe Gly Ser Val Val Gly Met Pro Trp Ile Gln Ser Leu Glu
 355 360 365

Pro Val Asn Leu Leu Ala Phe Ile Lys Asn Arg Tyr Thr Arg Asn Val
 370 375 380

Asn Met Gln Pro Asp Leu Gln Ser Val Trp Thr Phe Leu Glu Thr Ser
 385 390 395 400

Gly Leu Lys Thr Ile Val Pro Val Val Val Cys Gly Ser Leu Tyr Ile
 405 410 415

Cys Lys Glu Leu Leu Arg Leu His Asn Cys His Leu Pro Val
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 <211> 593
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (593)

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 1 5 10 15
 ata tct tcc ttt tct tct att gac tct taa aaa cag gag acc ttt act 96
 Ile Ser Ser Phe Ser Ser Ile Asp Ser Tyr Lys Pro Glu Pro Phe Thr
 20 25 30
 ggg ttc aaa gat tct gaa gct cca gaa cag cct att tta aaa aac gat 144
 Gly Phe Lys Asp Ser Glu Ala Pro Glu Gln Pro Leu Leu Lys Asn Asp
 35 40 45
 acc att gtt gga aag ggg caa ctg gaa gat gat agt aat gta gat gat 192
 Thr Ile Val Gly Lys Gly Gln Leu Glu Asp Asp Ser Asn Val Asp Asp
 50 55 60
 caa cac cgt cat tca gat gtg cat tct cat cac agt tct agt act tta 240
 Gln His Arg His Ser Asp Val His Ser His His Ser Ser Ser Thr Leu
 65 70 75 80
 aaa agg cca act tca act tct ata gaa aag atg gtt acc cac aat gct 288

Lys Arg Pro Thr Ser Asn Ser Ile Glu Tyr Met Val Thr His Asn Ala	
25 30 35	
tta gag ggc aac tca gaa aca gtt gal tcc tta aaa gaa gaa ggt tta	336
Leu Glu Gly Asn Ser Glu Thr Val Asp Ser Leu Lys Glu Asp Gly Leu	
100 105 110	
aat ttg aac aag aaa gct ctt ccy gat att ccc gcc cca gta aca aac	384
Asn Leu Asn Lys Lys Ala Leu Pro Asp Ile Thr Ala Pro Val Thr Asn	
115 120 125	
tca gct cag cat gct gca ttt cca gaa gag tat cgt tta gaa aca gaa	432
Ser Ala His Asp Ala Ala Phe Pro Glu Glu Tyr Arg Leu Glu Thr Glu	
130 135 140	
aac ccc ttg ctc aaa ttg aag acg ctt gaa agt ttg aag agg gag gaa	480
Thr Gly Leu Val Lys Leu Lys Thr Leu Glu Ser Leu Lys Arg Glu Asp	
145 150 155 160	
tct cgc gta tca tca act aaa aaa gag cat att aac gac cat aca gat	528
Ser Arg Val Ser Ser Thr Lys Lys Glu His Ile Asn Asp His Thr Asp	
165 170 175	
atg cat tgg acc cga tcc aag gtt act aca aat tct caa gct tct tct	576
Met His Ser Thr Arg Ser Lys Val Thr Thr Asn Ser Gln Gly Ser Ser	
180 185 190	
cta gaa cca aac aag ttg aac atg gca gta gag aag aat aag aag agg	624
Leu Glu Pro Asn Lys Leu Asn Met Ala Val Glu Lys Asn Lys Lys Arg	
195 200 205	
atc gaa aaa tat cca aaa cat aaa tca gaa aag ggg atc aag ggg ttt	672
Ile Glu Lys Tyr Gln Lys His Lys Ser Glu Lys Gly Ile Lys Gly Phe	
210 215 220	
ttt cat aga att ttc gat taa	693
Phe His Arg Ile Phe Asp	
225 230	

<210> 93

<211> 230

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 93

Met Pro Val Pro Ser Val Thr Val Thr Thr Asp Asn Glu Tyr Glu Asp
 1 5 10 15

Ile Ser Ser Phe Ser Ser Ile Asp Ser Tyr Lys Pro Glu Pro Phe Thr
 20 25 30

Gly Phe Lys Asp Ser Glu Ala Pro Glu Gln Pro Leu Leu Lys Asn Asp
 35 40 45

Thr Ile Val Gly Lys Gly Gln Leu Glu Asp Asp Ser Asn Val Asp Asp
 50 55 60

Gln His Arg His Ser Asp Val His Ser His His Ser Ser Met Thr Leu
 65 70 75 80

Lys Arg Pro Thr Ser Asn Ser Ile Glu Lys Met Val Thr His Asn Ala
 85 90 95

Leu Glu Gly Asn Ser Glu Thr Val Asp Ser Leu Lys Glu Asp Gly Leu
 100 105 110

Asn Leu Asn Lys Lys Ala Leu Pro Asp Ile Thr Ala Pro Val Thr Asn
 115 120 125

Ser Ala His Asp Ala Ala Phe Pro Glu Glu Tyr Arg Leu Glu Thr Glu
 130 135 140

Thr Gly Leu Val Lys Leu Lys Thr Leu Glu Ser Leu Lys Arg Glu Asp

145 150 155 160

Ser Arg Val Ser Ser Thr Lys Lys Glu His Ile Asn Arg His Thr Asp
165 170 175

Met His Ser Thr Arg Ser Lys Val Thr Thr Asn Ser Gln Gly Ser Ser
180 185 190

Leu Glu Pro Asn Lys Leu Asn Met Ala Val Glu Lys Asn Lys Lys Arg
195 200 205

Ile Gln Lys Tyr Gln Lys His Lys Ser Glu Lys Gly Ile Lys Gly Phe
210 215 220

Phe His Arg Ile Phe Asp
225 230

<210> 94
<211> 510
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(510)

<400> 54
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1 5 10 15
tta tca aaa aaa ccc ccc cta gga aca cta ttc tcc tct aag gct agc 96
Leu Ser Lys Lys Pro Pro Leu Gly Thr Leu Phe Ser Ser Lys Ala Ser
20 25 30

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agg caa ggt llu llo ggu lgg aya act tot tcc aat aaa gat gac ccc      144
Arg Gln Gly Phe Phe Gly Trp Arg Thr Ser Ser Asn Lys Asp Asp Pro
      35              40              45

gat ttt ggt atg tgc gca tca cat att cca ttt gta ttc gtg gag ttc      192
Asp Phe Gly Met Cys Ala Ser His Ile Pro Phe Val Phe Val Glu Phe
      50              55              60

gat aat gga gag val aaa cta att gca cat tta gaa cgg aag aat aaa      240
Asp Asn Gly Glu His Lys Leu Ile Ala His Leu Ala Arg Lys Asn Lys
      65              70              75              80

cat gtg gaa atg atg gaa aga gtt caa aaa tgc tta gtg gta ttt cag      280
His Val Glu Met Leu Glu Arg Val Glu Lys Cys Leu Val Val Phe Glu
      85              90              95

agc gtc gal lua lau atc tct ccg gcg tgg ttc ccc atg aag aaa aag      336
Ser Val Asp Ser Tyr Ile Ser Pro Ala Trp Phe Pro Met Lys Lys Lys
      100              105              110

acc cat aag ttc gta cca aca tgg gal lll gac gat gtg cac gtt tac      384
Thr His Lys Phe Val Pro Thr Trp Asp Phe Ala Ala Val His Val Tyr
      115              120              125

ggt aca cca agg att atc cgc gac gat aaa gac tgg ctc att act atg      432
Gly Val Pro Arg Ile Ile Arg Asp Asp Lys Asp Trp Leu Ile Asn Met
      130              135              140

tta tca act ttg act gac caa gaa gaa gag aaa aga cct gag gcg gaa      480
Leu Ser Thr Leu Thr Asp Gln Glu Glu Glu Lys Arg Pro Glu Gly Glu
      145              150              155              160

aat gta cga agt aaa gtg gag cgt ttc tga                                510
Asn Val Arg Ser Lys Val Glu Arg Phe
      165

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<210> 95

<211> 169

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 95

Met Tyr Ile Pro Lys His Phe Glu Ser Met Glu Leu Ser Arg Tyr Lys
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Leu Ser Lys Lys Pro Pro Leu Gly Thr Leu Phe Ser Ser Lys Ala Ser
 20 25 30

Arg Gln Gly Phe Phe Gly Trp Arg Thr Ser Ser Asn Lys Asp Asp Pro
 35 40 45

Asp Phe Gly Met Cys Ala Ser His Val Pro Phe Val Phe Val Glu Phe
 50 55 60

Asp Asn Gly Glu His Lys Leu Ile Ala His Leu Ala Arg Lys Asn Lys
 65 70 75 80

His Val Glu Met Leu Glu Arg Val Gln Lys Cys Leu Val Val Phe Glu
 85 90 95

Ser Val Asp Ser Tyr Ile Ser Pro Ala Trp Phe Pro Met Lys Lys Lys
 100 105 110

Thr His Lys Phe Val Pro Thr Trp Asp Phe Ala Ala Val His Val Tyr
 115 120 125

Gly Thr Pro Arg Ile Ile Arg Asp Asp Lys Asp Trp Leu Ile Asn Met
 130 135 140

Leu Ser Thr Leu Thr Asp Glu Glu Glu Glu Lys Arg Pro Glu Gly Glu
 145 150 155 160

aac ggg tct gga gat ago saa agl gta att tgg gtg gat aag ttg agg 336
asn cly ser cly asp scr gln scr val fte ser val asp lys leu arg

103

105

110

att gtg gca tgt aac tca aaa aag agc gag taa

369

Ile Val Ala Cys Asn Ser Lys Lys Ser Gln

115

120

<210> 97

<211> 122

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 97

Met Ala Val Pro Gly Tyr Tyr Glu Leu Tyr Arg Arg Ser Thr Ile Gly

1

5

10

15

Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile

20

25

30

Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val

35

40

45

Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly

50

55

60

Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val

65

70

75

80

Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln

85

90

95

Asn Gly Ser Gly Asp Ser Gln Ser Val Ile Ser Val Asp Lys Leu Arg

100

105

110

Ile Val Ala Cys Asn Ser Lys Lys Ser Glu

115

120

<210> 98

<211> 336

<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> CDS

<222> (1) .. (336)

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Met Thr Lys Ser Ile Tyr Ile Ile Ile Gly Tyr Met Leu His Asp Glu

1

5

10

15

gag ttt ttc tat ttc ttt ttt att tca ttc tat aca att tgg atc gtc 96

Glu Phe Phe Tyr Phe Phe Phe Ile Ser Phe Tyr Thr Leu Trp Ile Val

20

25

30

ttt ttt att ttg cac ttg agt ttc ttt tca aca tta tca ttc ggt ata 144

Phe Phe Leu Leu His Leu Ser Phe Phe Ser Thr Leu Ser Phe Gly Ile

35

40

45

ttt cac gat ttt gac acc gat gtc taa ata aaa gtc ggt aat tat att 192

Phe His Asp Phe Asp Thr Asp Val Tyr Ile Tyr Val Gly Asn Tyr Ile

50

55

60

ttg cat ttt ctc gaa ttg agt aaa aat agt aac att tta aag aat tct 240

Leu His Phe Leu Glu Ser Lys Asn Ser Asn Leu Leu Lys Asn Ser

65

70

75

80

tca gaa atg tta aag cat ttc cga ttg gca tca ttg atg tat atg taa 288

Ser Glu Met Leu Lys His Phe Arg Leu Ala Ser Leu Met Tyr Met Tyr

85

90

95

gta tat aat cag atg att tgc ccc tgg tta ctt ggc atc agg aat tag 336

Val Tyr Thr Glu Met Ile Cys Pro Ser Leu Leu Gly Ile Arg Asn

100

105

110

<210> 99

<211> 111

<212> PRT

<213> Saccharomyces cerevisiae

<400> 99

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Met Thr Lys Ser Ile Tyr Ile CLe CLe Gly Tyr Met Leu His Asp Glu
1             5             10             15

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Glu Phe Phe Tyr Phe Phe Phe Ile Ser Phe Tyr Thr Leu Trp Ile Val
                20                25                30

```

```

Phe Phe Leu Leu His Leu Ser Phe Phe Ser Thr Leu Ser Phe Gly CLe
35                40                45

```

```

Phe His Asp Phe Asp Thr Asp Val Tyr CLe Lys Val Gly Asn Tyr CLe
50                55                60

```

```

Leu His Phe Leu Glu Leu Ser Lys Asn Ser Asn Leu Leu Lys Asn Ser
65                70                75                80

```

```

Ser Glu Met Leu Lys His Phe Arg Leu Ala Ser Leu Met Tyr Met Tyr
85                90                95

```

```

Val Tyr Thr Gln Met Ile Cys Pro Ser Leu Leu Gly Ile Arg Asn
100                105                110

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<210> 100

<211> 991

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> {1} .. {801}

<400> 100

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Met Thr Leu Arg Ser Val Asn Arg Ala Val Thr Arg Ser Ile Leu Thr

1 5 10 15

acg ccc aag cca gcc gta gta aau tca tog tgg aga gtt ttt act gtt 96

Thr Pro Lys Pro Ala Val Val Lys Ser Ser Trp Arg Val Phe Thr Val

20 25 30

gct aac tct aag aga tgt ttc aca ucc gct gcc atc atg agg acc caa 144

Ala Asn Ser Lys Arg Cys Phe Thr Pro Ala Ala Ile Met Arg Asn Gln

35 40 45

gag acc caa aga gta gct gat att ttg caa tct gaa ttg aaa att gag 192

Glu Thr Gln Arg Val Gly Asp Ile Leu Gln Ser Glu Iau Lys Ile Glu

50 55 60

aag gaa aag tta cca gag tca acg tog tta gag tca ttt aat gac ttt 240

Lys Glu Thr Leu Pro Glu Ser Thr Ser Leu Asp Ser Phe Asn Asp Phe

65 70 75 80

ttg aac aaa taa aag ttc tca ttz gta gag cca ccc ggt aag aat gaa 288

Leu Asn Lys Tyr Lys Phe Ser Leu Val Glu Thr Pro Gly Lys Asn Glu

85 90 95

gct gaa ata gtt aga aga acc gaa taa gga gaa aca gtt cat gtt ttt 336

Ala Glu Ile Val Arg Arg Thr Glu Ser Gly Glu Thr Val His Val Phe

100 105 110

ttt gac gta gct cag att gct aat ctg cct tcc aac aac gcc atg gat 384

Phe Asp Val Ala Gln Ile Ala Asn Leu Pro Tyr Asn Asn Ala Met Asp

115 120 125

gaa aat acc gag caa aac gaa gac gcc att aat gag gat gal ttt gat 432

Glu Asn Thr Glu Gln Asn Glu Asp Gly Ile Asn Glu Asy Asp Phe Asp

130 135 140

240/762

gct tta tca gac aac ttt gcc aac gtt aat gtt gtt att tct aac gaa 480
 Ala Leu Ser Asp Asn Phe Ala Asn Val Asn Val Val Ile Ser Lys Glu
 145 150 155 160

agc gca agc gaa cct gca gtc tca ttt gaa tta cta atg aak tta dag 528
 Ser Ala Ser Glu Pro Ala Val Ser Phe Glu Leu Leu Met Asn Leu Gln
 165 170 175

gaa ggt tca ttt tat gtt gat agt gct act cca tac ccc tca gtt gat 576
 Glu Gly Ser Phe Tyr Val Asp Ser Ala Thr Pro Tyr Pro Ser Val Asp
 180 185 190

gct gct ttg aat cag tct gct gag ggc gaa ala aca aga gaa ttg gta 624
 Ala Ala Leu Asn Gln Ser Ala Glu Ala Glu Phe Thr Arg Glu Leu Val
 195 200 205

tac cat ggc cca cct ttt tca aac ttg gac gaa gaa cta cca gaa tat 672
 Tyr His Gly Pro Pro Phe Ser Asn Leu Asp Glu Glu Leu Gln Glu Ser
 210 215 220

ctg gaa gct tat ttg gaa agt aga ggt ctg aat gaa gag cta gcc tct 720
 Leu Glu Ala Tyr Leu Glu Ser Arg Gly Val Asn Glu Glu Leu Ala Ser
 225 230 235 240

ttc att agt gcc tat tcc gag ttc aaa gag aat aac gag tat att tct 768
 Phe Ile Ser Ala Tyr Ser Glu Phe Lys Glu Asn Asn Glu Tyr Ile Ser
 245 250 255

tgg ttg gaa aag atg aag aag ttt ttr cac taa 801
 Trp Leu Glu Lys Met Lys Lys Phe Phe His
 260 265

<210> 101

<211> 266

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 101

Met Phe Leu Arg Ser Val Asn Arg Ala Val Thr Arg Ser Ile Leu Thr
 1 5 10 15

Thr Pro Lys Pro Ala Val Val Lys Ser Ser Trp Arg Val Phe Thr Val
20 25 30

Ala Asn Ser Lys Arg Cys Phe Thr Pro Ala Ala Ile Met Arg Asn Glu
35 40 45

Glu Thr Gln Arg Val Gly Asp Ile Leu Gln Ser Glu Leu Lys Ile Glu
50 55 60

Lys Glu Thr Leu Pro Glu Ser Thr Ser Leu Asp Ser Phe Asn Asp Phe
65 70 75 80

Leu Asn Lys Tyr Lys Phe Ser Leu Val Glu Thr Pro Gly Lys Ser Glu
85 90 95

Ala Glu Thr Val Arg Arg Thr Glu Ser Gly Glu Thr Val His Val Phe
100 105 110

Phe Asp Val Ala Gln Ile Ala Asn Leu Pro Tyr Asn Asn Ala Met Asp
115 120 125

Glu Asn Thr Glu Gln Asn Glu Asp Gly Ile Asn Glu Asp Asp Phe Asp
130 135 140

Ala Leu Ser Asp Asn Phe Ala Asn Val Asn Val Val Ile Ser Lys Glu
145 150 155 160

Ser Ala Ser Glu Pro Ala Val Ser Phe Glu Leu Leu Met Asn Leu Gln
165 170 175

Glu Gly Ser Phe Tyr Val Asp Ser Ala Thr Pro Tyr Pro Ser Val Asp
130 185 190

Ala Ala Leu Asn Gln Ser Ala Glu Ala Glu Ile Thr Arg Glu Leu Val
195 200 205

Tyr His Gly Pro Pro Phe Ser Asn Leu Asp Glu Glu Leu Gln Glu Ser
210 215 220

Leu Glu Ala Tyr Leu Glu Ser Arg Gly Val Asn Glu Glu Leu Ala Ser
225 230 235 240

Phe Ile Ser Ala Tyr Ser Glu Phe Lys Glu Asn Asn Glu Tyr Ile Ser
245 250 255

Trp Leu Glu Lys Met Lys Lys Phe Phe His
260 265

<210> 102

<211> 366

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (966)

<430> 102

atg acg cgt ccc cca ttg gtt cgt gga atc ttt tgg tta ggt ctt tct 43
Met Thr Arg Pro Pro Leu Val Arg Gly Ile Phe Ser Leu Gly Leu Ser
1 5 10 15

gta gcc gtt ttg aaa ggt gtt gaa aaa aca gtt cgt aag cat ttg gaa 96
Val Ala Val Leu Tyr Gly Val Glu Lys Thr Val Arg Lys His Leu Glu

243/762

20	25	30	
aga gag gga tgg ata gag ccc cag aaa gtg gac tat gag tta att ttc			144
Arg Gln Gly Trp Ile Glu Pro Gln Lys Val Asp Tyr Glu Leu Ile Phe			
35	40	45	
act ata gat agg ttg aaa aac ttg gta gat aat aag cgt gag gct tta			192
Thr Ile Asp Arg Leu Lys Asn Leu Val Asp Asn Lys Arg Glu Ala Leu			
50	55	60	
act gcg gaa caa ccc gcc gct ggt gaa ctg agc tgg cgt aaa gta ttt			240
Thr Ala Glu Gln Pro Asp Ala Gly Glu Leu Ser Trp Arg Lys Val Phe			
65	70	75	80
aat ttc att tcc aga caa tcc agc gaa ttg gac aca cgc aca tac gtt			288
Asn Phe Ile Ser Arg Glu Ser Ser Glu Leu Asp Thr Arg Ile Tyr Val			
85	90	95	
ctt ata cta ctc cta tcc ttt cta cta cct ctg gag tgg act gta ctg			336
Leu Ile Leu Leu Leu Ser Phe Leu Leu Pro Ile Ala Trp Thr Val Leu			
100	105	110	
gac ggt gat cgc gag acc acg cta gaa cat aag gat aac gat tgt aat			384
Asp Gly Asp Arg Glu Thr Thr Leu Glu Asp Lys Asp Asn Asp Cys Asn			
115	120	125	
gta gat ctt att gaa aac gaa agg agg ctg aag cat tac aac gat ggt			432
Val Arg Leu Ile Glu Asn Glu Arg Arg Leu Lys His Tyr Asn Asp Gly			
130	135	140	
gaa aga gca gta ttg caa ttt ggt aaa aat aga tcc gaa cct att ata			480
Glu Arg Ala Val Leu Glu Phe Gly Lys Asn Arg Ser Glu Pro Ile Ile			
145	150	155	160
tta agc tat aag gac atg aac gtt ttg gaa ggg gaa cat gag ttt acc			528
Leu Ser Tyr Lys Asp Met Asn Val Leu Glu Gly Glu His Glu Phe Thr			
165	170	175	
tcc aaa gag gaa cac agt aac agc cat ttg aca agc aag agc gaa aat			576
Ser Lys Glu Glu His Ser Asn Ser His Leu Thr Ser Lys Ser Glu Asn			
180	185	190	

gca cta aac cca gta ggg agt gaa gat ttg tta ggt tgt cad ctg gaa	624
Ala Leu Asn Gln Val Gly Ser Glu Asp Leu Leu Gly Cys His Leu Glu	
195 200 205	
aag cca ttg gaa gaa gac aaa aat gaa cgg aat gga gaa gca gac ggt	672
Lys Gln Leu Glu Gln Asp Lys Asn Glu Pro Asn Gly Glu Ala Asp Gly	
210 215 220	
gaq gat gat aat aac cgg gaa aag gat tgc agc lcc agt tca gaa gtt	720
Glu Asp Asp Asn Asn Arg Glu Lys Asp Cys Ser Ser Ser Ser Glu Val	
225 230 235 240	
gaq tgg cag agt aaa tgc cga aag gaa agt act gca gag cct gac tct	768
Glu Ser Glu Ser Lys Cys Arg Tyr Glu Ser Thr Ala Glu Pro Asp Ser	
245 250 255	
ctc tca cgg gat acc aga aca acc tct tcc ctt aaa tca agt acc tca	816
Leu Ser Arg Asp Thr Arg Thr Thr Ser Ser Leu Lys Ser Ser Thr Ser	
260 265 270	
tto ccc ata tca ttc aag ggc tgg ata gac ctt aag tgg tta aac cag	864
Phe Pro Ile Ser Phe Lys Gly Ser Ile Asp Leu Lys Ser Ser Asn Gln	
275 280 285	
act tca tca ttg ttg cat ata caa gta tct ccc acc aaa tct agt aat	912
Pro Ser Ser Leu Leu His Ile Gln Val Ser Pro Thr Lys Ser Ser Asn	
290 295 300	
cta gat gca cca gtg aac act gaa caa gaa tac tct caa taa ttt aga	960
Leu Asp Ala Gln Val Asn Thr Glu Gln Ala Tyr Ser Gln Pro Phe Arg	
305 310 315 320	
tac taa	966
Tyr	

<210> 103

<211> 321

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 103

Met Thr Arg Pro Pro Leu Val Arg Gly Ile Phe Ser Leu Gly Leu Ser
 1 5 10 15

Val Ala Val Leu Lys Gly Val Glu Lys Thr Val Arg Lys His Leu Glu
 20 25 30

Arg Glu Gly Trp Ile Glu Pro Gln Lys Val Asp Tyr Glu Leu Ile Phe
 35 40 45

Thr Ile Asp Arg Leu Lys Asn Leu Val Asp Asn Lys Arg Glu Ala Leu
 50 55 60

Thr Ala Glu Gln Pro Asp Ala Gly Glu Leu Ser Trp Arg Lys Val Phe
 65 70 75 80

Asn Phe Ile Ser Arg Glu Ser Ser Glu Leu Asp Thr Arg Ile Tyr Val
 85 90 95

Leu Ile Leu Leu Leu Ser Phe Leu Leu Pro His Ala Trp Thr Val Leu
 100 105 110

Asp Gly Asp Arg Glu Thr Thr Leu Glu Asp Lys Asp Asn Asp Cys Asn
 115 120 125

Val Asp Leu Ile Glu Asn Glu Arg Arg Leu Lys His Tyr Asn Asp Gly
 130 135 140

Glu Arg Ala Val Leu Gln Phe Gly Lys Asn Arg Ser Glu Pro Ile Ile
 145 150 155 160

Leu Ser Tyr Lys Asp Met Asn Val Leu Glu Gly Glu His Glu Phe Thr
 165 170 175

Ser Lys Glu Glu His Ser Asn Ser His Leu Thr Ser Lys Ser Glu Asn
 180 185 190

Ala Leu Asn Gln Val Gly Ser Glu Asp Leu Leu Gly Cys His Leu Glu
 195 200 205

Lys Gln Leu Glu Glu Asp Lys Asn Glu Pro Asn Gly Glu Ala Asp Gly
 210 215 220

Glu Asp Asp Asn Asn Arg Glu Lys Asp Cys Ser Ser Ser Ser Glu Val
 225 230 235 240

Glu Ser Gln Ser Lys Cys Arg Lys Glu Ser Thr Ala Glu Pro Asp Ser
 245 250 255

Leu Ser Arg Asp Thr Arg Thr Thr Ser Ser Leu Lys Ser Ser Thr Ser
 260 265 270

Phe Pro Ile Ser Phe Lys Gly Ser Ile Asp Leu Lys Ser Leu Asn Gln
 275 280 285

Pro Ser Ser Leu Leu His Ile Gln Val Ser Pro Thr Lys Ser Ser Asn
 290 295 300

Leu Asp Ala Gln Val Asn Thr Glu Gln Ala Tyr Ser Gln Pro Phe Arg
 305 310 315 320

Tyr

<210> 104
 <211> 504
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(504)

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 1 5 10 15
 ttt gca tct ggt tac atg ttc tgg caa ggc tta gcc att gct act aac 95
 Phe Ala Ser Ala Tyr Met Phe Trp Gln Gly Leu Ala Ile Ala Thr Asn
 20 25 30
 ago gct tct cag att gtg gtg gty tta taa ggc taa atg gaa cca gct 144
 Ser Ala Ser Pro Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala
 35 40 45
 ttc caa agg ggt gaa atc ctt ttc cta tgg aat aga aat act ttc aac 192
 Phe Gln Arg Gly Asp Ile Leu Phe Leu Trp Asn Arg Asn Thr Phe Asn
 50 55 60
 caa gta ggt gat gtc gtg gtg tat gag gta gaa ggg aaa caa atc ccc 240
 Gln Val Gly Asp Val Val Val Tyr Glu Val Glu Gly Lys Gln Ile Pro
 65 70 75 80
 att gtg cat aga gtt ttg agg caa cat aac aat cag gcg gac aag caa 288
 Ile Val His Arg Val Leu Arg Gln His Asn Asn His Ala Asp Lys Gln
 85 90 95
 ttc ctc ctg acc aaa ggt gaa aat aac gcc ggc aat gat atc tca cta 336
 Phe Leu Leu Thr Lys Gly Asp Asn Asn Ala Gly Asn Asp Ile Ser Leu
 100 105 110
 tat gct aat aag aaa att tac ttg aac aag tca aag gag att gta ggg 384

Tyr Ala Asn Lys Lys Ile Tyr Leu Asn Tyr Ser Lys Gln Ile Val Gly
 115 120 125

acc gtc aag ggc tac ttt cca cca cta ggg tac att acg att tgg att 132
 Thr Val Lys Gly Tyr Phe Pro Gln Leu Gly Tyr Ile Thr Ile Trp Ile
 130 135 140

agc gag aac aaa tat gcc aag ttg gca ttg tta ggt acg ttg ggg ttg 480
 Ser Glu Asn Lys Tyr Ala Lys Phe Ala Leu Leu Gly Met Leu Gly Leu
 145 150 155 160

agt gcc ctg ctg ggg gcc gag tag 504
 Ser Ala Leu Leu Gly Gly Glu
 165

<210> 105
 <211> 15'
 <212> DRT
 <213> *Saccharomyces cerevisiae*

<400> 105

Met Asn Leu Arg Phe Glu Asn Gln Lys Leu Leu Asn Val Cys Phe Leu
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Phe Ala Ser Ala Tyr Met Phe Trp Gln Gly Leu Ala Ile Ala Thr Asn
 20 25 30

Ser Ala Ser Pro Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala
 35 40 45

Phe Gln Arg Gly Asp Ile Leu Phe Leu Trp Asn Arg Asn Thr Phe Asn
 50 55 60

Gln Val Gly Asp Val Val Val Tyr Glu Val Glu Gly Lys Gln Ile Pro
 65 70 75 80

Ile Val His Arg Val Leu Arg Gln His Asn Asn His Ala Asp Lys Glu
85 90 95

Phe Leu Leu Thr Lys Gly Asp Asn Asn Ala Gly Asn Asp Ile Ser Leu
100 105 110

Tyr Ala Asn Lys Lys Ile Tyr Leu Asn Lys Ser Lys Glu Ile Val Gly
115 120 125

Thr Val Lys Gly Tyr Phe Pro Gln Leu Gly Tyr Ile Thr Ile Trp Ile
130 135 140

Ser Glu Asn Lys Tyr Ala Lys Phe Ala Leu Leu Gly Met Leu Gly Leu
145 150 155 160

Ser Ala Leu Leu Gly Gly Gln
165

<210> 106
<211> 2490
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
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<222> (1)..(2490)

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1 5 10 15
tcc tgc agc aat aaa ctg ctg ata gta cca acc ggt caa agc tcc tct 96

250762																	
Ser	Cys	Ser	Asn	Tyr	Val	Ileu	Phe	Val	Pro	Thr	Gly	Gln	Ser	Ser	Ser		
20					25					30							
aac	gca	atc	act	gat	ttc	tct	glu	aga	aag	gag	cat	gct	tgc	gnt	aga	144	
Asn	Ala	Ile	Thr	Asp	Phe	Ser	Val	Arg	Iys	Ala	His	Ala	Tys	Asp	Arg		
35					40					45							
tgc	aga	ctg	aaa	aaa	atc	aag	tgt	gac	ggt	tta	aaa	cag	aac	tgt	toa	192	
Cys	Arg	Leu	Lys	Lys	Ile	Lys	Cys	Asp	Gly	Leu	Lys	Pro	Asn	Cys	Ser		
50					55					60							
aac	tgt	gag	aaa	att	gac	tto	out	tgu	aaa	acc	tgc	gat	aaa	ctg	tog	240	
Asn	Cys	Ala	Lys	Ile	Asp	Phe	Pro	Cys	Lys	Thr	Ser	Asp	Lys	Leu	Ser		
65					70					75					80		
agg	aga	ggt	ctt	cca	aag	ggg	tat	aca	gaa	cta	cta	gaa	aaa	gag	gtc	288	
Arg	Arg	Gly	Leu	Pro	Lys	Gly	Tyr	Thr	Glu	Leu	Leu	Glu	Lys	Glu	Val		
85					90					95							
gtc	cgt	tgg	aca	aat	atg	aat	ggc	agt	tcc	agc	gcc	aat	gca	aat	tct	336	
Val	Arg	Ileu	Thr	Asn	Met	Asn	Ala	Ser	Ser	Ser	Ala	Asn	Ala	Asn	Ser		
100					105					110							
aat	tgg	cng	ttc	att	aat	gat	aca	ttt	tat	tgt	ttt	gat	aat	tac	aac	384	
Asn	Leu	Pro	Phe	Ile	Asn	Asp	Thr	Phe	Tyr	Cys	Phe	Asp	Asn	Tyr	Asn		
115					120					125							
act	cag	tct	gaa	aat	caa	agg	ttt	ttg	gga	cat	ttg	aca	tgg	cat	att	432	
Thr	Glu	Ser	Glu	Asn	Gln	Arg	Phe	Leu	Gly	His	Leu	Thr	Trp	Asn	Ile		
130					135					140							
cta	act	aat	act	ttt	ctt	act	caa	aaa	gca	gta	ggt	ttt	aca	gac	gnt	480	
Leu	Thr	Asn	Thr	Phe	Pro	Thr	Gln	Lys	Ala	Val	Val	Phe	Thr	Asp	Asp		
145					150					155					160		
cga	aat	aat	att	gat	cta	caa	ctg	caa	ctg	tta	aca	aat	lll	ttg	aac	528	
Arg	Asn	Asn	Ile	Asp	Leu	Gln	Leu	Gln	Leu	Leu	Thr	Asn	Phe	Leu	Asn		
165					170					175							
ctg	aat	ggc	gac	ttt	act	cat	ctc	cca	aat	ttt	ctt	tta	ctt	aaa	tat	576	
Ileu	Asn	Gly	Asp	Phe	Asn	His	Leu	Pro	Asn	Phe	Leu	Leu	Leu	Lys	Tyr		
180					185					190							

Fig. 10a: E. coli sequence alignment

gat tat aac ctt cag ttt ttg aaa aat ttg ttg tct gtc att att aaa	624
Asp Tyr Asn Leu Gln Phe Leu Lys Asn Leu Leu Ser Val Ile Ile Lys	
195 200 205	
gat ttt ttt aac agg caa aat tct ttg cta ctt ctt tta tac cct aca	672
Asp Phe Phe Lys Arg Gln Asn Ser Leu Leu Leu Leu Leu Tyr Pro Thr	
210 215 220	
aat tta tgg aac aat ttg cta tta gac aag att aat tca acc gca atg	720
Asn Leu Trp Lys Asn Leu Leu Leu Asp Lys Ile Asn Ser Thr Ala Met	
225 230 235 240	
aaa ggt gaa cgc ata aat cta ctg gcg tta ctt tat att att caa ttt	768
Thr Gly Glu Pro Ile Thr Ser Leu Ala Leu Ser Tyr Ile Ile Gln Phe	
245 250 255	
aat tgg tct tgc ttt gat gat ttc aag ctt ttt aac gtc aag aag ctt	816
Thr Trp Ser Cys Phe Asp Asp Phe Lys Leu Phe Lys Val Thr Lys Leu	
260 265 270	
atc gll lut cly aca acc aac ayc aay tta gac ttg aac gtt ttg caa	864
Ile Val Ser Ser Thr Thr Asn Ser Lys Ser Asp Leu Lys Val Leu Gln	
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ttg gtt aac tta tcc atc ttt tat ttt atg ggc ggc lut gtt gac lut	912
Leu Val Asn Leu Ser Ile Phe Tyr Phe Met Gly Ala Ser Val Asp Ser	
290 295 300	
tgt aaa agt aaa ago tgc tta aca gaa cat tca aat gta aat tca gta	960
Cys Lys Ser Lys Ser Ser Leu Thr Glu His Ser Asn Val Asn Ser Val	
305 310 315 320	
ata tgg aac aat gat ttg cta aac cta aac ttt aca aat att ttg aat	1008
Ile Trp Thr Asn Asp Leu Leu Asn Leu Asn Phe Thr Asn Ile Leu Asn	
325 330 335	
atg gga ttg tac atc aat ccc aca aat tta uil cct ata leu ggc aac	1056
Met Gly Ser Tyr Ile Asn Pro Lys Asn Leu Ile Pro Ile Ser Gly Asn	
340 345 350	
aat aat aat aat aac tct aat gaa gag gat gat aga ata gtc aca ttt	1104

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 Trp Cys Phe Gln Phe Leu Ser Ser Trp Trp Ser Leu Ile Gln Gly Leu
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 Pro Lys Ser Asn Phe Leu Thr Glu Glu Phe Gln Pro Lys Ser Ile Ser
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gtt cta gaa atc ccc agg ctg aag ccc ttt gaa att tgg tta aac ttc 1248
 Val Leu Glu Ile Pro Arg Leu Lys Pro Phe Glu Ile Leu Leu Asn Phe
 405 410 415

atc ata tat tct ttg gat gga tgt aat ttg ttg aat atc taa taa tta 1296
 Ile Ile Tyr Ser Leu Asp Gly Cys Asn Leu Leu Asn Ile Ser Ser Leu
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aat gtt tgg gac cca aat ttc caa ttt ttc cag aat gaa ctg gaa agc 1344
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ttt aaa aaa aat tta tta ctg tgg aac ctt tat cac aat ttg agt gat 1392
 Phe Lys Lys Asn Leu Leu Leu Trp Asn Leu Tyr His Asn Leu Ser Asp
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cag gaa aac ttc aga ttc tta aca tcc agt taa aat aag aac cta aca 1440
 His Asp Asn Phe Arg Phe Leu Thr Ser Ser Ser Asn Lys Lys Leu Thr
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aca aat tta cta ctt aag aat ttg acg ggt cta aat cac aac ctc aat 1488
 Thr Asn Leu Leu Leu Lys Asn Leu Thr Thr Gln Asn His Lys Leu Asn
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caa cct gat ttt gtg gag att caa tta act tta ttt taa tgg agt tta 1536
 Gln Pro Asp Phe Val Gln Ile Gln Leu Thr Leu Phe Tyr Leu Ser Leu
 500 505 510

aac tta atg act tta aag gaa ggc gac caa gat ttg aag aaa gag gat 1584
 Lys Leu Met Thr Leu Lys Glu Gly Asp Gln Asp Leu Lys Lys Glu Asp
 515 520 525

cac tgg agt ttt ggc tcc aat ttc cta gat ggg tca cca tac gat ttt 2112

His Ser Ser Ser Asn Ser Asn Phe Leu Asp Ala Ser Pro Tyr Asp Phe		
690	695	700
Asn Lys Ile Phe Met Asn Asn Phe Glu Asn Tyr Asp Tyr Glu Thr Asp		2160
705	710	715 720
Glu Gly Tyr Ala Glu Asp Asp Asp Glu Glu Asp Ser Asp Ser Asp Asn		2208
725	730	735
Arg Trp Cys Cys Gln Asn Asn Arg Asn Asn Asn Asn Asn Asn		2256
Ser Leu Pro Leu Glu Ile Pro Phe Lys Lys Ser Lys Asn Lys Cys Lys		
740	745	750
Asn Arg Asn Lys Glu Leu Ser Glu Arg Leu Ser Leu Phe Glu Asn Arg		2304
755	760	765
Glu Arg Asn Lys Glu Leu Ser Glu Arg Leu Ser Leu Phe Glu Asn Arg		2352
770	775	780
Pro Asp Ser Pro Ser Val Thr Ser Ser Lys Lys Lys Tyr Leu Asp His		2400
785	790	795 800
Asn Ile Leu Asp Asn Arg Asp Ile Val Ser Asn His Asp Ser Ser Lys		2448
805	810	815
Gln Lys Phe Lys Ile Glu Asn Ile Leu Asn Ser Thr Phe		2496
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Asn Ala Ile Thr Asp Phe Ser Val Arg Lys Ala His Ala Cys Asp Arg
 35 40 45

Cys Arg Asn Lys Lys Ile Lys Cys Asp Gly Leu Lys Pro Asn Cys Ser
 50 55 60

Asn Cys Ala Lys Ile Asp Phe Pro Cys Lys Thr Ser Asp Lys Asn Ser
 65 70 75 80

Arg Arg Gly Leu Pro Lys Gly Tyr Thr Glu Leu Leu Glu Lys Glu Val
 85 90 95

Val Arg Leu Thr Asn Met Asn Ala Ser Ser Ser Ala Asn Ala Asn Ser
 100 105 110

Asn Asn Pro Phe Ile Asn Asp Thr Phe Tyr Cys Phe Asp Asn Tyr Asn
 115 120 125

Thr Gln Ser Glu Asn Gln Arg Phe Leu Gly His Leu Thr Trp Asn Ile
 130 135 140

Leu Thr Asn Thr Phe Pro Thr Glu Lys Ala Val Val Phe Thr Asp Asp
 145 150 155 160

Arg Asn Asn Ile Asp Leu Gln Leu Gln Leu Leu Thr Asn Phe Asn Asn

FIG. 10: Amino acid sequence of the protein.

165

170

175

Leu Asn Gly Asp Phe Asn His Leu Pro Asn Phe Leu Leu Leu Lys Tyr
180 185 190

Asp Tyr Asn Leu Gln Phe Leu Lys Asn Leu Leu Ser Val Ile Ile Lys
195 200 205

Asp Phe Phe Lys Arg Gln Asn Ser Leu Leu Leu Phe Leu Tyr Pro Thr
210 215 220

Asn Leu Trp Lys Asn Leu Leu Leu Asn Lys Ile Asn Ser Thr Ala Met
225 230 235 240

Thr Gly Glu Pro Ile Thr Leu Leu Ala Leu Leu Tyr Ile Ile Gln Phe
245 250 255

Thr Trp Ser Cys Phe Asp Asp Phe Lys Leu Phe Lys Val Thr Lys Leu
260 265 270

Ile Val Ser Leu Thr Thr Asn Ser Lys Leu Asp Leu Lys Val Leu Gln
275 280 285

Leu Val Asn Leu Ser Ile Phe Tyr Phe Met Gly Ala Ser Val Asp Ser
290 295 300

Cys Lys Ser Lys Ser Ser Leu Thr Glu His Ser Asn Val Asn Ser Val
305 310 315 320

Ile Trp Thr Asn Asp Leu Leu Asn Leu Asn Phe Thr Asn Ile Leu Asn
325 330 335

Protein Data Bank (PDB) Entry: 1A2Y

Met Gly Leu Tyr Ile Asn Pro Lys Asn Leu Ile Pro Ile Ser Gly Asn
310 345 350

Asn Asn Asn Asn Lys Ser Asn Glu Glu Asp Asp Arg Ile Val Thr Phe
355 360 365

Trp Cys Phe Gln Phe Leu Ser Ser Trp Trp Ser Leu Ile Gln Gly Leu
370 375 380

Pro Lys Ser Asn Phe Asn Thr Glu Glu Phe Glu Pro Lys Ser Ile Ser
385 390 395 400

Val Leu Glu Ile Pro Arg Leu Lys Pro Phe Glu Ile Leu Leu Asn Phe
405 410 415

Ile Ile Tyr Ser Leu Asp Gly Cys Asn Leu Leu Asn Ile Ser Ser Leu
420 425 430

Asn Val Ser Asp Pro Asn Phe Gln Phe Phe Gln Asn Glu Leu Glu Ser
435 440 445

Phe Lys Lys Asn Leu Leu Leu Trp Asn Leu Tyr His Asn Leu Ser Asp
450 455 460

His Asp Asn Phe Arg Phe Leu Thr Ser Ser Ser Asn Lys Lys Leu Thr
465 470 475 480

Thr Asn Leu Leu Leu Lys Asn Leu Thr Gly Leu Asn His Lys Leu Asn
485 490 495

Fig. 6. Amino acid sequence of the protein.

Gln Pro Asp Phe Val Glu Ile Gln Leu Thr Leu Phe Tyr Leu Ser Leu
500 503 510

Lys Leu Met Thr Leu Lys Glu Gly Asp Gln Asp Leu Lys Lys Glu Asn
515 520 525

Ile Ser Asn Glu Ile Leu Ser Leu Tyr Phe Leu Ile Leu Thr Asp Asp
530 535 540

Asn Asn Asn Asp Asp Asn Gln Gln Leu Gln Pro Gln Gln Leu Asn Leu
545 550 555 560

Tyr His Phe Thr Pro Phe Asn Ser Ile Asp Ile Ile Asp Leu Cys Leu
565 570 575

Asn Asn Leu Asn Asn Trp Ser Ser Leu Ser Leu Lys Tyr Glu Ser Gly Gln
580 585 590

Asn Gln Pro His Ser Ser Lys Ile Lys Phe Glu Lys Phe Gln Asn Phe
595 600 605

Leu Asn His Trp Cys Pro Ile Trp Tyr Tyr Asp Glu Phe Ser Thr Asn
610 615 620

Pro Phe Leu Gln Ile Leu Lys Ile Asn Phe Lys Leu Leu Pro Phe Glu
625 630 635 640

Thr Ile His Tyr Ser Gln Glu Glu Gln Arg Leu Leu Ile Ser Leu Asn
645 650 655

Lys Leu Arg Tyr Leu Asp Ala Val Ser Ser Phe Asn Ser Ser Ser Val
660 665 670

Lys Ser Asn Phe Ala Ser Lys Val Asn Thr Gln Leu Asn Leu Gln
 675 680 685

His Ser Ser Ser Asn Ser Asn Phe Leu Asp Ala Ser Pro Tyr Asp Phe
 690 695 700

Asn Lys Ile Phe Met Asn Asn Phe Gln Asn Tyr Asp Tyr Glu Thr Asp
 705 710 715 720

Glu Gly Tyr Ala Glu Asp Asp Asp Gln Glu Asp Ser Asp Ser Asp Asn
 725 730 735

Ser Leu Pro Leu Gln Ile Pro Phe Lys Lys Ser Lys Asn Lys Cys Lys
 740 745 750

Asn Arg Asn Lys Gln Leu Ser Gln Arg Leu Ser Leu Phe Glu Asn Arg
 755 760 765

Asp Ser Asn Ser Val Asp Phe Asn Thr Asp Thr Asn Leu Asn Leu Asn
 770 775 780

Pro Asp Ser Pro Ser Val Thr Ser Ser Lys Lys Lys Tyr Leu Asp His
 785 790 795 800

Ile Ile Leu Asp Asn Arg Asp Ile Val Ser Asn His Asp Ser Ser Lys
 805 810 815

Gln Lys Phe Lys Ile Gln Asn Ile Leu Asn Ser Thr Phe
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Seq. ID No. 1

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 agy ccc aga gcu ttt att agt gga ata gtt gcc ctt att atc atc ggc 86
 Arg His Arg Ala Phe Ile Ser Gly Ile Val Ala Leu Ile Ile Ile Gly
 20 25 30
 acc ttc ttc ctg act tgg ggt ctg cag cca gca cca cct cat gag gca 144
 Thr Phe Phe Leu Thr Ser Gly Leu His Pro Ala Pro Pro His Glu Ala
 35 40 45
 aag cgt cca cag cat gga aaa ggt ccc atg cag tca ccc aaa tgt gag 192
 Lys Arg Pro His His Gly Lys Gly Pro Met His Ser Pro Lys Cys Glu
 50 55 60
 aag att gan cca tta agt cca tca ttc aza cat tcc gtc gac aca att 240
 Lys Ile Glu Pro Leu Ser Pro Ser Phe Lys His Ser Val Asp Thr Ile
 65 70 75 80
 ctc cat gcc cct gcc ttt aga aac ago tcc att gag aac ctg tcc aat 288
 Leu His Asp Pro Ala Phe Arg Asn Ser Ser Ile Glu Lys Leu Ser Asn
 85 90 95
 gct gtt aga atc ccc act gta gtc cca gac aaa aac ccc aag ccc gca 336
 Ala Val Arg Ile Pro Thr Val Val Glu Asp Lys Asn Pro Asn Pro Ala
 100 105 110
 gat gat cgg gat ttc tat aag cat ttt tat gaa cta cag gac cat ttt 384
 Asp Asp Pro Asp Phe Tyr Lys His Phe Tyr Glu Leu His Asp Tyr Phe
 115 120 125

gag aag act ttc cct aat att caa aag cat ttg aaa ttg gag aaa gtc

422

Gln Tyr Thr Phe Pro Asn Ile His Lys His Leu Lys Leu Glu Lys Val

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140

aat gag ctg ggt ctt cta cac aca tgg gaa ggt tot gat cct gat cta

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Asn Glu Leu Gly Leu Leu Tyr Thr Trp Glu Gly Ser Asp Pro Asp Leu

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160

aaa caa tta ttg tta atg gcc cat caa gat gtt gta cct gta aac aac

528

Lys Pro Leu Leu Leu Met Ala His Gln Asp Val Val Pro Val Asn Asn

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175

gaa aot tta caa tcc tgg aag ttc cct caa ttt tct qgt cac tac gnt

376

Glu Thr Leu Ser Ser Trp Lys Phe Pro Pro Phe Ser Gly His Tyr Asp

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cca gaa ada gat ttt gtt tgg ggg cgt ggt tot aac gat tgt aag aac

624

Pro Glu Thr Asp Phe Val Trp Gly Arg Gly Ser Asn Asp Cys Lys Asn

195

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ttg tta att gcc aag ttt gaa gct aac gaa caa ctg ttg ata gat gga

572

Leu Leu Ile Ala Glu Phe Glu Ala Ile Glu Gln Leu Leu Ile Asp Gly

210

215

220

ctc aag ccc aac aga act att gtt atg tgg ctt ggt ttc gat gaa gaa

720

Phe Lys Pro Asn Arg Thr Ile Val Met Ser Leu Gly Phe Asp Glu Glu

225

230

235

240

gca ago ggc aac ctc ggt gct gac ago tta gcc tca ttt ctt cac gaa

760

Ala Ser Gly Thr Leu Gly Ala Ala Ser Leu Ala Ser Phe Leu His Glu

245

250

255

aga tal ggt gat gat ggt att tac agt atc alc gac gag ggt gaa ggt

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Arg Tyr Gly Asp Asp Gly Ile Tyr Ser Ile Ile Asp Glu Gly Glu Gly

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265

270

atc atg gaa gtc gac aag gat gtc ttt gtt gcc aot caa atc aac gct

864

Ile Met Glu Val Asp Lys Asp Val Phe Val Ala Thr Pro Ile Asn Ala

275

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285

gaa aaa ggc tat gtc gac ttc gaa gtc agt att cta ggc cat ggt ggt

912

Glu Iys Gly Tyr Val Asp Phe Glu Val Ser Ile Leu Gly His Gly Gly	
290	295 300
cat tcc tct gtc cca cct gat cat acc aca alc ygt atc get tca gaa	960
His Ser Ser val Pro Pro Asp His Thr Thr Ile Gly Ile Ala Ser Glu	
305	310 315 320
ctg att act gaa ttt gaa gcc aac cca ttt gac tac gaa ttt gag ttt	1008
Leu Ile Thr Glu Phe Glu Ala Asn Pro Phe Asp Tyr Glu Phe Glu Phe	
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gac aat cca atc tat gga ttg ttg aca tgt got got gaa cat tct aaa	1056
Asp Asn Pro Ile Tyr Gly Leu Leu Thr Cys Ala Ala Glu His Ser Tyr	
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tct tta agt aag gat gtg aag aag aca att ttg ggc gaa aca ttc tgt	1104
Ser Leu Ser Lys Arg Val Lys Lys Thr Ile Leu Gly Ala Pro Phe Cys	
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cct age agt aag gac aag ctc gtt gag tac att tcc aac aca taa cat	1152
Pro Arg Arg Lys Asp Lys Leu Val Glu Tyr Ile Ser Asn Gln Ser His	
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Leu Arg Ser Leu Ile Arg Thr Thr Glu Ala Val Asp Ile Ile Asn Gly	
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ggt gat aaa got aat gct ctg ccc gaa aat acc aga ttc ttg atc aat	1248
Gly Val Lys Ala Asn Ala Leu Pro Glu Thr Thr Arg Phe Leu Ile Asn	
405	410 415
cac aga att aat tta cat tct tct gtg got gaa gtc ttt gaa aga aac	1296
His Arg Ile Asn Leu His Ser Ser Val Ala Glu Val Phe Glu Arg Asn	
420	425 430
ata gaa tat gag aaa aag att gct gag aag tat ggc tat ggt tta tct	1344
Ile Glu Tyr Ala Lys Lys Ile Ala Glu Lys Tyr Gly Tyr Gly Leu Ser	
435	440 445
aag aac ggt gac gat tac att atc cct gaa acc gag tta ggt aca att	1392
Lys Asn Gly Asp Asp Tyr Ile Ile Pro Glu Thr Glu Leu Gly His Ile	
450	455 460

Fig. 4. Sequence alignment of the protein sequences.

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gac att act ctc ttg aga gaa ttg gaa deu gca cca ctt tgg cca agt      1440
Asp Ile Thr Leu Leu Arg Glu Leu Glu Pro Ala Pro Leu Ser Pro Ser
465              470              475              480

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tca ggc cct ggt tgg gac att ttg gca ggt act att caa gat gtt ttt      1488
Ser Gly Pro Val Trp Asp Ile Leu Ala Gly Thr Ile Glu Asp Val Phe
485              490              495

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gaa aac ggt gtt cta caa aac aac gaa gag ttc tat gcy act act ggt      1536
Glu Asn Gly Val Leu Glu Asn Asn Glu Glu Phe Tyr Val Thr Thr Gly
500              505              510

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tta ttc tct ggt aac acc gat act aaa tac tac tgg aal ttg tcc aag      1584
Leu Phe Ser Gly Asn Thr Asp Thr Lys Tyr Tyr Trp Asn Leu Ser Lys
515              520              525

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530              535              540

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con ttg cat tgg gtt aat gaa ccc ptg gat gtc cca ggt cat tta tcl      1680
Thr Leu His Ser Val Asn Glu His Val Asp Val Pro Gly His Leu Ser
545              550              555              560

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gac att ggc ttt gtt tac gag tat atc gtt aat gtt aac gaa tac gct      1728
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<212> PRT

<213> Saccharomyces cerevisiae

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10

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Fig. 1: Amino acid sequence of the protein

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Thr Phe Phe Leu Thr Ser Gly Leu His Pro Ala Pro Pro His Glu Ala
35 40 45

Lys Arg Pro His His Gly Lys Gly Pro Met His Ser Pro Lys Cys Glu
50 55 60

Lys Ile Glu Pro Leu Ser Pro Ser Phe Lys His Ser Val Asp Thr Ile
65 70 75 80

Leu His Asp Pro Ala Phe Arg Asn Ser Ser Ile Glu Lys Leu Ser Asn
85 90 95

Ala Val Arg Ile Pro Thr Val Val Glu Asp Lys Asn Pro Asn Pro Ala
100 105 110

Asp Asp Pro Asp Phe Tyr Lys His Phe Tyr Glu Leu His Asp Tyr Phe
115 120 125

Glu Lys Thr Phe Pro Asn Ile His Lys His Leu Lys Leu Glu Lys Val
130 135 140

Asn Glu Leu Gly Leu Leu Tyr Thr Trp Glu Gly Ser Asp Pro Asp Leu
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Lys Pro Leu Leu Leu Met Ala His Gln Asp Val Val Pro Val Asn Asn
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Glu Thr Leu Ser Ser Trp Lys Phe Pro Pro Phe Ser Gly His Tyr Asp

Protein Data Bank

265/762

190

185

190

Pro Glu Thr Asp Phe Val Trp Gly Arg Gly Ser Asn Asp Cys Lys Asn
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Phe Lys Pro Asn Arg Thr Ile Val Met Ser Leu Gly Phe Asp Glu Glu
225 230 235 240

Ala Ser Gly Thr Leu Gly Ala Ala Ser Leu Ala Ser Phe Leu His Glu
245 250 255

Arg Tyr Gly Asp Asp Gly Ile Tyr Ser Ile Ala Asp Glu Gly Glu Gly
260 265 270

Ile Val Glu Val Asp Lys Asp Val Phe Val Ala Thr Pro Ile Asn Ala
275 280 285

Glu Lys Gly Tyr Val Asp Phe Glu Val Ser Ile Leu Gly His Gly Gly
290 295 300

His Ser Ser Val Pro Pro Asp His Thr Thr Ile Gly Ile Ala Ser Glu
305 310 315 320

Leu Ile Thr Glu Phe Glu Ala Asn Pro Phe Asp Tyr Glu Phe Glu Phe
325 330 335

Asp Asn Pro Ile Tyr Gly Leu Leu Thr Cys Ala Ala Glu His Ser Lys
340 345 350

Ser Leu Ser Lys Asp Val Lys Lys Thr Ile Leu Gly Ala Pro Phe Cys
355 360 365

Pro Arg Arg Lys Asp Lys Leu Val Glu Tyr Ile Ser Asn Gln Ser His
370 375 380

Leu Arg Ser Leu Ile Arg Thr Thr Gln Ala Val Asp Ile Ile Asn Gly
385 390 395 400

Gly Val Lys Ala Asn Ala Leu Pro Glu Thr Thr Arg Phe Leu Ile Asn
405 410 415

His Arg Ile Asn Leu His Ser Ser Val Ala Gly Val Phe Glu Arg Asn
420 425 430

Ile Glu Tyr Ala Lys Lys Ile Ala Glu Lys Tyr Gly Tyr Gly Leu Ser
435 440 445

Lys Asn Gly Asp Asp Tyr Ile Ile Pro Cys Thr Glu Leu Gly His Ile
450 455 460

Asp Ile Thr Asn Lys Arg Glu Leu Glu Pro Ala Pro Leu Ser Pro Ser
465 470 475 480

Ser Gly Pro Val Trp Asp Ile Leu Ala Gly Thr Ile Gln Asp Val Phe
485 490 495

Glu Asn Gly Val Leu Glu Asn Asn Glu Cys Phe Tyr Val Thr Thr Gly
500 505 510

Leu Phe Ser Gly Asn Thr Asp Thr Lys Tyr Tyr Trp Asn Leu Ser Lys

515

520

525

Asn Ile Tyr Arg Phe Val Gly Ser Ile Ile Asp Ile Asp Leu Leu Lys
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Thr Leu His Ser Val Asn Glu His Val Asp Val Pro Gly His Leu Ser
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 Asp Tyr Pro Lys Glu Phe Val Ser Phe Leu Asn Ser Ser His Ser Pro
 20 25 30

tac cat aca gtt cat aac atc aaa aag cat ctg gtg tca aat ggc ttc 144
 Tyr His Thr Val His Asn Ile Lys Lys His Leu Val Ser Asn Gly Phe
 35 40 45

aac gag ttg agc gaa cgt gac tgg tgg got ggc cag gtc gaa caa aac 192
 Lys Glu Leu Ser Glu Arg Asp Ser Trp Ala Gly His Val Ala Gln Lys
 50 55 60

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Gly Lys Tyr Phe Val Thr Arg Asn Gly Ser Ser Ile Ile Ala Phe Ala	
65 70 75 80	
ctt ggt gaa aag tgg gag cct ggt aat cca att gcc att acg ggt gct	288
Val Gly Gly Lys Trp Glu Pro Gly Asn Pro Ile Ala Ile Thr Gly Ala	
85 90 95	
cad acc gac tcc ccc gca tta agg att aag cct all tct aza aga gtc	336
His Thr Asp Ser Pro Ala Leu Arg Ile Lys Pro Ile Ser Lys Arg Val	
100 105 110	
agt gag aag tat tta caa gtg ggc gtg gaa act tat ggt ggc gct att	384
Ser Glu Lys Tyr Leu Gln Val Gly Val Glu Thr Tyr Gly Ala Ile	
115 120 125	
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Trp His Ser Trp Phe Asp Lys Asp Leu Gly Val Ala Gly Arg Val Phe	
130 135 140	
gta aag gat ggc aaa act ggc aaa tcc att gct aga ttg gtg gat ttg	480
Val Lys Asp Ala Lys Thr Gly Lys Ser Ile Ala Arg Leu Val Asp Leu	
145 150 155 160	
aat aga cct ctg tta aag att cct act ttg gct att cat ctg gcc agc	528
Asn Arg Pro Leu Leu Lys Ile Pro Thr Leu Ala Ile His Leu Asp Arg	
165 170 175	
gac gta aat caa aax ttr gag ttt sat aga gaa act caa ctg ttg ccg	576
Asp Val Asn Gln Lys Phe Glu Phe Asn Arg Glu Thr Gln Leu Ser Pro	
180 185 190	
att ggt ggt ctg caa gaa gac aaa act gaa gcg aaa act gaa aag gaa	624
Ile Gly Gly Leu Gln Glu Asp Lys Thr Glu Ala Lys Thr Glu Lys Glu	
195 200 205	
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Ile Asn Asn Gly Glu Phe Thr Ser Ile Lys Thr Ile Val Gln Arg His	
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ile glu asp ile glu asp phe glu ser ile leu tyr asp his asn ala				
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leu acg cta ggt ggg ttc aac gat gag ttt gtc ttc tct ggt cga ttg				816
ser thr leu gly gly phe asn asp glu phe val phe ser gly arg leu				
260	265		270	
gat aat tly acg leu lyl ile acu tca atg cac ggt tta acg ttg gcg				864
asp asn leu thr ser cys phe thr ser met his gly leu thr leu ala				
275	280		285	
gct gac aca gaa ttt gac cga gaa tca ggc att aga ttg atg gca tgc				912
ala asp thr glu ile asp arg glu ser gly ile arg leu met ala cys				
290	295		300	
ttt gal cat gag gag att ggc tca tcc tcc gcc caa ggg gca gat tct				960
phe asp his glu glu ile gly ser ser ser ala gln gly ala arg ser				
305	310	315	320	
aac ttc ttg cct aat ata ttg gaa agg ttg tcc atc cly aag ggg gac				1008
asn phe leu pro asn ile leu glu arg leu ser ile leu tyr gly asp		330	335	
325				
ggc tct gat cca act aaa cct ttg ttt cac tcc gca ata tgg gaa act				1056
gly ser asp gln thr lys pro leu phe his ser ala ile leu glu thr				
340	345	350		
tac gct aag tgg ttt ttc ctt tca tct gat gct gct cat gca gtt cat				1104
ser ala lys ser phe phe leu ser ser asp val ala his ala val his				
355	360	365		
cca aac tat gca aac aaa tac gaa agc caa cac aaa ccc ttc ttg ggc				1152
pro asn tyr ala asn lys tyr glu ser gln his lys pro leu leu gly				
370	375	380		
gct ggt ccc gta atc aag att aac gcg aat caa cgt tac atg acc aat				1200
gly gly pro val ile lys ile asn ala asn gln arg tyr met thr asn				
385	390	395	400	

tca	aca	ggg	tgg	gtc	tgg	ggg	aaa	aga	cta	gca	gag	gct	gct	aaa	gtc	1240
Ser	Pro	Gly	Leu	Val	Leu	Val	Lys	Arg	Leu	Ala	Glu	Ala	Ala	Lys	Val	
			405					410						415		

cct ttg aaa ttg ttt gtc gta gct aac gac tca cca tgc ggt tct acc 1296
 Pro Leu Gln Leu Phe Val Val Ala Arg Asp Ser Pro Cys Gly Ser Thr
 420 425 430

atc ggc ccc att ttg gcc tca aag aca ggt att aga act cta gac ttg 1344
 Val Gly Pro Ile Leu Ala Ser Lys Thr Gly Ile Arg Thr Leu Arg Leu
 435 440 445

ygt aak uol ylg lbg agt atg cat tgg act aga gag aou gyl ygr tct 1322
 Gly Asp Pro Val Leu Ser Met His Ser Tle Arg Glu Thr Gly Gly Ser
 450 455 460

gca gac ctg gag ttc caa atc aag tta ttt aag gaa ttt ttt gaa cgc 1440
Ala Asp Leu Glu Phe Gln Ile Lys Leu Phe Lys Glu Phe Phe Glu Arg
465 470 475 480

LAG AOT TCG AIA GAA IGT GAA ATT GTT GTC TAA
 Tyr Thr Ser Ile Glu Ser Glu Ile Val Val
 485 490

c210> 111

411 490

<212> FRT

<31.3> Saccharomyces carvinaliae

400 111

Met Phe Arg Ile Gln Leu Arg Thr Met Ser Ser Lys Thr Cys Lys Ser
1 5 10 15

Asp Tyr Pro Lys Glu Phe Val Ser Phe Leu Asn Ser Ser His Ser Pro
20 25 30

Tyr His Thr Val His Asn Ile Lys Lys His Leu Val Ser Asn Gly Phe
35 40 45

FIG. 10 is a schematic diagram of a protein structure.

Lys Glu Leu Ser Glu Arg Asp Ser Trp Ala Gly His Val Ala Gln Lys
50 55 60

Gly Lys Tyr Phe Val Thr Arg Asn Gly Ser Ser Ile Ile Ala Phe Ala
65 70 75 80

Val Gly Gly Lys Trp Glu Pro Gly Asn Pro Ile Ala Ile Thr Gly Ala
85 90 95

His Thr Asp Ser Pro Ala Leu Arg Ile Lys Pro Ile Ser Lys Arg Val
100 105 110

Ser Glu Lys Tyr Leu Gln Val Gly Val Glu Thr Tyr Gly Gly Ala Ile
115 120 125

Trp His Ser Trp Phe Arg Tyr Asp Leu Gly Val Ala Gly Arg Val Phe
130 135 140

Val Lys Asp Ala Lys Thr Gly Lys Ser Ile Ala Arg Leu Val Asp Leu
145 150 155 160

Asn Arg Pro Leu Leu Lys Ile Pro Thr Leu Ala Ile His Leu Asp Arg
165 170 175

Asp Val Asn Gln Lys Phe Glu Phe Asn Arg Glu Thr Gln Leu Leu Pro
180 185 190

Ile Gly Gly Leu Gln Glu Asp Lys Thr Gln Ala Lys Thr Gln Lys Glu
195 200 205

1000 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Ile Asn Asn Gly Glu Phe Thr Ser Ile Lys Thr Ile Val Gln Arg His
210 215 220

His Ala Glu Leu Leu Gly Leu Ile Ala Lys Glu Leu Ala Ile Asp Thr
225 230 235 240

Ile Glu Asp Ile Glu Asp Phe Glu Leu Ile Leu Tyr Asp His Asn Ala
245 250 255

Ser Thr Leu Gly Gly Phe Asn Asp Glu Phe Val Phe Ser Gly Arg Leu
260 265 270

Asp Asn Leu Thr Ser Cys Phe Thr Ser Met His Gly Leu Thr Leu Ala
275 280 285

Ala Asp Thr Glu Ile Asp Arg Glu Ser Gly Ile Arg Leu Met Ala Cys
290 295 300

Phe Asp His Glu Glu Ile Gly Ser Ser Ser Ala Gln Gly Ala Asp Ser
305 310 315 320

Asn Phe Leu Pro Asn Ile Leu Glu Arg Leu Ser Ile Leu Lys Gly Asp
325 330 335

Gly Ser Asp Glu Thr Lys Pro Leu Phe His Ser Ala Ile Leu Glu Thr
340 345 350

Ser Ala Lys Ser Phe Phe Leu Ser Ser Asp Val Ala His Ala Val His
355 360 365

Pro Asn Tyr Ala Asn Lys Tyr Glu Ser Gln His Lys Pro Leu Leu Gly
370 375 380

Gly Gly Pro Val Ile Lys Ile Asn Ala Asp Gln Arg Tyr Met Thr Asn
 305 350 395 400

Ser Pro Gly Leu Val Leu Val Lys Arg Leu Ala Glu Ala Ala Lys Val
 405 410 415

Pro Leu Gln Leu Phe Val Val Ala Asn Asp Ser Pro Cys Gly Ser Thr
 420 425 430

Ile Gly Pro Ile Leu Ala Ser Lys Thr Gly Ile Arg Thr Leu Asp Leu
 435 440 445

Gly Asn Pro Val Leu Ser Met His Ser Ile Arg Glu Thr Gly Cys Ser
 450 455 460

Ala Asp Leu Glu Phe Gln Ile Lys Leu Phe Lys Glu Phe Phe Glu Arg
 465 470 475 480

Tyr Thr Ser Ile Glu Ser Glu Ile Val Val
 485 490

<210> 112

<211> 570

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(570)

<400> 112

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Met Asp Asp Lys Lys Thr Trp Ser Thr Val Thr Leu Arg Thr Phe Asn			
1	5	10	15
cag ctg gta acg tct tog tta att gga tac tca aaa aag atg gal ugc			96
Gln Leu Val Thr Ser Ser Leu Ile Gly Tyr Ser Lys Lys Met Asp Ser			
20	25	30	
atg aat cac aag atg gaa gga aat gcg ggc cac gac cgc agt gat atg			144
Met Asn His Lys Lys Met Gln Gly Asn Ala Gly His Asp His Ser Asp Met			
35	40	45	
cat atg gga gat gga gat gat aac tgt tgg atg aat atg cta ttt tog			192
His Met Gly Asp Gly Asp Asp Thr Cys Ser Met Asn Met Leu Phe Ser			
50	55	60	
tgg tca taa aag aat acg tgt gtc gtc ttt gaa tgg tgg cat atc aag			240
Trp Ser Tyr Lys Asn Thr Cys Val Val Phe Gln Trp Trp His Ile Lys			
65	70	75	80
acc ctg aat gga atg att tta agt tgt tta gca att ttt ggt cta gcc			288
Thr Leu Pro Gly Leu Ile Leu Ser Cys Leu Ala Ile Phe Gly Leu Ala			
85	90	95	
tac ctg tat gag tac tta aag tgc tgc cat aag aga caa tta tcc			336
Tyr Leu Tyr Gln Tyr Leu Lys Tyr Cys Val His Lys Arg Gln Leu Ser			
100	105	110	
cag aga gta ttg tta cca aat aga tct ctg acc aag atc aac caa gcc			384
Gln Arg Val Leu Leu Pro Asn Arg Ser Leu Thr Lys Ile Asn Gln Ala			
115	120	125	
gac aaa gtg tcc sat agt att cta tat ggt ttg caa gtg gga ttc tca			432
Asp Lys Val Ser Asn Ser Ile Leu Tyr Gly Leu Gln Val Gly Phe Ser			
130	135	140	
ttc atg ctg atg ctt gta ttc atg act tat aat ggt tgg tta atg tta			480
Phe Met Leu Met Leu Val Phe Met Thr Tyr Ser Gly Trp Leu Met Leu			
145	150	155	160
gct gtc gtg tgt ggg gca ata tgg ggt aat tac agc tgg tgt act tgg			528
Ala Val Val Cys Gly Ala Ile Trp Gly Asn Tyr Ser Trp Cys Thr Ser			
165	170	175	

tat agt cct gag ata gat gac agc tcc ctc gcc tgc gat lan 573
 Tyr Ser Pro Glu Ile Asp Asp Ser Ser Leu Ala Cys His

180

185

<210> 113

<211> 163

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 113

Met Asp Asp Lys Lys Thr Trp Ser Thr Val Thr Leu Arg Thr Phe Asn

1

5

10

15

Gln Leu Val Thr Ser Ser Leu Ile Gly Tyr Ser Lys Lys Met Asp Ser

20

25

30

Met Asn His Lys Met Glu Gly Asn Ala Gly His Asp His Ser Asp Met

35

40

45

His Met Gly Asn Gly Asp Asp Thr Cys Ser Met Asn Met Leu Phe Ser

50

55

60

Trp Ser Tyr Lys Asn Thr Cys Val Val Phe Glu Trp Trp His Phe Lys

65

70

75

80

Thr Leu Pro Gly Leu Ile Leu Ser Cys Leu Ala Ile Phe Gly Leu Ala

85

90

95

Tyr Leu Tyr Glu Tyr Leu Lys Tyr Cys Val His Lys Arg Gln Leu Ser

100

105

110

Gln Arg Val Leu Leu Pro Asn Arg Ser Leu Thr Lys Ile Asn Gln Ala

115

120

125

Asp Lys Val Ser Asn Ser Ile Leu Tyr Gly Leu Glu Val Gly Phe Ser
 130 135 140

Phe Met Leu Met Leu Val Phe Met Thr Tyr Asn Gly Trp Leu Met Leu
 145 150 155 160

Ala Val Val Cys Gly Ala Ile Trp Gly Asn Tyr Ser Trp Cys Thr Ser
 165 170 175

Tyr Ser Pro Glu Ile Asp Asp Ser Ser Leu Ala Cys His
 180 185

<210> 114

<211> 585

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> [1]..(585)

<400> 114

atg att cat gca gtt cta ata ttc aat aag aaa tgc caa cca aga tta 48

Met Ile His Ala Val Leu Ile Phe Asn Lys Lys Cys Gln Pro Arg Leu

1

5

10

15

gtg aaa ttc tac acg ccg gtc gac ctt cca aag caa aaa ctg cta tta 96

Val Lys Phe Tyr Thr Pro Val Asp Leu Pro Lys Gln Lys Leu Leu Leu

20

25

30

gag caa gta tac gaa ttg att tct caa agg aat agc gat ttt caa agt 144

Glu Glu Val Tyr Gln Leu Ile Ser Gln Arg Asn Ser Asp Phe Gln Ser

35

40

45

277/762

tat ttt tta gtc aag aca cga cag att ctg tta agc aat gaa aat aat	192
<div> <div>Ser Phe Leu Val Thr Pro Pro Ser Leu Leu Leu Ser Asn Glu Asn Asn</div> <div>50 58 60</div> </div>	
aat gat gag gta aac aat gaa gat att caa atc atc tat aaa aac tac	240
<div> <div>Asn Asp Glu Val Asn Asn Glu Asp Ile Gln Ile Ile Tyr Lys Asn Tyr</div> <div>65 70 75 80</div> </div>	
gct aca cta tat ttc act ttc atc gtc gat gat caa gaa tca gaa ctg	288
<div> <div>Ala Thr Leu Tyr Phe Thr Phe Ile Val Asp Asp Gln Glu Ser Glu Leu</div> <div>85 90 95</div> </div>	
gac ata tta gat ctg atc caa act ttt gtc gaa tca ttg gac cgt tgt	336
<div> <div>Ala Ile Leu Asp Leu Ile Gln Thr Phe Val Glu Ser Leu Asp Arg Cys</div> <div>100 105 110</div> </div>	
ttt act gaa gtc aat gaa att gat ttg att ttt aac tgg caa cct ttg	384
<div> <div>Phe Thr Glu Val Asn Glu Leu Asp Leu Ile Phe Asn Trp Gln Thr Leu</div> <div>115 120 125</div> </div>	
gaa agt gta tta gaa gaa atc gtc cag cag gtc atg gtc att gaa aca	432
<div> <div>Glu Ser Val Leu Glu Glu Ile Val Gln Gly Gly Met Val Ile Glu Thr</div> <div>130 135 140</div> </div>	
aac ctg ttc aga ata gtt gct tct gtt gac gaa ctc aca aac gct gac	480
<div> <div>Asn Val Asn Arg Ile Val Ala Ser Val Asp Glu Leu Asn Lys Ala Ala</div> <div>145 150 155 160</div> </div>	
gag tcc aca gat agt aaa att gga aga cta aag tcc act gga ttt gga	528
<div> <div>Glu Ser Thr Asp Ser Lys Ile Gly Arg Leu Thr Ser Thr Gly Phe Gly</div> <div>165 170 175</div> </div>	
agc gca cta cca ggc ttt gct caa ggc gga ttt gca caa tgg gca aag	576
<div> <div>Ser Ala Leu Gln Ala Phe Ala Gln Gly Gly Phe Ala Gln Trp Ala Thr</div> <div>180 185 190</div> </div>	
ggg caa taa	585
Gly Gln	

<211> 194

<212> PPT

<213> *Saccharomyces cerevisiae*

<400> 115

Met	Ile	His	Ala	Val	Ileu	Ile	Phe	Asn	Lys	Lys	Cys	Glu	Pro	Arg	Leu
1				5						10				15	

Val	Lys	Phe	Tyr	Thr	Pro	Val	Asp	Leu	Pro	Lys	Gln	Lys	Leu	Leu	Leu
			30					25					30		

Glu	Gln	Val	Tyr	Glu	Leu	Ile	Ser	Gln	Arg	Asn	Ser	Asp	Phe	Gln	Ser
		35					40					45			

Ser	Phe	Leu	Val	Thr	Pro	Pro	Ser	Leu	Leu	Leu	Ser	Asn	Glu	Asn	Asn
	50						55					60			

Asn	Asp	Glu	Val	Asn	Asn	Glu	Asp	Ile	Gln	Ile	Ile	Tyr	Lys	Asn	Tyr
65					70					75				80	

Ala	Thr	Leu	Tyr	Phe	Thr	Phe	Ile	Val	Asp	Asp	Gln	Glu	Ser	Glu	Leu
			85						90					95	

Ala	Ile	Leu	Asp	Leu	Ile	Gln	Thr	Phe	Val	Glu	Ser	Leu	Asp	Arg	Cys
		100						105					110		

Phe	Thr	Glu	Val	Asn	Glu	Leu	Asp	Leu	Ile	Phe	Asn	Trp	Gln	Thr	Leu
		115						120					125		

Glu	Ser	Val	Ileu	Gln	Gln	Ile	Val	Gln	Gly	Gly	Met	Val	Ile	Glu	Thr
	130					135						140			

Asn Val Asn Arg Ile Val Ala Ser Val Asp Glu Leu Asn Lys Ala Ala
 145 150 155 160

Glu Ser Thr Asp Ser Lys Ile Gly Arg Leu Thr Ser Thr Gly Phe Gly
 165 170 175

Ser Ala Leu Glu Ala Phe Ala Gln Gly Gly Phe Ala Glu Trp Ala Thr
 180 185 190

Gly Glu

<210> 116
 <211> 1038
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1)..(1038)

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 1 5 10 15
 gat atg aaa gaa gct gaa aag gat gaa atc ctt ttg atg gaa aac agc 96
 Asp Met Lys Glu Ala Glu Lys Asp Glu Ile Leu Leu Met Glu Asn Ser
 20 25 30
 cgt aga ttc gtg atg ttc cct atc aaa tac cac gaa atc tgg gct gcc 144
 Arg Arg Phe Val Met Phe Pro Ile Lys Tyr His Glu Ile Trp Ala Ala
 35 40 45
 tac aag aag gtt gaa gcc tcc ttc tgg act gcg gaa gaa atc gca ttg 192
 Tyr Lys Lys Val Glu Ala Ser Phe Trp Thr Ala Glu Glu Ile Glu Leu
 50 55 60

gct aag gac act gaa gat ttc caa aaa ttg act gat gac cag aag acc	240
Ala Lys Asp Thr Glu Asp Phe Gln Lys Leu Thr Asp Asp Gln Lys Thr	
65 70 75 80	
tac atc ggt aac ttg tta gcc ttg tcc att tct tct gac aac dtt gtc	288
Tyr Ile Gly Asn Leu Leu Ala Leu Ser Ile Ser Ser Asp Asn Leu Val	
85 90 95	
aac aag tac ttg atc gaa aac ttt tct gcc caa ttg caa aag act gaa	336
Asn Lys Tyr Leu Ile Glu Asn Phe Ser Ala Gln Leu Gln Asn Pro Glu	
100 105 110	
ggc aag agt ttc tac ggt ttc cag att atg atg gaa aac atc tac tct	384
Gly Lys Ser Phe Tyr Gly Phe Gln Ile Met Met Glu Asn Ile Tyr Ser	
115 120 125	
gaa gtt tac tcc atg atg gtt gat gcc ttc ttc aag gac cct aag aac	432
Glu Val Tyr Ser Met Met Val Asp Ala Phe Phe Lys Asp Pro Lys Asn	
130 135 140	
atc acc cta ttc aag gaa att gcc aat ttg cct gaa gcc aag tac aag	480
Ile Pro Leu Phe Lys Gln Ile Ala Asn Leu Pro Glu Val Tyr His Tyr	
145 150 155 160	
gct gcc ttc atc gag aga tgg att tcc aac gal gac aac ttg tat gct	528
Ala Ala Phe Ile Glu Arg Trp Ile Ser Asn Asp Asp Ser Leu Tyr Ala	
165 170 175	
gaa aga cta gta gca ttt gct gca aag gaa ggt att ttc caa gct ggt	576
Glu Arg Leu Val Ala Phe Ala Ala Lys Glu Gly Ile Phe Gln Ala Gly	
180 185 190	
aac tat gct tct atg ttc tgg ttg act gac aaa aag att atg cca ggt	624
Asn Tyr Ala Ser Met Phe Trp Leu Thr Asp Lys Lys Ile Met Pro Gly	
195 200 205	
tta gca atg gcc aac aga aac atc tgt aga gaa aga ggt gaa leu act	672
Leu Ala Met Ala Asn Arg Asn Ile Tyr Arg Asp Arg Gly Ala Tyr Thr	
210 215 220	
gac ttt tca tgc ttg cta ttc gcc cat ttg aga acc aag cca aac gcc	720

281/762

Asp Phe Ser Cys Leu Leu Phe Ala His Ileu Arg Thr Lys Pro Asn Pro
 225 230 235 240

 aag atc att gaa aaa atc att acc gaa gcc gtg gaa att gaa aag gaa 768
 Lys Ile Ile Glu Lys Ile Ile Thr Glu Ala Val Glu Ile Glu Lys Glu
 245 250 255

 tac tac tca aac tct ttg cca gta gaa aaa ttt ggt atg gat ttg aag 816
 Tyr Tyr Ser Ser Leu Pro Val Glu Lys Phe Gly Met Asp Leu Lys
 260 265 270

 aag att cac acc tac ata gaa ttt gtc gct gac ggt ata tta cca ggt 864
 Ser Ile His Thr Tyr Ile Glu Phe Val Ala Asp Gly Leu Leu Gln Gly
 275 280 285

 tto ggt aac gaa aaa tac tac aac gcc gtc aac cca ttc gaa ttc atg 912
 Phe Gly Asn Glu Lys Tyr Tyr Asn Ala Val Asn Pro Phe Glu Phe Met
 290 295 300

 gag gaa gtc gct acc gct ggt aag acc acc ttc ttt gaa aag aag gtt 960
 Glu Asp Val Ala Thr Ala Gly Lys Thr Thr Phe Phe Glu Lys Lys Val
 305 310 315 320

 tcc gac tac cca aag gcc agt gac atg tct aag tcc gct acc cca tcc 1008
 Ser Asp Tyr Glu Lys Ala Ser Asp Met Ser Lys Ser Ala Thr Pro Ser
 325 330 335

 aag gaa att aac ttt gat gat gac ttc taa 1038
 Lys Glu Ile Asn Phe Asp Asp Asp Phe
 340 345

<210> 117

<211> 345

<212> PPT

<213> *Saccharomyces cerevisiae*

<400> 117

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Asp Met Lys Glu Ala Glu Lys Asp Glu Ile Leu Leu Met Glu Asn Ser
30 25 30

Arg Arg Phe Val Met Phe Pro Ile Lys Tyr His Glu Ile Trp Ala Ala
35 40 45

Tyr Lys Lys Val Glu Ala Ser Phe Trp Thr Ala Glu Glu Ile Glu Leu
50 55 60

Ala Lys Asp Thr Glu Asp Phe Gln Lys Leu Thr Asp Asp Gln Lys Thr
65 70 75 80

Tyr Ile Gly Asn Leu Leu Ala Leu Ser Ile Ser Ser Asp Asn Leu Val
85 90 95

Asn Lys Tyr Leu Ile Glu Asn Phe Ser Ala Glu Leu Gln Asn Pro Glu
100 105 110

Gly Lys Ser Phe Tyr Gly Phe Gln Ile Met Met Glu Asn Ile Tyr Ser
115 120 125

Glu Val Tyr Ser Met Met Val Asp Ala Phe Phe Lys Asp Pro Lys Asn
130 135 140

Ile Pro Leu Phe Lys Glu Ile Ala Asn Leu Pro Glu Val Lys His Lys
145 150 155 160

Ala Ala Phe Ile Glu Arg Trp Ile Ser Asn Asp Asp Ser Leu Tyr Ala
165 170 175

Glu Arg Leu Val Ala Phe Ala Ala Lys Glu Gly Ile Phe Gln Ala Gly

180

185

190

Asn Tyr Ala Ser Met Phe Trp Leu Thr Asp Lys Lys Ile Met Pro Gly
195 200 205

Leu Ala Met Asn Asn Arg Asn Ile Cys Arg Asp Arg Gly Ala Tyr Thr
210 215 220

Asp Phe Ser Cys Leu Leu Phe Ala His Leu Arg Thr Lys Pro Asn Pro
225 230 235 240

Lys Ile Ile Glu Lys Ile Ile Thr Glu Ala Val Glu Ile Glu Lys Glu
245 250 255

Tyr Tyr Ser Asn Ser Leu Pro Val Glu Lys Phe Gly Met Asp Leu Lys
260 265 270

Ser Ile His Thr Tyr Ile Glu Phe Val Ala Asp Gly Leu Leu Gln Gly
275 280 285

Phe Gly Asn Glu Lys Tyr Tyr Asn Ala Val Asn Pro Phe Glu Phe Met
290 295 300

Glu Asp Val Ala Thr Ala Gly Lys Thr Thr Phe Phe Glu Lys Lys Val
305 310 315 320

Ser Asp Tyr Glu Lys Ala Ser Asp Met Ser Lys Ser Ala Thr Pro Ser
325 330 335

Lys Glu Ile Asn Phe Asp Asp Asp Phe
340 345

<210> L18
 <211> 330
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <220>
 <221> CDS
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 1 5 10 15

 aca caa ttg gat atg gtc aat cag cag cta gca tat ttg gac aga caa 96
 Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln
 20 25 30

 gaa aag ctt gct gaa ttg aca aag aaa gaa cta gag tct tat aca aag 144
 Gln Lys Leu Ala Gln Leu Thr Lys Lys Gln Leu Glu Ser Tyr Pro Thr
 35 40 45

 gac aca gta tgg aag tct agc ggt aca tgg ttt atc tta cag gat aac 192
 Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys
 50 55 60

 tcc aaa tac gtt aat gat tta tca cat gcc gaa act gtt ctt atg gat 240
 Ser Lys Tyr Val Asn Asp Leu Ser Ala Ala Gln Thr Val Leu Leu asp
 65 70 75 80

 cea aga aaa aca tta aag ulu aag aag aac tat tta gaa act act gtt 288
 Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val
 85 90 95

 gaa aaa aca ata gac aat cta aag gca ttg atg aag aat taa 330
 Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn
 100 105

 <210> L19

<211> 109

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 119

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20 25 30

Glu Lys Leu Ala Glu Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr

35 40 45

Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys

50 55 60

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Glu Thr Val Leu Leu Asp

65 70 75 80

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val

85 90 95

Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn

100 105

<210> 120

<211> 648

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (648)

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 1 5 10 15

agt tta ggt acc tca att atg ggc gtg acn ttt aag gat ggt gcg ata 96
 Ser Leu Gly Thr Ser Ile Met Ala Val Thr Phe Lys Asp Gly Val Ile
 20 25 30

cta ggt gct gat tca cgt acc acc acf ggt ggc tac ata gct aac cgt 144
 Leu Gly Ala Asp Ser Arg Thr Thr Thr Gly Ala Tyr Ile Ala Asn Arg
 35 40 45

gtg acc gat aaa tta acg aga gta cat gac aaa att tgg tgt tgt agg 192
 Val Thr Asp Lys Leu Thr Arg Val His Asp Lys Ile Trp Cys Cys Arg
 50 55 60

tcg ggt tct gca gca gac aag cag gcg att gcc gac ala gtt cag tac 240
 Ser Gly Ser Ala Ala Asp Thr Gln Ala Ile Ala Asp Ile Val Gln Tyr
 65 70 75 80

cat ttg gaa tta tat act tcc caa tat ggt acc ccu tcc acc gag act 288
 His Leu Glu Leu Tyr Thr Ser Gln Tyr Gly Thr Pro Ser Thr Glu Thr
 85 90 95

gct gcc tgg gtg ttc aaa gaa tta tgt tac gaa aat aaa gat aac gtt 336
 Ala Ala Ser Val Phe Lys Glu Leu Cys Tyr Glu Asn Lys Asp Asn Leu
 100 105 110

act gct ggt ata att gtg gct ggt tat gat gac aaa aac aaa ggg gaa 384
 Thr Ala Gly Ile Ile Val Ala Gly Tyr Asp Asp Lys Asn Lys Gly Glu
 115 120 125

gta tat act att cca ttg ggt ggc tcc gtc cat aag ctg cct cai ggg 432
 Val Tyr Thr Ile Pro Leu Gly Gly Ser Val His Lys Leu Pro Tyr Ala
 130 135 140

atn gaa gga tct ggc tct act ttc ata lat ggg tat tgt gat aac aac 480
 Ile Ala Gly Ser Gly Ser Thr Phe Ile Tyr Gly Tyr Cys Asp Lys Asn
 145 150 155 160

Utt aga gaa aat atg tca aag gaa gaa acc gta gat ttc ala aag cat 528
 Phe Arg Glu Asn Met Ser Lys Glu Glu Thr Val Asp Phe Ile Lys His
 165 170 175

tgg cta tgg caa gcc att aaa tgg gac gga tct tcc ggt ggt gtt ata 576
 Ser Leu Ser Glu Ala Ile Lys Trp Asp Gly Ser Ser Gly Gly Val Ile
 180 185 190

aga atg gtt gtt ttg aca gct gct ggt gtg gaa cgt ttg ata ttc tac 624
 Arg Met Val Val Leu Thr Ala Ala Gly Val Glu Arg Leu Ile Phe Tyr
 195 200 205

cct gat gaa tat gaa caa cta taa 548
 Pro Asp Glu Tyr Glu Glu Leu
 210 215

<110> 121

<111> 215

<113> PRT

<213> Saccharomyces cerevisiae

<400> 121

Met Asn Gly Thr Gln Val Asp Ile Asn Arg Leu Lys Lys Gly Glu Val
 1 5 10 15

Ser Leu Gly Thr Ser Ile Met Ala Val Thr Phe Lys Asp Gly Val Ile
 20 25 30

Leu Gly Ala Asp Ser Arg Thr Thr Thr Gly Ala Tyr Ile Ala Asn Arg
 35 40 45

Val Thr Asp Lys Leu Thr Arg Val His Asp Lys Ile Trp Cys Cys Arg
 50 55 60

Ser Gly Ser Ala Ala Asp Thr Gln Ala Ile Ala Asp Ile Val Gln Tyr

65 79 75 80

His Leu Gln Leu Tyr Thr Ser Gln Tyr Gly Thr Pro Ser Thr Glu Thr
85 90 95

Ala Ala Ser Val Phe Lys Glu Leu Cys Tyr Glu Asn Lys Asp Asn Leu
100 105 110

Thr Ala Gly Ile Ile Val Ala Gly Tyr Asp Asp Lys Asn Lys Gly Glu
115 120 125

Val Tyr Thr Ile Pro Leu Gly Gly Ser Val His Lys Leu Pro Tyr Ala
130 135 140

Ile Ala Gly Ser Gly Ser Thr Phe Ile Tyr Gly Tyr Cys Asp Lys Asn
145 150 155 160

Phe Arg Glu Asn Met Ser Lys Glu Glu Thr Val Asp Phe Ile Lys His
165 170 175

Ser Leu Ser Gln Ala Ile Lys Trp Asp Gly Ser Ser Gly Gly Val Ile
180 185 190

Arg Met Val Val Leu Thr Ala Ala Gly Val Glu Arg Leu Ile Phe Tyr
195 200 205

Pro Asp Glu Tyr Glu Gln Leu
210 215

<210> 122

<211> 990

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(990)

<400> 132

atg tgc agt agg ata ctc ttg tcc ggt tta gtc gga ctg ggt gct ggt 48

Met Cys Ser Arg Ile Leu Leu Ser Gly Leu Val Gly Leu Gly Ala Gly

1 5 10 15

act ggc tta acc tat ctt ctt ttg aac aaa cat tct cca acg cca atc 96

Thr Gly Leu Thr Tyr Leu Leu Leu Asn Lys His Ser Pro Thr Gln Ile

20 25 30

att gag aca cct tat cca cct acc cag aaa cct aat agt aat att caa 144

Ile Glu Thr Pro Tyr Pro Pro Thr Gln Lys Pro Asn Ser Asn Ile Gln

35 40 45

tct cac tct ttc aac gtc gat cct tcc ggg ttc ttc aag tat ggt ttt 192

Ser His Ser Phe Asn Val Asp Pro Ser Gly Phe Phe Lys Tyr Gly Phe

50 55 60

cct ggt cag att cat gct atg cag aac cgt gaa gag ttt atc tca tgt 240

Pro Gly Pro Ile His Asp Asn Gln Asn Arg Glu Glu Phe Ile Ser Cys

65 70 75 80

cac aac agc cca act caa aat cct tat tgg gtc ctg gaa cat atc aag 288

Tyr Asn Arg Gln Thr Gln Asn Pro Tyr Trp Val Leu Gln His Ile Thr

85 90 95

cca gaa tca ttg gct cca agg aat gct gac aga aua aac tcc ttt ttc 336

Pro Glu Ser Leu Ala Ala Arg Asn Ala Asp Arg Lys Asn Ser Phe Phe

100 105 110

aag gaa gat gaa gta att cca gaa aag ttt aga ggt aaa cta aga gaa 384

Lys Glu Asp Glu Val Ile Pro Glu Lys Phe Arg Gly Lys Leu Arg Asp

115 120 125

cac ttt agg tgg ggc tat gat cga ggc ctt caa gcc cca gct gca gac 432

Tyr Phe Arg Ser Gly Tyr Asp Arg Gly His Gln Ala Pro Ala Ala Asp

290/762

130	135	140	
gca aca ttt tct cca cag gcc atg gat gat aca ttc tac tta tcc aat			480
Ala Lys Phe Ser Glu Glu Ala Met Asp Asp Thr Phe Tyr Leu Ser Asn			
145	150	155	160
atg tac cct caa gta cga gaa ggt ttc aat aga gac tat tgg cgc cat			528
Met Cys Pro Glu Val Gly Glu Gly Phe Asn Arg Asp Tyr Trp Ala His			
165	170	175	
ttg gag cac ttt tgt agg gga ttg aat aag aaa tat aag agt gta aga			576
Leu Glu Tyr Phe Cys Arg Gly Leu Thr Lys Lys Tyr Lys Ser Val Arg			
180	185	190	
atc gtg aot ggt cca ttg tat cta ccc aac aag gat ccc ata gat aat			624
Ile Val Thr Gly Pro Leu Tyr Leu Pro Lys Lys Asp Pro Ile Asp Asn			
195	200	205	
aaa ttc agg gtt aat tat gaa gtt atg ggc aat cca ccc agt att gct			672
Lys Phe Arg Val Asn Tyr Glu Val Ile Gly Asn Pro Pro Ser Ile Ala			
210	215	220	
gtt cca aag cac ttt ttt aaa ttg att gtt gca gaa gca cca aca gcc			720
Val Pro Thr His Phe Phe Lys Leu Ile Val Ala Glu Ala Pro Thr Ala			
225	230	235	240
aac cca gat aga gag gat att gct gtc gcg gca ttt gta ttg cca aac			768
Asn Pro Ala Arg Glu Asp Ile Ala Val Ala Ala Phe Val Leu Pro Asn			
245	250	255	
gac cag ata tca aat gag cag aac ttg act gac ttt gaa gtt cct ata			816
Glu Pro Ile Ser Asn Glu Thr Lys Leu Thr Asp Phe Glu Val Pro Ile			
260	265	270	
gat gct tta gag aga agt cct ggg cta gaa ctt ctg caa aaa gta cca			864
Asp Ala Leu Glu Arg Ser Thr Gly Leu Glu Leu Leu Glu Lys Val Pro			
275	280	285	
cct tca asg aag aag gca tta tgc aac gag gta aat tgt caa att gta			912
Pro Ser Lys Lys Lys Ala Leu Cys Lys Glu Val Asn Cys Glu Ile Val			
290	295	300	

gtg aga gat ttc tct aac gcg gcg atc aac cca tcc aaa gat gtg aaa 960
 Val Arg Asp Phe Ser Asn Ala Ala Ile Lys Gln Ser Lys Asp Val Lys
 305 310 315 320

tgg tta cct cct cca aaa aaa agg aat tga 990
 Leu Leu Pro Pro Pro Lys Lys Arg Asn
 325

<213> 123
 <211> 329
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 123

Met Cys Ser Arg Ile Leu Leu Ser Gly Leu Val Gly Leu Gly Ala Gly
 1 5 10 15

Thr Gly Leu Thr Tyr Leu Leu Leu Asn Lys His Ser Pro Thr Gln Ile
 20 25 30

Ile Glu Thr Pro Tyr Pro Pro Thr Gln Lys Pro Asn Ser Asn Ile Gln
 35 40 45

Ser His Ser Phe Asn Val Asp Pro Ser Gly Phe Phe Lys Tyr Gly Phe
 50 55 60

Pro Gly Pro Ile His Asp Leu Gln Asn Arg Glu Glu Phe Ile Ser Cys
 65 70 75 80

Tyr Asn Arg Gln Thr Gln Asn Pro Tyr Trp Val Leu Glu His Ile Thr
 85 90 95

Pro Glu Ser Leu Ala Ala Arg Asn Ala Asp Arg Lys Asn Ser Phe Phe
 100 105 110

Lys Glu Asp Glu Val Ile Pro Glu Lys Phe Arg Gly Lys Leu Arg Asp
115 120 125

Tyr Phe Arg Ser Gly Tyr Asp Arg Gly His Gln Ala Pro Ala Ala Asp
130 135 140

Ala Lys Phe Ser Glu Gln Ala Met Asp Asp Thr Phe Tyr Leu Ser Asn
145 150 155 160

Met Cys Pro Gln Val Gly Glu Gly Phe Asn Arg Asp Tyr Trp Ala His
165 170 175

Leu Glu Tyr Phe Cys Arg Gly Leu Thr Lys Lys Tyr Lys Ser Val Arg
180 185 190

Ile Val Thr Gly Pro Leu Tyr Leu Pro Lys Lys Asp Pro Ile Asp Asn
195 200 205

Lys Phe Arg Val Asn Tyr Glu Val Ile Gly Asn Pro Pro Ser Ile Ala
210 215 220

Val Pro Thr His Phe Phe Lys Leu Ile Val Ala Glu Ala Phe Thr Ala
225 230 235 240

Asn Pro Ala Arg Glu Asp Ile Ala Val Ala Ala Phe Val Leu Pro Asn
245 250 255

Glu Pro Ile Ser Asn Glu Thr Lys Leu Thr Asp Phe Glu Val Pro Ile
260 265 270

Asp Ala Leu Glu Arg Ser Thr Gly Leu Glu Leu Leu Gln Lys Val Pro
 275 280 285

Pro Ser Lys Lys Lys Ala Leu Cys Lys Glu Val Asn Cys Gln Ile Val
 290 295 300

Val Arg Asp Phe Ser Asn Ala Ala Ile Lys Glu Ser Lys Asp Val Lys
 305 310 315 320

Leu Leu Pro Pro Pro Lys Lys Arg Asn
 325

<210> 124
 <211> 160
 <212> CNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(160)

<400> 124
 atg cgg cat tta gcc gcc gaa ggg ggt aol lgg gct cgg cat att tca 48
 Met Pro His Leu Ala Ala Glu Ala His Thr Trp Pro Pro His Ile Ser
 1 5 10 15

cat tta aca ctt cgg att cgg cat gaa acc cgg gaa cac cgg cac gta 56
 His Ser Thr Leu Ser Ile Pro His Pro Thr Pro Glu His Arg His Val
 20 25 30

ttt cat aag aag gac gtg aag aac aac aag aac gaa gaa aaa ggc aat 144
 Phe His Lys Lys Asp Val Lys Asn Lys Arg Asn Glu Gln Lys Gly Asn
 35 40 45

aat tta ctc tat gtg tta ttt aga act cgg gtg ata aag aac cgg ttc 192
 Asn Leu Leu Tyr Val Leu Phe Arg Thr Thr Val Ile Lys Ser Ser Phe
 50 55 60

aga	tca	cta	agt	acg	gcc	gga	aga	gag	atg	tig	ttt	gtt	gtc	cat	caa	240
Arg	Ser	Leu	Ser	Thr	Ala	Gly	Arg	Gln	Leu	Leu	Phe	Val	Val	His	Gln	
55					70					75					80	

ggg	gac	atc	ggc	acc	ggc	ctc	atc	gtc	ttc	atc	ata	tgc	tgg	agg	ctg	288
Gly	His	Ile	Gly	Thr	Gly	Leu	Ile	Val	Phe	Ile	Ile	Cys	Trp	Arg	Leu	
			85						90						95	

tgc	tig	aga	ttc	ctc	tgc	agg	gtg	agc	tcc	cag	gtc	acg	gtc	tac	ggc	336
Cys	Leu	Arg	Phe	Leu	Cys	Arg	Val	Ser	Phe	Gln	Val	Thr	Val	Tyr	Gly	
			100						105						110	

ggg	cgc	agt	cgc	atg	tct	ggg	tga									360
Gly	Arg	Ser	Arg	Met	Ser	Ala										
																115

<210> 125

<211> 119

<212> PRT

<213> Saccharomyces cerevisiae

<400> 125

Met	Pro	His	Leu	Ala	Ala	Glu	Ala	His	Thr	Trp	Pro	Pro	His	Ile	Ser
1			5							10					15

His	Ser	Thr	Leu	Ser	Ile	Pro	His	Pro	Thr	Pro	Gln	His	Arg	His	Val
			20						25						30

Phe	His	Lys	Lys	Asp	Val	Lys	Asn	Lys	Arg	Asn	Glu	Gln	Lys	Gly	Asn
			35						40						45

Asn	Leu	Leu	Tyr	Val	Leu	Phe	Arg	Thr	Thr	Val	Ile	Lys	Ser	Ser	Phe
			50					55							60

Arg	Ser	Leu	Ser	Thr	Ala	Gly	Arg	Glu	Leu	Leu	Phe	Val	Val	His	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65 70 75 80

Gly His Ile Gly Thr Gly Leu Ile Val Phe Ile Ile Cys Trp Arg Leu
85 90 95

Cys Leu Arg Phe Leu Cys Arg Val Ser Phe Gln Val Thr Val Tyr Gly
100 105 110

Gly Arg Ser Arg Met Ser Ala
215

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<210> 126
<211> 1071
<212> DNA
<213> Saccharomyces cerevisiae
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<220>
<221> CDS
<222> (1)..(1071)
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<E00> 126
atg tta aaa gtt cct ttg agt gat gti cik leu cag aag atg ctg ttt 48
Met Leu Lys Val Pro Leu Ser Asp Val Leu Ser Gln Lys Met Ile Phe
1 5 10 15

ttt aaa agt ttt aga tat ttt cgt tgc aca aaa tac ttc agc aya gac 95
Leu Lys Ser Phe Arg Tyr Phe His Cys Thr Lys Tyr Phe Ser Arg Asp
20 25 30

aat gca tca tct acc aca gat ata ttt ggc aac gca atg aaa cgt aaa 144
 asn ala ser ser thr thr asp ile phe arg asn ala met lys arg lys
 35 40 45

cat gag ctg gca aat ctt aac gag caa agt cat gga aat gtg gca aga 132
Arg Glu Leu Ala Asn Leu Lys Glu Cln Ser His Gly Asn Val Ala Arg
50 55 60

aat	gct	gct	ttt	ctt	aaa	gag	tat	att	aag	ggc	ccg	aaa	caa	gtg	cca	240
Asn	Ala	Ala	Phe	Pro	Lys	Glu	Tyr	Ile	Lys	Arg	Pro	Lys	Gln	Val	Pro	
65					70				75					80		
agg	aat	gct	act	aac	agg	aaa	aaa	atc	ctg	att	act	tgg	ago	acc	ggg	288
Arg	Asn	Ala	Thr	Asn	Arg	Lys	Lys	Ile	Leu	Ile	Thr	Trp	Ser	Thr	Gly	
				85					90					95		
aca	gat	cga	gct	aaa	gag	gca	gct	aat	tca	gll	glt	agt	gag	ata	ttc	336
Thr	Asp	Arg	Ala	Lys	Gln	Ala	Ala	Asn	Ser	Val	Val	Ser	Gln	Ile	Phe	
				100					105					110		
aaa	aaa	aat	cac	aag	gga	aac	atc	aaa	gtt	gig	gal	ccc	acg	acc	cac	384
Lys	Lys	Asn	His	Lys	Gly	Asn	Ile	Lys	Val	Val	Asp	Pro	Thr	Thr	His	
				115					120					125		
cga	att	gaa	gca	tcc	aat	att	egg	tat	ttt	goc	aag	ggc	att	gcl	ctc	432
Arg	Ile	Glu	Ala	Ser	Asn	Ile	Arg	Tyr	Phe	Ala	Lys	Gly	Ile	Asp	Leu	
				130					135					140		
gat	aaa	gtt	gga	ctc	agt	att	gtt	aat	gta	gag	caa	atc	gal	aat	gaa	480
Asp	Lys	Val	Gly	Leu	Ser	Ile	Val	Asn	Val	Glu	Glu	Ile	Asp	Asn	Glu	
				145					150					155		
aat	caa	att	cca	ctt	gtt	aag	ata	gtc	gaa	agt	cgt	gta	gcc	tta	aaa	528
Asn	Gln	Ile	Pro	Leu	Val	Lys	Ile	Val	Glu	Ser	Arg	Val	Ala	Leu	Lys	
				165					170					175		
aaa	tat	tca	gac	ttt	ctg	gct	aaa	aaa	aag	gaa	uag	gaa	ctg	atg	gaa	576
Lys	Tyr	Ser	Asp	Phe	Leu	Ala	Lys	Lys	Lys	Gln	Lys	Glu	Leu	Met	Glu	
				180					185					190		
tgg	gga	gta	ctg	aat	aag	tct	tac	aag	atc	tgg	gtg	act	gat	aaa	aaa	624
Leu	Gly	Val	Leu	Asn	Lys	Ser	Tyr	Lys	Asn	Leu	Val	Thr	Asp	Lys	Lys	
				195					200					205		
gaa	gat	aac	tgg	aag	cat	att	aaa	ata	tca	tgg	cag	att	gaa	ago	gat	672
Glu	Asp	Asn	Leu	Lys	His	Ile	Lys	Ile	Ser	Trp	Gln	Ile	Glu	Ser	Asp	
				210					215					220		
gal	lla	aaa	agg	cag	aag	gct	cac	gaa	ata	ctt	cgg	cta	tgg	aaa	aaa	720
Asp	Leu	Lys	Arg	Gln	Lys	Ala	His	Glu	Ile	Val	Ser	Leu	Leu	Lys	Lys	

225	230	235	240	
ggg aat aaa gta acg tta tat att gat gac aag aat aac ata aat tca				768
Gly Asn Lys Val Thr Leu Tyr Leu Asp Asp Lys Asn Asn Ile Asn Ser				
245	250	255		
aac aat tgg att gaa aat ttt gag gag atg gac cgc tct cca aac ggt				816
Asn Asn Trp Leu Glu Asn Phe Glu Glu Leu Asp Arg Ser Gln Lys Gly				
260	265	270		
gaa cca ccc agg cta cca gaa tca gtt tcc cag aaa aga gct gct gtc				864
Glu Pro Pro Arg Leu Pro Glu Ser Val Phe Gln Lys Arg Ala Ala Val				
275	280	285		
ttg gag aca ttg aaa gag ata gtt agc gaa tat gct aat gat cct gtc				912
Leu Gln Thr Leu Lys Glu Ile Val Ser Glu Tyr Ala Asn Asp Pro Val				
290	295	300		
cag cta ggt aac atg aac tgg aac atg ata atg aac ctt ata cca aag				960
Leu Leu Gly Asn Met Asn Ser Lys Met Ile Met Lys Leu Ile Pro Lys				
305	310	315	320	
gac gtt aaa cca cca aac aac gat aag aag gcg tta aag gaa ttg aga				1008
Asp Val Tyr Pro Gln Asn Asn Asp Lys Arg Ala Leu Lys Glu Leu Arg				
325	330	335		
aag aag gag agg caa gaa aca ttg cca aaa agg att cag aga aca aac				1056
Lys Lys Glu Arg Gln Glu Lys Leu Gln Lys Arg Ile Gln Arg Lys Lys				
340	345	350		
atg aat gaa atg taa				1071
Met Asn Glu Met				
355				

<210> 127

<211> 356

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 127

Met Leu Lys Val Pro Leu Ser Asp Val Leu Ser Gln Lys Met Ile Phe
 1 5 10 15

Leu Lys Ser Phe Arg Tyr Phe His Cys Thr Lys Tyr Phe Ser Arg Asp
 20 25 30

Asn Ala Ser Ser Thr Thr Asp Ile Phe Arg Asn Ala Met Lys Arg Lys
 35 40 45

Arg Gln Leu Ala Asn Leu Lys Glu Gln Ser His Gly Asn Val Ala Arg
 50 55 60

Asn Ala Ala Phe Pro Lys Glu Tyr Ile Lys Arg Pro Lys Gln Val Pro
 65 70 75 80

Arg Asn Ala Thr Asn Arg Lys Lys Ile Leu Ile Thr Trp Ser Thr Gly
 85 90 95

Thr Asp Arg Ala Lys Gln Ala Ala Asn Ser Val Val Ser Glu Ile Phe
 100 105 110

Lys Lys Asn His Lys Gly Asn Ile Lys Val Val Asp Pro Thr Thr His
 115 120 125

Arg Ile Glu Ala Ser Asn Ile Arg Tyr Phe Ala Lys Gly Ile Asp Leu
 130 135 140

Asp Lys Val Gly Leu Ser Ile Val Asn Val Gln Gln Ile Asp Asn Glu
 145 150 155 160

Asn Gln Ile Pro Leu Val Lys Ile Val Gln Ser Arg Val Ala Leu Lys
 165 170 175

Lys Tyr Ser Asp Phe Leu Ala Lys Lys Lys Glu Lys Glu Leu Met Glu
 180 185 190

Leu Gly Val Leu Asn Lys Ser Tyr Lys Asn Leu Val Thr Asp Lys Lys
 195 200 205

Glu Asp Asn Leu Lys His Ile Lys Ile Ser Trp Gln Ile Glu Ser Asp
 210 215 220

Asp Leu Lys Arg Gln Lys Ala His Glu Ile Val Ser Leu Leu Lys Lys
 225 230 235 240

Gly Asn Lys Val Thr Leu Tyr Leu Asp Asp Lys Asn Asn Ile Asn Ser
 245 250 255

Asn Asn Trp Leu Glu Asn Phe Glu Gly Leu Asp Arg Ser Gln Lys Gly
 260 265 270

Glu Pro Pro Arg Leu Pro Glu Ser Val Phe Gln Lys Arg Ala Ala Val
 275 280 285

Leu Glu Thr Leu Lys Glu Ile Val Ser Glu Tyr Ala Asn Asp Pro Val
 290 295 300

Leu Leu Gly Asn Met Asn Ser Lys Met Ile Met Lys Leu Ile Pro Lys
 305 310 315 320

Asp Val Lys Pro Gln Asn Asn Asp Lys Arg Ala Leu Lys Glu Leu Arg
 325 330 335

Lys Lys Glu Arg Glu Glu Lys Leu Glu Lys Arg Phe Glu Arg Lys Lys
 340 345 350

Met Asn Glu Met
 355

<210> 128
 <211> 402
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(402)

<400> 128
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 5 10 15
 atc aac aag gac gac ttg ttg tta atg gct ttg gcg gtt ttc att taa 96
 Ile Asn Lys Asp Asp Leu Leu Leu Met Val Leu Ala Val Phe Ile Pro
 20 25 30
 cca gcg gcc gtc tgg aag cgt aag ggt atg ttc aac agg gat aca cta 144
 Pro Val Ala Val Trp Lys Arg Lys Gly Met Phe Asn Arg Asp Thr Leu
 35 40 45
 ttg aac tta ctt ctg ttc cta ctg tta ttc ttc aca gca acc att cac 192
 Leu Asn Leu Leu Leu Phe Leu Leu Leu Phe Pro Ala Ile Ile His
 50 55 60
 gct tgc tcc gtt gta tat gaa acg agt agt gaa cgt tcc tac gat ctt 240
 Ala Cys Tyr Val Val Tyr Glu Thr Ser Ser Glu Arg Ser Tyr Asp Leu
 55 70 75 80
 tca cgc aga cat gcg acg gcg ccc gcc gta gac cgt gac ctg gaa gct 288
 Ser Arg Arg His Ala Thr Ala Pro Ala Val Asp Arg Asp Leu Glu Ala
 85 90 95

cac cct gca gag gaa tct caa gca cag cct cca gca tat gat gaa gac 336
 His Pro Ala Glu Glu Ser Gln Ala Glu Pro Pro Ala Tyr Asp Glu Arg
 100 105 110

gat gag gcc ggt gcc gat ggg ccc ttg atg gac aac aaa caa cag ctc 384
 Asp Glu Ala Gly Ala Asp Val Pro Leu Met Asp Asn Lys Gln Gln Leu
 115 120 125

tct taa gcc cgt aat tag 402
 Ser Ser Gly Arg Thr
 130

<210> 128

<211> 133

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 129

Met Asp Arg Asp His Ile Asn Asp His Asp His Arg Met Ser Tyr Ser
 1 5 10 15

Ile Asn Lys Asp Asp Leu Leu Leu Met Val Leu Ala Val Phe Ile Pro
 20 25 30

Pro Val Ala Val Tyr Lys Arg Lys Gly Met Phe Asn Arg Asp Thr Leu
 35 40 45

Leu Asn Leu Leu Leu Phe Leu Leu Leu Phe Phe Pro Ala Ile Ile His
 50 55 60

Ala Cys Tyr Val Val Tyr Glu Thr Ser Ser Glu Arg Ser Tyr Asp Met
 65 70 75 80

Ser Arg Arg His Ala Thr Ala Pro Ala Val Asp Arg Asp Leu Glu Ala

85

96

95

His Pro Ala Glu Glu Ser Glu Ala Gly Pro Pro Ala Tyr Asp Glu Asp
 100 105 110

Asp Glu Ala Gly Ala Asp Val Pro Leu Met Asp Asn Lys Gln Gln Leu
 115 120 125

Ser Ser Gly Arg Thr
 130

<210> 130

<211> 768

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(768)

<400> 130

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 Met Ala Val Gly Lys Asn Lys Arg Leu Ser Tyr Gly Tyr Tyr Gly Gln
 1 5 10 15

aag aag aga gtc gtt gac cca ttt acc aga aag gaa tgg ttc gac att 36
 Lys Lys Arg Val Val Asp Pro Phe Thr Arg Lys Glu Tyr Phe Asp Ile
 20 25 30

aaa gct cca tcc act ttt gaa aac aga aat gtt ggt aag act tta gtt 144
 Lys Ala Pro Ser Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Val
 35 40 45

aac aag tcc act ggt ttg aag agt ggt tca gat ggt ttg aaa ggt aga 192
 Asn Lys Ser Thr Gly Leu Lys Ser Ala Ser Asp Ala Leu Lys Gly Arg
 50 55 60

gtt gtc gaa gtt tgc ttg gct gac tta cag ggt tct gaa gac cac tct	240
Val Val Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser	
65 70 75 80	
ttc aga aaa atc aac tta aga gtt gac gaa gtc caa ggt aag aat tta	360
Phe Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu	
85 90 95	
ttg acc aac ttc cac ggt atg gac ttc act act gat aaa ttg aga tcc	366
Leu Thr Asn Phe His Gly Met Asp Phe Thr Thr Asp Lys Leu Arg Ser	
100 105 110	
atg gtt aga aag tgg caa act ttg atc gaa gct aac gtt act gtt aag	384
Met Val Arg Lys Trp Gln Thr Leu Ile Glu Ala Asn Val Thr Val Lys	
115 120 125	
act tct gat gat tac gtt ttg aga atc ttt gct atc gcc ttc acc aga	432
Thr Ser Asp Asp Tyr Val Leu Arg Ile Phe Ala Ile Ala Phe Thr Arg	
130 135 140	
aag caa gct aac caa gtt aag aga ccc tct tac gct caa tct tac aac	480
Lys Gln Ala Asn Gln Val Lys Arg His Asn Tyr Ala Gln Ser Ser His	
145 150 155 160	
atc aga gct acc aga aag gtt att tcc gaa acc ttg act aag gaa gtc	528
Ile Arg Ala Ile Arg Lys Val Ile Ser Glu Ile Leu Thr Lys Glu Val	
165 170 175	
caa aga tct acc ttc gcc caa ttg acc tcc aag ttg att cca gaa gtc	576
Gln Gly Ser Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val	
180 185 190	
atc aac aag gaa att gaa aac gcc acc aag gac att ttc cca cta caa	624
Ile Asn Lys Glu Ile Glu Asn Ala Thr Lys Asp Ile Phe Pro Leu Gln	
195 200 205	
aac atc cat gtt aga aag gtt aag ttg ttg aac cca cca aag ttc gat	672
Asn Ile His Val Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp	
210 215 220	
gtc ggt gct ttg atg gct ttg caa ggt gaa ggt tct ggt gaa gaa aag	720
Val Gly Ala Leu Met Ala Leu His Gly Glu Gly Ser Gly Glu Glu Lys	

225	230	235	240	
ggg aag aag ggt acc ggt ttc aag gac gaa gtc ttg gaa act gtg taa	768			
Gly Lys Lys Val Thr Gly Phe Lys Asp Glu Val Leu Glu Thr Val				
	245	250	255	

<210> 131
 <211> 255
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <430> 131

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Gln
1 5 10 15

Lys Lys Arg Val Val Asp Pro Phe Thr Arg Lys Glu Trp Phe Asp Ile
20 25 30

Lys Ala Pro Ser Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Val
35 40 45

Asn Lys Ser Thr Gly Leu Lys Ser Ala Ser Asp Ala Leu Lys Gly Arg
50 55 60

Val Val Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser
65 70 75 80

Phe Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu
85 90 95

Leu Thr Asn Phe His Gly Met Asp Phe Thr Thr Asp Lys Leu Arg Ser
100 105 110

Met Val Arg Lys Trp Glu Thr Leu Ile Gly Ala Asn Val Thr Val Lys
 115 120 125

Thr Ser Asp Asp Tyr Val Leu Arg Ile Phe Ala Ile Ala Phe Thr Arg
 130 135 140

Lys Glu Ala Asn Gln Val Lys Arg His Ser Tyr Ala Gln Ser Ser His
 145 150 155 160

Ile Arg Ala Ile Arg Lys Val Ile Ser Glu Ile Leu Thr Lys Glu Val
 165 170 175

Gln Gly Ser Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val
 180 185 190

Ile Asn Lys Gly Ile Glu Asn Ala Thr Lys Asp Ile Phe Pro Leu Glu
 195 200 205

Asn Ile His Val Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp
 210 215 220

Val Gly Ala Leu Met Ala Leu His Gly Gln Gly Ser Gly Glu Glu Lys
 225 230 235 240

Gly Lys Lys Val Thr Gly Phe Lys Asp Glu Val Leu Glu Thr Val
 245 250 255

<210> 132

<211> 339

<212> DNA

<213> Saccharomyces cerevisiae

-320-

«221» CHB

222 (1) - (339)

<400> -32

atg tat ctd agt ggc cag ctt atg aga act gtc aca ggc tcc cao ttg 48
Met Tyr Leu Ser Ala Gln Leu Met Arg Thr Val Thr Ala Ser His Leu
1 5 10 15

acc cnc aga gcc cnc tcc act cnc ccc ctc ttt naa caa cgc cag ata 96
 Thr Leu Arg Ala Leu Ser Thr Pro Pro Leu Phe Gln His Arg Gln Ile
 20 25 30

gnc gnc gtt gaa tgg tgc ggg aca acc egg cct ggc ctg gcc agg aac 144
Ala Ala Val Glu Trp Cys Gly Thr Thr Arg Pro Gly Leu Ala Arg Glu
35 40 45

aaa agg acg cag cac ggc tgg agc gtt att tgc aaa tgg ggc gta ota 192
Lys Arg Thr Gln His Ala Ser Ser Val Ile Ser Lys Ser Gly Val Leu
50 55 60

Lex	guc	acg	guc	acg	luc	guc	lil	lta	guc	all	guc	gga	aaa	lty	240
Ser	Ala	Lys	Pro	Ser	Ser	Val	Phe	Leu	Ala	Ileu	Ileu	Ala	Gly	Tyr	Leu
65					70					75				80	

[illegible]

gta aat gag tgt cca gtg grg ttt cat tct gga cca gtt gnt tgg aag 336
Val Asn Glu Cys Pro Val Val Phe His Ser Gly Pro Val Val Trp Lys
100 105 110

tag 339

c210s 133

211 112

<212> PR1

<213> Saccharomyces cerevisiae

c400s 133

Met Tyr Leu Ser Ala Glu Leu Met Arg Thr Val Thr Ala Ser His Leu
1 5 10 15

Thr Leu Arg Ala Leu Ser Thr Pro Pro Leu Phe Glu His Arg Glu Ile
20 25 30

Ala Ala Val Glu Trp Cys Gly Thr Thr Arg Pro Gly Leu Ala Arg Glu
35 40 45

Lys Arg Thr Gln His Ala Ser Ser Val Ile Ser Lys Ser Gly Val Leu
50 55 60

Ser Ala Tyr Pro Ser Ser Val Phe Leu Ala Leu Ala Gly Lys Leu
65 70 75 80

Ala Glu Lys Tyr Ile Tyr Ala Arg Met Leu Leu Phe His Val Ser Val
85 90 95

Val Asn Glu Cys Pro Val Val Phe His Ser Gly Pro Val Val Trp Tyr
100 105 110

<210> 134

<211> 1422

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1422)

<400> 134

atg ggt gga gaa att att act ttg caa gca ggt caa tgc ggg aac cac
Met Gly Gly Glu Ile Ile Thr Leu Glu Ala Gly Gln Cys Gly Asn His

1	5	10	15	
gtt ggt aag ttt ctg tgg tat caa tgg ggg aaa gaa cac gat ata ggc				26
Val Gly Lys Phe Leu Trp Ser Gln Leu Ala Lys Glu His Ala Ile Gly				
	20	25	30	
adu gat ggg cta tat cag ctt cct gat tcc agt aag gaa aga gat gat				144
Thr Asp Gly Leu Ser Gln Leu Pro Asp Ser Ser Thr Glu Arg Asp Asp				
	35	40	45	
gac aca aag cct ttc ttc cgc gaa aac agt agg aat aag ttt acg cca				192
Asp Thr Lys Pro Phe Phe Arg Glu Asn Ser Arg Asn Lys Phe Thr Pro				
	50	55	60	
agg gct att atg atg gat tcc gag cct ayt glu atc gcc gac gtg gag				240
Arg Ala Ile Met Met Asp Ser Glu Pro Ser Val Ile Ala Asp Val Glu				
	65	70	75	80
aac aca ttt cgt ggg ttt ttc gac cca aga aat acc tgc gta gct tcc				288
Asn Thr Phe Arg Gly Phe Phe Asp Pro Arg Asn Thr Trp Val Ala Ser				
	85	90	95	
gat ggc gct agt gct ggt aat tct tgg gcc aat ggg tat gat ata gga				336
Asp Gly Ala Ser Ala Gly Asn Ser Trp Ala Asn Gly Tyr Asp Ile Gly				
	100	105	110	
act cct aac cag gat gat att ctt aac aag atc gcc aag gag att gat				384
Thr Arg Asn Gln Asp Asp Ile Leu Asn Lys Ile Asp Lys Glu Ile Asp				
	115	120	125	
tct acc gac aat ttc gaa ggt ttc cag ttg ctg can tca gta gcc gga				432
Ser Thr Asp Asn Phe Glu Gly Phe Gln Val Leu His Ser Val Ala Gly				
	130	135	140	
ggg acc ggt tca ggg ctg gga tcc aac ctc tta gaa gcg ctg tgt gat				480
Gly Thr Gly Ser Gly Leu Gly Ser Asn Leu Leu Glu Ala Leu Cys Asp				
	145	150	155	160
aga tat cct aca aaa ata ctc acg aca tat tct gtg ttc cct gaa aga				528
Arg Tyr Pro Lys Lys Ile Leu Thr Thr Tyr Ser Val Phe Pro Ala Arg				
	165	170	175	

340	345	350	
cac gtt aac att gga aga aga tgg cca tac ttg cct tta caa cca aat			1104
His Val Asn Ile Gly Arg Arg Ser Pro Tyr Leu Pro Leu Gly Pro Asn			
355	360	365	
gaa aac gaa gtt agc ggc atg atg tta agc aat atg tct acc gtg gtg			1152
Glu Asn Glu Val Ser Gly Met Met Leu Ser Asn Met Ser Thr Val Val			
370	375	380	
aac gtc ttt gag aat gcg tgc aat act ttt gac aaa gta ttt gcc aag			1200
Asn Val Phe Glu Asn Ala Cys Asn Thr Phe Asp Lys Val Phe Ala Lys			
385	390	395	400
ggc gca ttt tta aat aat tat aat gta ggc gac ttg ttc caa tca atg			1248
Gly Ala Phe Leu Asn Asn Tyr Asn Val Gly Asp Leu Phe Gln Ser Met			
405	410	415	
cag aac gtt caa get gaa ttc gcc gag tca agc gaa gta gta caa agc			1296
Gln Asn Val Gln Asp Glu Phe Ala Glu Ser Arg Glu Val Val Gln Ser			
420	425	430	
ctg atg gag gat tat gta gct gca gaa caa gat lug cac ttg gac gat			1344
Leu Met Glu Asp Tyr Val Ala Ala Glu Gln Asp Ser Tyr Leu Asp Asp			
435	440	445	
gta cct gtt gaa gat gaa aat atg gtt ggc gag ttg gaa gag gac ctg			1392
Val Leu Val Asp Asp Glu Asn Met Val Gly Glu Leu Glu Asp Leu			
450	455	460	
gat ggc gac ggt gat cat aaa tta gta taa			1440
Asp Ala Asp Gly Asp His Lys Leu Val			
465	470		

<210> 135

<211> 473

<212> DRT

<213> *Saccharomyces cerevisiae*

<400> 135

Met Gly Gly Glu Ile Ile Thr Leu Gln Ala Gly Gln Cys Gly Asn His
 1 5 10 15

Val Gly Lys Phe Leu Trp Ser Gln Leu Ala Lys Glu His Ala Ile Gly
 20 25 30

Thr Asp Gly Leu Ser Gln Leu Pro Asp Ser Ser Thr Glu Arg Asp Asp
 35 40 45

Asp Thr Lys Pro Phe Phe Arg Glu Asn Ser Arg Asn Lys Phe Thr Pro
 50 55 60

Arg Ala Ile Met Met Asp Ser Glu Pro Ser Val Ile Ala Asp Val Glu
 65 70 75 80

Asn Thr Phe Arg Gly Phe Phe Asp Pro Arg Asn Thr Trp Val Ala Ser
 85 90 95

Asp Gly Ala Ser Ala Gly Asn Ser Trp Ala Asn Gly Tyr Asp Ile Gly
 100 105 110

Thr Arg Asn Gln Asp Asp Ile Leu Asn Lys Ile Asp Lys Glu Ile Asp
 115 120 125

Ser Thr Asp Asn Phe Gln Gly Phe Gln Leu Leu His Ser Val Ala Gly
 130 135 140

Gly Thr Gly Ser Gly Leu Gly Ser Asn Leu Leu Glu Ala Leu Cys Asp
 145 150 155 160

Arg Tyr Pro Lys Lys Ile Leu Thr Thr Tyr Ser Val Phe Pro Ala Arg
 165 170 175

Ser Ser Glu Val Val Val Glu Ser Tyr Asn Thr Ile Leu Ala Leu Arg
 180 185 190

Arg Leu Ile Glu Asp Ser Asp Ala Thr Val Val Phe Asp Asn Ala Ser
 195 200 205

Leu Leu Asn Ile Ser Gly Lys Val Phe Arg Asn Pro Asn Ile Asp Leu
 210 215 220

Gln His Thr Asn Glu Leu Ile Ser Thr Ile Ile Ser Ser Val Thr Asn
 225 230 235 240

Ser Ile Arg Phe Pro Ser Tyr Met Tyr Ser Ser Met Ser Ser Ile Tyr
 245 250 255

Ser Thr Leu Ile Pro Ser Pro Glu Leu His Phe Leu Ser Pro Ser Phe
 260 265 270

Thr Pro Phe Thr Ser Asp Tyr Ile His Asp Asp Ile Ala His Lys Gly
 275 280 285

His Ser Ser Tyr Asp Val Met Leu Asp Leu Leu Asp Pro Ser Asn Ser
 290 295 300

Leu Val Ser Thr Ala Met Asn Asn Pro Thr Tyr Phe Asn Val Tyr Asn
 305 310 315 320

Thr Ile Ile Gly Asn Val Glu Pro Arg Gln Ile Ser Arg Ala Met Thr
 325 330 335

Lys Leu Gln Gln Arg Ile Lys Phe Pro Ser Thr Ser Ser Ala Met
 340 345 350

His Val Ser Ile Gly Arg Arg Ser Pro Tyr Leu Pro Leu Gln Pro Asn
 355 360 365

Glu Asn Glu Val Ser Gly Met Met Leu Ser Asn Met Ser Thr Val Val
 370 375 380

Asn Val Phe Glu Asn Ala Cys Asn Thr Phe Asp Lys Val Phe Ala Lys
 385 390 395 400

Gly Ala Phe Leu Asn Asn Tyr Asn Val Gly Asp Leu Phe Glu Ser Met
 405 410 415

Gln Asn Val Gln Asp Glu Phe Ala Glu Ser Arg Glu Val Val Gln Ser
 420 425 430

Asp Met Glu Asp Tyr Val Ala Ala Glu Gln Asp Ser Tyr Leu Asp Asp
 435 440 445

Val Leu Val Asp Asp Glu Asn Met Val Gly Gln Leu Glu Gln Asp Leu
 450 455 460

Asp Ala Asp Gly Asp His Lys Leu Val
 465 470

<210> 136

<211> 615

<212> DNA

<213> *Saethamysa corviciac*

<400> 136

atgggtgcct ccaaatattt ggaagatttg caaagaaga agcaatctga tgttttgaga 60

ttcttgcaaa gactcagagt ctgggaatac agacaaaaga atgtcattca cagagccgct 120

agaccaacta gaccagacaa ggcctagaaga ttgggttaca aagctaagca aggtttcgtt 180

atctaccgtg tcagagttag ccgtggtaac agaagagac ctgttcacaa gggtgctact 240

tcgggttaag caactaacca aggtgtcaal gaattgaaat acaaaagata cttagagagt 300

aaugctyug aaagayttg: teygtgtgcc gctaacttga gactctttaa ctccactcgg 360

gttaaccaag attctactta caagtacttc gaagttalul lygluyacuu lwaacacag 420

gctatccagc gagatgtctg ttacaactgg atctgtgacc cagttacaaa gcacccgtga 480

gctataggtt tgactgcac ttgtaagaaa tccagaggtt tcaacaaggg tcacaaaltc 540

acacacacca aggtcgttag aagaagacc ttgaagagac caacactttt gtacctgtgg 600

agatacagaa aataa 665

<210> 137

<211> 801

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(801)

<400> 137

atg ttg aac gtg cta ttg aga agg aag gcc ttt tgt ttg gtg aag aag 48

Met Leu Asn Val Leu Ile Arg Arg Lys Ala Phe Cys Leu Val Thr Lys

1 5 10 15

aag ggt atg gct acf gcc aca aca gct gcc gct aag cat acc ccc aga 96

Lys Gly Met Ala Thr Ala Thr Thr Ala Ala Ala Thr His Thr Pro Arg

20 25 30

ttg aaa acg ttt aaa gtt tac aga tgg aat cca gac gag cca agt gct	141
Leu Lys Thr Phe Lys Val Tyr Arg Trp Asn Pro Asp Glu Pro Ser Ala	
35 40 45	
aaa cct cat tta caa tca tat cca gtc gat ctg aat gac tgt ggg ccc	192
Lys Pro His Leu Gln Ser Tyr Gln Val Asp Leu Asn Asp Cys Gly Pro	
50 55 60	
atg gta ctt gat gch ctg tta aag atc aat gaa gaa cag gat tct acc	240
Met Val Leu Asp Ala Phe Leu Lys Thr Tyr Asp Glu Gln Asp Ser Thr	
65 70 75 80	
cta acg ttt aga aga tca tgt aga gaa ggc atc tgc ggt tca tgt gcc	288
Leu Thr Phe Arg Arg Ser Cys Arg Glu Gly Ile Cys Gly Ser Cys Ala	
85 90 95	
atg aac att ggc ggt aga aac acg cta gct tgt ata tgt aag atc gac	336
Met Asn Ile Gly Gly Arg Asn Thr Leu Ala Cys Ile Cys Lys Ile Asp	
100 105 110	
cag aac gaa tcc aaa cca ctc aag atc tat cca tta ccc acg atg ttt	384
Gln Asn Glu Ser Lys Gln Leu Lys Ile Tyr Pro Leu Pro His Met Phe	
115 120 125	
att gtc aaa gat ttg gta cct gat tta acg and ttc taa caa cca taa	432
Ile Val Lys Asp Leu Val Pro Asp Leu Thr Asn Phe Tyr Gln Gln Tyr	
130 135 140	
aaa tct atc caa cct taa tta cag aga tca tgg ttt cca aag gat gga	480
Lys Ser Ile Gln Pro Tyr Leu Gln Arg Ser Ser Phe Pro Lys Asp Gly	
145 150 155 160	
acg gaa gtg cta caa agt att gaa gat cgt aag aaa ctg gal ggt ctt	528
Thr Glu Val Leu Gln Ser Ile Glu Asp Arg Lys Lys Leu Asp Gly Leu	
165 170 175	
taa gaa tgt att ctg tgt gca tgc tgc tct act tca tgt cca tgg taa	576
Tyr Glu Cys Ile Leu Cys Ala Cys Cys Ser Thr Ser Cys Pro Ser Tyr	
180 185 190	
lyg lgg aac caa gaa cag tat ttg ggc cct gcc gtg cta atg cca gcc	624
Trp Trp Asn Gln Glu Gln Tyr Leu Gly Pro Ala Val Leu Met Gln Ala	

316/762

195	230	265	
taa cgt tgg cta att gac tct aga gac caa gcc aca aag aca aga aag			672
tyr arg trp leu ile asp ser arg asp gln ala thr lys thr arg lys			
210	215	220	
gcc atg cta aac aac tcc atg tca tgg tac aga tgt cca acc atc atg			720
ala met leu asn asn ser met ser leu tyr arg cys his thr ile met			
225	230	235	240
uuu tgt act aga act tgt cca aag gcc ttg aat cct ggt ttg gct att			768
asn cys thr arg thr cys pro lys gly leu asn pro gly leu ala ile			
245	250	255	
gct gaa att aag aaa tct ttg gca ttt gcc tag			801
ala glu ile lys lys ser leu ala phe ala			
260	265		
<210> 138			
<211> 266			
<212> FRT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 138			
ket leu asn val leu leu arg arg lys ala phe cys leu val thr lys			
1	5	10	15
lys gly met ala thr ala thr thr ala ala ala thr his thr pro arg			
20	25	30	
leu lys thr phe lys val tyr arg trp asn pro asp glu pro ser ala			
35	40	45	
lys pro his leu glu ser tyr glu val asp leu asn asp cys gly pro			
50	55	60	

Met Val Ten Asp Ala Leu Leu Lys Ile Lys Asp Glu Gln Asp Ser Thr
65 70 75 80

Leu Thr Phe Arg Arg Ser Cys Arg Gln Gly Ile Cys Gly Ser Cys Ala
85 90 95

Met Asn Ile Gly Gly Arg Asn Thr Leu Ala Cys Ile Cys Tyr Ile Asp
100 105 110

Gln Asn Glu Ser Lys Gln Leu Lys Ile Tyr Pro Leu Pro His Met Phe
115 120 125

Ile Val Lys Asp Leu Val Pro Asp Leu Thr Asn Phe Tyr Gln Gln Tyr
130 135 140

Lys Ser Ile Gln Pro Tyr Leu Gln Arg Ser Ser Phe Pro Lys Asp Gly
145 150 155 160

Thr Glu Val Leu Gln Ser Ile Glu Asp Arg Tyr Lys Leu Asp Gly Leu
165 170 175

Tyr Glu Cys Ile Leu Cys Ala Cys Cys Ser Thr Ser Cys Pro Ser Tyr
180 185 190

Trp Trp Asn Gln Glu Gln Tyr Leu Gly Pro Ala Val Leu Met Gln Ala
195 200 205

Tyr Arg Trp Leu Ile Asp Ser Arg Asp Gln Ala Thr Lys Thr Arg Lys
210 215 220

Ala Met Leu Asn Asn Ser Met Ser Leu Tyr Arg Cys His Thr Ile Met
225 230 235 240

Asn Cys Thr Arg Thr Cys Pro Iys Gly Leu Asn Pro Gly Leu Ala Ile
 245 250 255

Ala Glu Ile Lys Lys Ser Leu Ala Phe Ala
 260 265

<210> 139
 <211> 1134
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1134)

<400> 159
 atg ttt aaa ggg agg gtc aat cag aag cgt tac aag tat cct ctt cca 45
 Met Ser Iys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro
 1 5 10 15
 att cag ccc gta gat gac ctt cca gag tta atc ctt cat aat cag tta 96
 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
 20 25 30
 tct tgg cta tat tgg gca tac cgc tat tac aag agt aag aac gca cgg 144
 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
 35 40 45
 aac gat aaa gta cat gta gat ttt ata gga gat acc act ctt cag atc 192
 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Phe Leu His Ile
 50 55 60
 acg gtl aaq gat gac aag caa atg cta tat ctt tgg aat aat gga ttt 240
 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
 65 70 75 80
 ttt ggc act ggt caa ttt agc agg agt gag cct aca cgg aaa ggt aga 288

Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg	
85 90 95	
aca gag gcc aga ctg cgt ctc aat gat act ccc ctc cac aat cgg gga	336
Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly	
100 105 110	
gga aca aag agt aat act gaa acg gag atg act tlu gag aag gtc aca	384
Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr	
115 120 125	
caa cag agg aga tta caa aga tta gag ttc aag aaa gaa cgl gcy aag	432
Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys	
130 135 140	
tta gaa aga gaa tta cta gaa tta aga aaa ggt ggt cat atc gal	480
Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp	
145 150 155 160	
gag gaa aac atc ctc att gag aac cgc cga gaa tca tta aga aaa ttt	528
Gln Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe	
165 170 175	
aaa cta aaa caa aca gaa gac gcg ggc atc gtt gca caa cag caa gac	576
Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp	
180 185 190	
att tcc gaa tca aat tta aga gat gaa gaa aac aat att att gat gag	624
Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu	
195 200 205	
aac ggt gat att ttg cca cta gag tca cta gaa ala atg cca gtg gaa	672
Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Met Pro Val Glu	
210 215 220	
gct atg ttt tta act ttt gca att cct gtt att gac ata tct ccc gag	720
Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala	
225 230 235 240	
tgc ccg gca ggg aac ctg ttt caa ttc gat gcc aac taa aaa gat att	768
Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile	
245 250 255	

cac tcc ttt gtc aga tca tuc gtt ata tac cat cnc tac aga tca cac	816
His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His	
260 263 270	

ggc tgg tgc gta aga tct ggt ata aca ttc ggc tgc gat tat tta tta	864
Gly Trp Cys val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu	
275 280 285	

tat aag aga ggg cca cca ttt caa cac gct gaa ttt tgt gtt atg ggt	912
Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly	
290 295 300	

ctt gac cac gac gtc tct aca gat tat acg tgg tat tct agc ata gcc	960
Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala	
305 310 315 320	

cgt gtt gtc ggc ggc gca aag aag acg ttt gtc tta tgc tac gtc gag	1036
Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu	
325 330 335	

aga cta atc tgc gaa cag gag ggc aca gca cta tgg aac tca aac aac	1088
Arg Leu Ile Ser Glu Gln Glu Ala Ile Asn Asn Trp Lys Ser Asn Asn	
340 345 350	

ttt act aca tgg ttc aat agt ttt caa gtt ggc gaa gta tgg tat aag	1104
Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys	
355 360 365	

aga tgg gtt ccc gga aga aat aga gac tag	1134
Arg Trp Val Pro Gly Arg Asn Arg Asp	
370 375	

<210> 140

<211> 377

<212> PRT

<213> Saccharomyces cerevisiae

<400> 140

Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro

1 5 10 15

Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
20 25 30

Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
35 40 45

Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
50 55 60

Thr Val Glu Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
 65 70 75 80

Phe Gly Thr Gly Cln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
85 90 95

Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly
100 103 110

Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr
115 120 125

Gln Gln Arg Arg Leu Glu Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys
130 135 140

Leu Glu Arg Glu Neu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp
145 150 155 160

Glu Glu Asn Ile Leu Leu Glu Lys Cln Arg Glu Ser Leu Arg Lys Phe
165 170 175

Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp
 180 185 190

Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
 195 200 205

Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Gln Leu Met Pro Val Glu
 210 215 220

Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
 225 230 235 240

Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
 245 250 255

His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
 260 265 270

Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
 275 280 285

Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
 290 295 300

Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
 305 310 315 320

Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu
 325 330 335

Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn

340

345

350

Phe Thr Lys Leu Phe Asa Ser Phe Gln Val Gly Glu Val Leu Tyr Lys
 355 360 365

Arg Trp Val Pro Gly Arg Asn Arg Asp
 370 375

<210> 141
 <211> 1182
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1182)

<400> 141
 atg tca tca aga atc att gtc ggc agt gca gca ttg gca gct gcc atc 40
 Met Ser Ser Arg Ile Ile Val Gly Ser Ala Ala Leu Ala Ala Ala Ile
 1 5 10 15
 acc gct agc atc atg gtc aga gaa cag aag gcc aag ggt cag aga aga 95
 Thr Ala Ser Ile Met Val Arg Glu Gln Lys Ala Lys Gly Gln Arg Arg
 20 25 30
 gag ggc aac gtc tcc gct tac tac aac ggc cag gag tac ggc agt tca 144
 Glu Gly Asn Val Ser Ala Tyr Tyr Asn Gly Gln Glu Tyr Gly Ser Ser
 35 40 45
 gca ccc cca cag ttg gga aag cta cat aac ata aag cca ggc ata aag 192
 Ala Pro Pro Gln Leu Gly Lys Leu His Asn Ile Lys Gln Gly Ile Lys
 50 55 60
 gaa gat gcc ttg tog tta aaa gac gag att ctg ggc gta tct oaa aag 240
 Glu Asp Ala Leu Ser Leu Lys Asp Ala Leu Leu Gly Val Ser Gln Lys
 65 70 75 80

ggt agg gaa gag gct cca aag gta act aag cgt gty ata tca cag gaa	288
Ala Arg Glu Glu Ala Pro Lys Val Thr Lys Arg Val Ile Ser Pro Glu	
85 90 95	
gag gaa gct caa aca cgc aag cag cta ggc caa aaa gcc aag gat tct	336
Glu Asp Ala Glu Thr Arg Lys Glu Leu Gly Glu Lys Ala Lys Asp Ser	
100 105 110	
tcc tgg caa agc atc ttc aat tgg ggg ttt agt gag gct gaa aga agg	384
Ser Ser Gln Ser Ile Phe Asn Trp Gly Phe Ser Glu Ala Glu Arg Arg	
115 120 125	
aaa gcc ata gcc atc ggg gaa ttt gat act gct aag aag cgt ttc gaa	432
Lys Ala Ile Ala Le Gly Glu Phe Asp Thr Ala Lys Tyr Arg Phe Glu	
130 135 140	
gag gaa gtg gat cgt aat gaa aag gag ctc ttg tcc acg gtg atg aga	480
Glu Ala Val Asp Arg Asn Glu Lys Glu Leu Leu Ser Thr Val Met Arg	
145 150 155 160	
gag aag aag gcc gct ctg gac aga gca tcc att gag tac gaa aag tac	528
Glu Lys Lys Ala Ala Leu Asp Arg Ala Ser Ile Glu Tyr Glu Arg Tyr	
165 170 175	
ggg aag gcc agc gac ttt aat gag ctt tgg gac aag cta gac caa cag	576
Gly Arg Ala Arg Asp Phe Asn Glu Leu Ser Asp Lys Leu Asp Gln Glu	
180 185 190	
gaa agg aac agt aat cct ttg aaa cgc ctg ttg aag aat aac aag ggt	624
Glu Arg Asn Ser Asn Pro Leu Lys Arg Leu Leu Lys Asn Asn Thr Gly	
195 200 205	
gac gct aat act gaa gaa gcc gct gca aga agt gtc caa gcc tgg ggt	672
Asp Ala Asn Thr Glu Glu Ala Ala Ala Arg Ser Val Gln Gly Trp Gly	
210 215 220	
gat acg gca cag gag ttt ggt aga gaa gag tgg gag gaa gcc aag aga	720
Arg Thr Ala Gln Glu Phe Gly Arg Glu Glu Leu Glu Glu Ala Lys Arg	
225 230 235 240	
aat gct tct leu gag cca agc gag gog caa aaa cgt ctc gac gag ctg	768
Asn Ala Ser Ser Glu Pro Ser Glu Ala Gln Lys Arg Leu Asp Glu Leu	

245	250	255	
aag aag atc aag gaa aag ggc tgg ttt ggt tac aac aaa ggg gag caa			816
Lys Lys Ile Lys Glu Lys Gly Trp Phe Gly Tyr Asn Lys Gly Glu Gln			
240	265	270	
agc gag caa cag att gct gaa cgg gta gcc aga ggt tta gaa gga tgg			864
Ser Glu Gln Gln Ile Ala Glu Arg Val Ala Arg Gly Leu Glu Gly Trp			
275	280	285	
ggc gaa aca gaa gct caa ctt tcc aag gac gaa atg gac gat tta aga			912
Gly Ala Thr Ala Ala Gln Leu Ser Lys Asp Glu Met Asn Asp Leu Arg			
290	295	300	
tgg aat tat gag act tca aag aaa caa ctg gat aag aac gtg tcc gac			960
Trp Asn Tyr Glu Asn Ser Lys Lys Gln Leu Asp Lys Asn Val Ser Arg			
305	310	315	320
gaa atg gac cag tta tct aag cgc aag gag gaa ttg aac cag tcc ggc			1008
Ala Met Asn Ser Leu Ser Lys Ala Lys Glu Asp Leu Lys Gln Tyr Gly			
325	330	335	
agc cac tgg tgg tct gga tgg act tca aag gtc gac aat gac aag cag			1056
Ser His Trp Trp Ser Gly Trp Thr Ser Lys Val Asp Asn Asp Lys Gln			
340	345	350	
gct ctc aaa gat gac gcc caa aag aag tac gat gaa ggc ttg aaa aag			1104
Ala Leu Lys Asp Glu Ala Gln Lys Lys Tyr Asp Glu Ala Leu Lys Lys			
355	360	365	
tac gat gaa gcc aag aac aaa ttc aaa gaa tgg aat gat aag ggt gac			1152
Tyr Asp Glu Ala Lys Asn Lys Phe Lys Glu Trp Asn Asp Lys Gly Asp			
370	375	380	
ggt aaa ttc tgg agc tcc aaa aag gac tag			1192
Gly Lys Phe Trp Ser Ser Lys Lys Asp			
385	390		
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<212>	PRP		

<213> *Saccharomyces cerevisiae*

<430> 142

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Thr Ala Ser Ile Met Val Arg Glu Gln Lys Ala Lys Gly Gln Arg Arg
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Glu Gly Asn Val Ser Ala Tyr Tyr Asn Gly Glu Glu Tyr Gly Ser Ser
35 40 45

Ala Pro Pro Gln Leu Gly Lys Leu His Asn Ile Lys Glu Gly Ile Lys
50 55 60

Glu Asp Ala Leu Ser Leu Lys Asp Ala Leu Leu Gly Val Ser Gln Lys
65 70 75 80

His Arg Glu Glu Ala Pro Lys Val Thr Lys Arg Val Ile Ser Pro Glu
85 90 95

Glu Asp Ala Glu Thr Arg Lys Gln Leu Gly Gln Lys Ala Lys Asp Ser
100 105 110

Ser Ser Gln Ser Ile Phe Asn Trp Gly Phe Ser Glu Ala Glu Arg Arg
115 120 125

Lys Ala Ile Ala Ile Gly Glu Phe Asp Thr Ala Lys Lys Arg Phe Glu
130 135 140

Glu Ala Val Asp Arg Asn Glu Lys Glu Leu Leu Ser Thr Val Met Arg
145 150 155 160

Glu Lys Lys Ala Ala Leu Asp Arg Ala Ser Ile Glu Tyr Glu Arg Tyr
165 170 175

Gly Arg Ala Arg Asp Phe Asn Glu Leu Ser Asp Lys Leu Asp Gln Gln
180 185 190

Glu Arg Asn Ser Asn Pro Leu Lys Arg Leu Leu Lys Asn Asn Thr Gly
195 200 205

Asp Ala Asn Thr Glu Glu Ala Ala Ala Arg Ser Val Gln Gly Trp Gly
210 215 220

Asp Thr Ala Glu Glu Phe Gly Arg Glu Glu Leu Glu Glu Ala Lys Arg
225 230 235 240

Asn Ala Ser Ser Glu Pro Ser Glu Ala Gln Lys Arg Ser Asp Glu Leu
245 250 255

Lys Lys Ile Lys Glu Lys Gly Trp Phe Gly Tyr Asn Lys Gly Glu Gln
260 265 270

Ser Glu Gln Gln Ile Ala Glu Arg Val Ala Arg Gly Leu Glu Gly Trp
275 280 285

Gly Glu Thr Ala Ala Gln Leu Ser Lys Asp Glu Met Asp Asp Leu Arg
290 295 300

Trp Asn Tyr Glu Asn Ser Lys Lys Gln Leu Asp Lys Asn Val Ser Asp
305 310 315 320

Ala Met Asp Ser Leu Ser Lys Ala Lys Glu Asp Leu Lys Gln Tyr Gly
 325 330 335

Ser His Trp Trp Ser Gly Trp Thr Ser Lys Val Asp Asn Asp Lys Gln
 340 345 350

Ala Leu Lys Asp Glu Ala Gln Lys Lys Tyr Asp Glu Ala Leu Lys Tyr
 355 360 365

Tyr Asp Glu Ala Lys Asn Lys Phe Lys Glu Trp Asn Asp Lys Gly Asp
 370 375 380

Gly Lys Phe Trp Ser Ser Lys Lys Asp
 385 390

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 <212> DNA
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gcg cag gtt gaa cgc tgc tct tac tcy ttt tgg tcc tca ctg tat ccc 96
 Ala Gln Val Gln His Cys Ser Tyr Ser Phe Thr Ser Ser Leu Tyr Pro
 20 25 30

aaa tat gtg cca aaa tcc ata gtg tta aaa tcc tta ccg aaa aaa ttt 142
 Lys Tyr Val Pro Lys Ser Ile Val Leu Lys Ser Leu Pro Lys Lys Phe
 35 40 45

atL uaa tat ttg gaa caa gaa ggt atc aag cta ccc caa gag gaa aac	192
Ile Gln Tyr Leu Glu Gln Asp Gly Ile Lys Leu Pro Gln Glu Glu Arg	
50 55 60	
tcc agg tct gty tac acc gag gaa ata ata aga aat gaa gat aat gac	240
Ser Arg Ser Val Tyr Thr Glu Glu Ile Ile Arg Asn Glu Asp Asn Asp	
65 70 75 80	
tat agt gat tgg gag gac gat gag gat acc gcc acc gaa ttt gtc caa	288
Tyr Ser Asp Trp Glu Asp Asp Glu Asp Thr Ala Thr Glu Phe Val Gln	
85 90 95	
gaa gtt gag cca ttg ata gat ttt cca gaa tta ccc cag aaa tta aag	336
Glu Val Glu Pro Leu Ile Asp Phe Pro Glu Leu His Gln Lys Leu Lys	
100 105 110	
gat gct ttg aac gaa tta ggt gca gtg got ccc aag tta aac tgg tct	384
Asp Ala Leu Asn Glu Leu Gly Ala Val Ala Pro Lys Leu Asn Trp Ser	
115 120 125	
gca ccc aga gac got ccc tgg att tly ccy aat aac act atg cag tgt	432
Ala Pro Arg Asp Ala Thr Trp Ile Leu Pro Asn Thr Met Lys Cys	
130 135 140	
aac gag gta aat gag ctt cac cta ttg ttg aac gca tcc aat tac ata	480
Asn Glu Val Asn Glu Leu Tyr Leu Leu Leu Asn Ala Ser Asn Tyr Ile	
145 150 155 160	
atg cat gac ctt caa aga gca ttt aaa ggc tgc gtc gaa ggg gat gat	528
Met His Asp Leu Gln Arg Ala Phe Lys Gly Cys Val Asp Gly Asp Asp	
165 170 175	
ata aaa gga ttg aaa ttt gac ttg gta ctt aga caa tgg tgt gat atg	576
Ile Lys Gly Leu Lys Phe Asp Leu Val Leu Arg Gln Trp Cys Asp Met	
180 185 190	
aat ccg gca atc gaa ttt agg gtc ttc gtt aag aal gcy cat atc gtt	624
Asn Pro Ala Leu Glu Phe Arg Val Phe Val Lys Asn Ala His Ile Val	
195 200 205	
ggg gcc acc aag ogt gat tta aat tat tat gac tat tta gat gag tly	672

Gly Ala Thr Gln Arg Asp Leu Asn Tyr Tyr Asp Tyr Leu Asp Glu Leu	
210 215 220	
tca gat acc ttc aag gac ctt att gal gaa ata gtt cat gat gtc gtc	720
Ser Asp Thr Phe Lys Asp Leu Ile Asp Glu Ile Val His Asp Val Val	
225 230 235 240	
ctg acc aag tct cct gat aaa agl LLe gtt ctt gac gtt tat att cca	768
Leu Pro Lys Phe Pro Asp Lys Ser Phe Val Leu Asp Val Tyr Ile Pro	
245 250 255	
aga cct ttc aat aaa atc ttc att gtt gat ata aat ccg ttt gcc agg	816
Arg Pro Phe Asn Lys Ile Phe Ile Val Asp Ile Asn Pro Phe Ala Arg	
260 265 270	
aag acc gat tct ttg cta ttt tca tgg aac gag att gct gag ala gaa	864
Lys Thr Asp Ser Leu Leu Phe Ser Trp Asn Glu Ile Ala Ala Ile Ala	
275 280 285	
cct ccg aag aat gat gtt gaa gat tat gag tta agg tta gtc acc agg	912
Pro Pro Lys Asn Asp Val Glu Asp Tyr Glu Leu Arg Leu Val Thr Arg	
290 295 300	
cat acc acg ggg aga ttc gct tca aaa gag cac tcc gaa aat cat gtt	960
His Asn Thr Gly Arg Phe Ala Ser Lys Glu His Ser Glu Asn His Val	
305 310 315 320	
caa cag gat ctg gta gaa gct agt tta aat cct gaa gca atc cga gag	1008
Pro Glu Asp Leu Val Glu Ala Ser Leu Asn Pro Glu Ala Ile Arg Glu	
325 330 335	
ctc act caa aaa tgg aaa gaa cta ctg tct caa cag gca aag gaa gaa	1056
Leu Thr Gln Lys Trp Lys Glu Leu Leu Ser Gln Gln Ala Lys Glu Gln	
340 345 350	
agc agt gat agt gag aat gaa act lag	1083
Ser Ser Asp Ser Glu Asn Glu Thr	
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<210> 111	
<211> 360	

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 144

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20           25           30
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Lys Tyr Val Pro Lys Ser Ile Val Leu Lys Ser Leu Pro Lys Lys Phe
35           40           45
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Ile Gln Tyr Leu Glu Gln Asp Gly Ile Lys Leu Pro Gln Glu Glu Asn
50           55           60
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Ser Arg Ser Val Tyr Thr Glu Glu Ile Ile Arg Asn Glu Asp Asn Asp
65           70           75           80
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Tyr Ser Asp Trp Glu Asp Asp Glu Asp Thr Ala Thr Glu Phe Val Gln
85           90           95
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Glu Val Glu Pro Leu Ile Asp Phe Pro Glu Leu His Gln Lys Leu Lys
100          105          110
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Asp Ala Leu Asn Glu Leu Gly Ala Val Ala Pro Lys Leu Asn Trp Ser
115          120          125
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Ala Pro Arg Asp Ala Thr Trp Ile Leu Pro Asn Asn Thr Met Lys Cys
130          135          140
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Asn Glu Val Asn Glu Leu Tyr Leu Leu Leu Asn Ala Ser Asn Tyr Ile
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145	150	155	160
Met His Asp Leu Glu Arg Ala Phe Lys Gly Cys Val Asp Gly Asp Asp			
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Ile Lys Gly Met Lys Phe Asp Leu Val Leu Arg Gln Trp Cys Asp Met			
	180	185	190
Asn Pro Ala Leu Glu Phe Arg Val Phe Val Lys Asn Ala His Ile Val			
	195	200	205
Gly Ala Thr Glu Arg Asp Leu Asn Tyr Tyr Asp Tyr Leu Asp Glu Leu			
	210	215	220
Ser Asp Thr Phe Lys Asp Leu Ile Asp Glu Ile Val His Asp Val Val			
	225	230	235
Leu Pro Lys Phe Pro Asp Lys Ser Phe Val Leu Asp Val Tyr Ile Pro			
	240	245	250
Arg Pro Phe Asn Lys Ile Phe Ile Val Asp Ile Asn Pro Phe Ala Arg			
	255	260	265
Lys Thr Asp Ser Leu Leu Phe Ser Trp Asn Glu Ile Ala Ala Ile Ala			
	270	275	280
Pro Pro Lys Asn Asp Val Glu Asp Tyr Gln Leu Arg Leu Val Thr Arg			
	285	290	295
His Asn Thr Gly Arg Phe Ala Ser Lys Glu His Ser Glu Asn His Val			
	300	305	310
		315	320

Pro Gln Asp Leu Val Glu Ala Ser Leu Asn Pro Glu Ala Ile Arg Glu
 325 330 335

Leu Thr Glu Lys Trp Lys Glu Leu Leu Ser Gln Gln Ala Lys Glu Glu
 340 345 350

Ser Ser Asp Ser Gln Asn Glu Thr
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<210> 145
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 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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 cat aac aga tgg aca aac gaa gat gat ggt aac ccc atc ttt aca atg 96
 His Asn Arg Leu Thr Asn Glu Asp Asp Gly Ile Pro Ile Phe Thr Met
 20 25 30
 gct cca cca aca agt cag cat aaa agt gct aac gtg gtc aac tat gcg 144
 Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala
 35 40 45
 gaa tat gac aac gat ctc ttt gat gaa ttc aat atg aac ggt tct aat 192
 Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn
 50 55 60
 llu aau aat gct gat aca ccc tat aaa qat aat qca gtg tct cat gaa 240
 Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu

65	70	75	80	
aat act cag gca ctt gca aat ggt gtt acc atg gac ggt tcc gaa tac				388
Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asn Gly Ser Glu Tyr				
	85	90	95	
aat gtc cta gag aac atg aat gga gct gat agt att atc lct aac aac				386
Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn				
	100	105	110	
aaa tuc gat gcg ggt tca aac atg gtt gtg gaa tct tta tcc ggt ttg				384
Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu				
	115	120	125	
aat agc aat aac aac gcc agc aac ggt cag agc aac aaa gcg cag gca				432
Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Glu Ala				
	130	135	140	
cag gat att gga aac gcc gtt cta cag gat ctg cca gac caa ctc caa				480
Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Glu His His				
	145	150	155	160
aac ccc ttc aac ala ttg aga tac ccc aac ata aga gat act ttc att				520
Asn Pro Phe Asn Ile Asn Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile				
	165	170	175	
aac gga aac gtc gtc tct cca tat aga ctg aac act gat caa gaa acg				576
Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Glu Thr				
	180	185	190	
cag gcc aac gcc aat tct gga gag gca atc atg ata cca att act ttg				624
Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Ile Pro Ile Thr Leu				
	195	200	205	
gat ata gaa cat atg ggt cat acc ata aaa gac cag ttt ctc tgg aac				672
Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn				
	210	215	220	
lac aat gac gac tcc ata tct cag gag gaa ttt gcc tct ata tcc tgt				720
Tyr Asn Asp Arg Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Cys				
	225	230	235	240

aaa gat ctt gat atg act tcc gct acc tta cca act cca att ggg aat	788
Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Glu Thr Glu Ile Ala Asn	
345 250 255	
ata ata aaa gag cag ttg aaa gac ctc gaa aat att gca gcc act gag	876
Ile Ile Lys Glu Glu Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu	
260 265 270	
ata atg tct gac ctc cac gtg ata atu aag cta acc tgc aad tta cca	884
Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Glu	
275 280 285	
gac aga ttt ttt gaa gat aac ttc cag tgg aac tly aau gaa aaa tca	912
Asp Arg Phe Phe Glu Asp Asn Phe Glu Trp Asn Leu Asn Asp Tyr Ser	
290 295 300	
att act cca gaa aga ttt gct aca tcc att gta cag gac ctt ggc tta	960
Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Glu Asp Leu Cys Leu	
305 310 315 320	
aca aga gag ttc atc acc tta ata tct cca tgg ctt cat gaa aul atc	1008
Thr Arg Glu Phe Ile Pro Leu Ile Ser Glu Ser Leu His Glu Thr Ile	
325 330 335	
ttg aag ata aag aag gac ggg gta gat cgc ctc ttg att cag gac cat	1056
Leu Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Glu Asp His	
340 345 350	
glt cca aac gat gcc gca ttt ggg tac tta tct ggt ata agg cng gat	1104
Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp	
355 360 365	
att gat gaa ctg ggc tcc aat tgg tgc cca ugg gtg gaa ata tta aca	1152
Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Ile Leu Thr	
370 375 380	
aaa gaa gaa ata cca aag aga gaa att gaa aaa gaa aga aac tta aga	1200
Lys Glu Glu Ile Glu Lys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg	
385 390 395 400	
uga tgg aaa aga gaa act gat aga tta tct aga aag ggc agg aga aga	1248
Arg Leu Tyr Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg	

105

410

415

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1281

Leu Asp Asp Leu Glu Thr Thr Met Arg Met

420

425

<210> 146

<211> 426

<212> PRT

<213> Saccharomyces cerevisiae

<400> 146

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1

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10

15

His Asn Arg Leu Thr Asn Glu Asp Asp Gly Ile Pro Ile Phe Thr Met

20

25

30

Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala

35

40

45

Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn

50

55

60

Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu

65

70

75

80

Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asp Gly Ser Glu Tyr

85

90

95

Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn

100

105

110

Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu
 115 120 125

Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Gln Ala
 130 135 140

Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Glu His His
 145 150 155 160

Asn Pro Phe Asn Ile Leu Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile
 165 170 175

Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Gln Glu Thr
 180 185 190

Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Thr Pro Ile Thr Leu
 195 200 205

Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn
 210 215 220

Tyr Asn Asp Asp Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Lys
 225 230 235 240

Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Gln Thr Gln Ile Ala Asn
 245 250 255

Ile Ile Lys Glu Gln Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu
 260 265 270

Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln
 275 280 285

Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser
 290 295 300

Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Gly Leu
 305 310 315 320

Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile
 325 330 335

Leu Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Gln Asp His
 340 345 350

Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp
 355 360 365

Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Thr Leu Thr
 370 375 380

Lys Glu Glu Ile Glu Tyr Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg
 385 390 395 400

Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg
 405 410 415

Leu Asp Asp Leu Glu Thr Thr Met Arg Met
 420 425

<210> 147

<211> 462

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> [1]..(462)

<400> 147

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Met	Gly	Lys	Lys	Asn	Thr	Lys	Gly	Gly	Lys	Lys	Gly	Arg	Arg	Gly	Lys
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1				5					10					15	
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aac	gac	tct	gac	ggc	cca	aag	cgt	gaa	ctt	att	tat	aag	gaa	ggc	96
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Asn	Asp	Ser	Asp	Gly	Pro	Lys	Arg	Glu	Leu	Ile	Tyr	Lys	Glu	Glu	Gly
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			20					25					30		
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caa	gaa	tat	aaa	caa	atc	acc	aag	atg	tty	ggc	aat	gga	aga	gtc	gaa	144
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Gln	Glu	Tyr	Ala	Gln	Ile	Thr	Lys	Met	Leu	Gly	Asn	Gly	Arg	Val	Glu
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			35					40					45		
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gcc	agt	tgc	ttc	gat	ggc	aat	aag	aga	atg	gcc	cat	att	aga	ggc	aag	192
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Ala	Ser	Cys	Phe	Asp	Gly	Asn	Lys	Arg	Met	Ala	His	Ile	Arg	Gly	Lys
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			50					55					60		
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tta	aga	aag	aaa	gtc	tgg	atg	ggc	caa	ggc	gat	att	att	ctt	gtt	tcc	240
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Leu	Arg	Lys	Lys	Val	Trp	Met	Gly	Gln	Gly	Asp	Ile	Ile	Leu	Val	Ser
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65					70					75				80	
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tta	aga	gat	ttc	caa	gat	gac	caa	tgl	gat	gtt	gtc	caa	aaa	tat	aat	288
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Leu	Arg	Asp	Phe	Gln	Asp	Asp	Glu	Cys	Asp	Val	Val	His	Lys	Tyr	Asn
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			85					90					95		
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tta	gat	gaa	gcc	aga	aca	ctg	aaa	aac	caa	ggt	gaa	ctt	ctt	gaa	aac	336
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Ieu	Asp	Glu	Ala	Arg	Thr	Leu	Lys	Asn	Gln	Gly	Glu	Leu	Pro	Glu	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

			100					105					110		
--	--	--	-----	--	--	--	--	-----	--	--	--	--	-----	--	--

gcc	aaa	att	aat	gaa	aca	gac	aac	ttt	ggt	ttc	gaa	tct	gat	gaa	gac	384
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala	Lys	Ile	Asn	Glu	Thr	Asp	Asn	Phe	Gly	Phe	Glu	Ser	Asp	Glu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

			115					120					125		
--	--	--	-----	--	--	--	--	-----	--	--	--	--	-----	--	--

gtt	aaa	ttt	gaa	ttt	ggc	aac	gct	gat	gaa	gat	gat	gag	gaa	ggc	gaa	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val	Asn	Phe	Glu	Phe	Gly	Asn	Ala	Asp	Glu	Asp	Asp	Glu	Glu	Gly	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

			130					135					140		
--	--	--	-----	--	--	--	--	-----	--	--	--	--	-----	--	--

Gat Gaa Gaa Ctt Gat Att Ggt Gac Att Taa 462
 Asp Glu Glu Asp Asp Ile Asp Asp Ile
 145 150

<213> 140
 <211> 153
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 140

Met Gly Lys Lys Asn Thr Lys Gly Gly Lys Lys Gly Arg Arg Gly Lys
 1 5 10 15

Asn Asp Ser Asp Gly Pro Lys Arg Glu Leu Ile Tyr Lys Glu Glu Gly
 20 25 30

Gln Glu Tyr Ala Glu Ile Thr Lys Met Leu Gly Asn Gly Arg Val Glu
 35 40 45

Ala Ser Cys Phe Asp Gly Asn Lys Arg Met Ala His Ile Arg Gly Lys
 50 55 60

Leu Arg Lys Lys Val Trp Met Gly Gln Gly Asp Ile Ile Leu Val Ser
 65 70 75 80

Leu Arg Asp Phe Glu Asp Asp Glu Cys Asp Val Val His Lys Tyr Asn
 85 90 95

Leu Asp Glu Ala Arg Thr Leu Lys Asn Glu Gly Glu Leu Pro Glu Asn
 100 105 110

Ala Lys Ile Asn Glu Thr Asp Asn Phe Gly Phe Glu Ser Asp Glu Asp

341/762

115	120	125
Val Asn Phe Glu Phe Gly Asn Ala Asp Glu Asp Asp Glu Glu Gly Glu		
130	135	140

Asp Glu Glu Leu Asp Ile Asp Asp Ile
145
150

<210> 149
 <211> 406
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(486)

<400> 149	
atg aia aaa gtc gat act tcc gat gca tgg ttg aaa aat tgg tta aca	48
Met Ile Lys Val Asp Thr Ser Asp Ala Leu Leu Lys Asn Ser Leu Thr	
1 5 10 15	
Leu ata aaa tgg aca tta aat atg ttg gat att tta tta agt tgt gac	55
Ser Ile Lys Trp Thr Leu Asn Met Leu Asp Ile Leu Phe Ser Cys Asp	
20 25 30	
att ttt taa tta atc aag gat tcc ata cgt tct ttg ata aca gaa aua	144
Ile Phe Ser Leu Ile Lys Asp Ser Ile Arg Ser Leu Ile Thr Glu Thr	
35 40 45	
ttt tcc tgg gtg aat acc gtg agt aca tgg aag gta aag cct gta cga	192
Phe Ser Ser Val Asn Thr Val Ser Thr Ser Thr Val Lys Pro Val Arg	
50 55 60	
tta ttg tgt tgc tta gtt tgt tcc aat agc aag tgg tgg aca ata tct	240
Leu Leu Cys Cys Leu Val Cys Ser Asn Ser Lys Ser Cys Thr Ile Ser	
65 70 75 80	

aac ata acc aga gat cct gaa tca gaa tgt gat aag ggg agc aga atc 288
 Asn Ile Thr Arg Asp Pro Glu Ser Glu Cys Asp Lys Gly Ser Arg Ile
 85 90 95

tta gag acg gat cct tcl ttt tca aat ggg tat ata act tta aat agg 336
 Leu Glu Thr Asp Pro Ser Phe Ser Asn Gly Tyr Ile Thr Leu Asn Arg
 100 105 110

ttc ctg aaa tat tca tcc ttc atc att tgt ttc ctt tgt tta gta cta 384
 Phe Leu Lys Tyr Ser Ser Phe Ile Ile Cys Phe Phe Cys Leu Val Leu
 115 120 125

aca aac ttg atg aaa cat tca tgg cca aac tcl tcc ttt cta gac tca 432
 Thr Asn Leu Met Lys His Ser Ser Glu Asn Phe Ser Phe Leu Asp Ser
 130 135 140

cct gtc gct gga ttt ctg gca gat gca ggg cac ctc tgg nac tcc ata 480
 Thr Val Ala Gly Phe Leu Ala Asp Ala Gly His Leu Trp His Ser Ile
 145 150 155 160

act tga 486
 Thr

<210> 150

<211> 161

<212> PRT

<213> *Seccharomyces cerevisiae*

<100> 150

Met Ile Lys Val Asp Thr Ser Asp Ala Leu Leu Lys Asn Ser Leu Thr
 1 5 10 15

Ser Ile Lys Trp Thr Leu Asn Met Leu Asp Ile Leu Phe Ser Cys Asp
 20 25 30

Ile Phe Ser Leu Ile Lys Asp Ser Ile Arg Ser Leu Ile Thr Glu Thr
 35 40 45

Phe Ser Ser Val Asn Thr Val Ser Thr Ser Thr Val Lys Pro Val Arg
 50 55 60

Leu Leu Cys Cys Leu Val Cys Ser Asn Ser Lys Ser Cys Thr Ile Ser
 65 70 75 80

Asn Ile Thr Arg Asp Pro Glu Ser Glu Cys Asp Lys Gly Ser Arg Ile
 85 90 95

Leu Glu Thr Asp Pro Ser Phe Ser Asn Gly Tyr Ile Thr Leu Asn Arg
 100 105 110

Phe Leu Lys Tyr Ser Ser Phe Ile Ile Cys Phe Ser Cys Leu Val Leu
 115 120 125

Thr Asn Leu Met Lys His Ser Ser Glu Asn Phe Ser Phe Leu Asp Ser
 130 135 140

Thr Val Ala Gly Phe Leu Ala Asp Ala Gly His Leu Trp His Ser Ile
 145 150 155 160

Thr

<210> 151

<211> 690

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(690)

<430> 151

atg act gtt tct act tcc aag aou uuu aaa aag aal att aag tat acc 48

Met Thr Val Ser Thr Ser Lys Thr Pro Lys Lys Asn Ile Lys Tyr Thr

1 5 10 15

tta aca cat act tta caa aaa tgg aaa gaa aat tta aag aaa att acc 96

Leu Thr His Thr Leu Gln Lys Trp Lys Glu Thr Leu Lys Lys Ile Thr

20 25 30

cac gaa acg ttg agt agt atc gat gaa tct agl gga agc gat gaa aaa 144

His Glu Thr Leu Ser Ser Ile Asp Asp Ser Ser Gly Ser Asn Glu Lys

35 40 45

ata gag gat ctg ttt act gtg tct cag cct gcc gtc gta gcc tcc aag 192

Ile Glu Ala Leu Phe Thr Val Ser Gln Pro Ala Val Val Ala Ser Lys

50 55 60

ggc ata gac aga gaa ugt ggt gct tct atg tgg cag gta gga gga ggt 240

Gly Ile Asp Arg Asp Ser Gly Ala Ser Met Ser Gln Val Gly Gly Gly

65 70 75 80

gtc aat agt aca ttg gag arg aag ctc aca gat gag agt gag gaa tct 288

Val Asn Ser Thr Leu Glu Met Lys Leu Thr Asp Glu Ser Glu Glu Ser

85 90 95

aga tct gct aat aac aag acc aca aac gcc tgg cat act cta tgg aat 336

Ser Ser Ala Asn Asn Thr Thr Thr Thr Ala Ser His Thr Leu Ser Asn

100 105 110

tcg aag aag tct acg cag aac ttt gaa aac tat aac gta gtg gag gaa 384

Ser Lys Lys Ser Thr Glu Asn Phe Glu Asn Tyr Asn Val Val Glu Glu

115 120 125

cgc ata aaa tta gca cag aaa agt aag gcg cgg ttt lgt aac gct gag 432

Arg Ile Lys Leu Ala Gln Lys Ser Lys Ala Pro Phe Cys Asn Ala Glu

130 135 140

aaa atc tgg aaa cga aga cga caa ctc tgg aca caa ccc act gag caa 480

Lys Ile Trp Lys Arg Arg Arg Gln Leu Trp Thr Gln Pro Thr Glu Gln

145 150 155 160

agc gaa agc gcc aac cat gac gga gtt act cga aag aag att ctc caa 528
 Ser Glu Ser Ala Asn Asn Asp Gly Val Thr Arg Arg Glu Ile Phe Gln
 165 170 175

gct ata cct cag gaa tat tat gct cga gtt tac aag aaa ctg gtg gta 576
 Ala Ile Pro Gln Glu Tyr Tyr Ala Arg Val Tyr Lys Lys Leu Val Val
 180 185 190

gat gat aag cca tgg aga gag cct cta aat ctg gaa gat gct cta caa 624
 Asp Asp Lys Pro Leu Arg Glu Pro Leu Asn Leu Glu Asp Ala Leu Gln
 195 200 205

gtc ata aat gca gcc tgg aag gaa aag aga aag tgg gct aat gct gcc 672
 Val Ile Asn Ala Gly Trp Thr Glu Thr Arg Lys Trp Ala Asn Ala Ala
 210 215 220

aag gca tgc cat gac tga 690
 Lys Ala Cys His Asp
 225

<210> 152
 <211> 229
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 152

Met Thr Val Ser Thr Ser Lys Thr Pro Lys Lys Asn Ile Lys Tyr Thr
 1 5 10 15

Leu Thr His Thr Leu Gln Lys Trp Lys Glu Thr Leu Lys Lys Ile Thr
 20 25 30

His Glu Thr Leu Ser Ser Ile Asp Asp Ser Ser Gly Ser Asp Glu Lys
 35 40 45

Tyr Glu Ala Leu Phe Thr Val Ser Gln Pro Ala Val Val Ala Ser Lys

50		55		60
Gly Ile Asp Arg Asp Ser Gly Ala Ser Met Ser Glu Val Gly Gly Gly				
65		70		80
Val Asn Ser Thr Leu Glu Met Lys Leu Thr Asp Glu Ser Glu Glu Ser				
	85		90	95
Ser Ser Ala Asn Asn Thr Thr Thr Thr Ala Ser His Thr Leu Ser Asn				
	100		105	110
Ser Lys Lys Ser Thr Gln Asn Phe Glu Asn Tyr Asn Val Val Gln Gln				
	115		120	125
Arg Ile Lys Leu Ala Gln Lys Ser Lys Ala Pro Phe Cys Asn Ala Glu				
	130		135	140
Lys Ile Trp Lys Arg Arg Arg Gln Leu Trp Thr Gln Pro Thr Glu Gln				
	145		150	155
Ser Glu Ser Ala Asn Asn Asp Gly Val Thr Arg Arg Glu Ile Phe Gln				
	165		170	175
Ala Ile Pro Gln Glu Tyr Tyr Ala Arg Val Tyr Lys Lys Leu Val Val				
	180		185	190
Asp Asp Lys Pro Leu Arg Glu Pro Leu Asn Leu Glu Asp Ala Leu Gln				
	195		200	205
Val Ile Asn Ala Gly Trp Thr Glu Thr Arg Lys Trp Ala Asn Ala Ala				
	210		215	220

Lys Ala Cys His Asp

225

<210> 153

<211> 654

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (654)

<400> 153

atg	agt	ccc	cta	tta	ata	tca	tac	gaa	tct	gac	tac	aaa	aaa	ccc	tta	48
Met	Ser	Ser	Leu	Leu	Ile	Ser	Tyr	Glu	Ser	Asp	Phe	Lys	Thr	Thr	Leu	
1			5					10						15		

gaa	caa	ccc	aaa	ggc	agg	tta	gca	gag	ccc	ccc	tca	caa	ccg	tta	tca	96
Glu	Gln	Ala	Lys	Ala	Ser	Leu	Ala	Glu	Ala	Pro	Ser	Gln	Pro	Leu	Ser	
			20					25						30		

ccg	aga	aat	act	cca	ctg	aga	cac	gta	gaa	cag	caa	caa	gat	gag	tgg	144
Gln	Arg	Asn	Thr	Thr	Leu	Lys	His	Val	Glu	Gln	Gln	Gln	Asp	Glu	Leu	
			35					40						45		

ttt	gac	ctg	cta	gac	uag	atg	gat	gta	gaa	gtt	aat	aac	agg	ata	ggc	192
Phe	Asp	Leu	Leu	Asp	Gln	Met	Asp	Val	Gln	Val	Asn	Asn	Ser	Ile	Gly	
			50					55						60		

gat	gac	tca	gaa	cgt	gct	acg	tac	aag	ggc	aag	tta	aga	gaa	tgg	aag	240
Asp	Ala	Ser	Glu	Arg	Ala	Thr	Tyr	Lys	Ala	Lys	Leu	Arg	Gln	Trp	Lys	
			65					70						75		80

aag	act	ata	cag	agg	gat	atc	aaa	aga	cca	ctg	caa	tcc	tta	gta	gac	288
Lys	Thr	Ile	Gln	Ser	Asp	Ile	Iys	Arg	Pro	Leu	Gln	Ser	Leu	Val	Asp	
								95						95		

tca	ggc	gat	cgt	gat	aga	ctt	ttt	gga	gat	ctt	aac	gca	tct	aat	att	336
Ser	Gly	Asp	Arg	Asp	Arg	Leu	Phe	Gly	Asp	Leu	Asn	Ala	Ser	Asn	Ile	

348/762

100	105	110	
gac gal gac caa agg caa cng ttg ttg agc aac cat gca atc tta cag			384
Asp Asp Asp Gln Arg Gln Gln Leu Ser Asn His Ala Ile Leu Gln			
115	120	125	
aaa tgg gga gat aga cta aau gat gcc agt aga ata gca aat gaa act			432
Lys Ser Gly Asp Arg Ile Lys Asp Ala Ser Arg Ile Ala Asn Glu Thr			
130	135	140	
gaa gga ata ggg tca caa aia atg atg gat tta agg tca cag aga gaa			480
Glu Gly Ile Gly Ser Gln Phe Met Met Asp Leu Arg Ser Gln Arg Glu			
145	150	155	160
act tgg gaa aat gca aga cag aac ttg ttt caa gcg gat tca tat gty			528
Thr Leu Glu Asn Ala Arg Gln Thr Leu Phe Gln Ala Asp Ser Tyr Val			
165	170	175	
gat aaa agt ata aag aca cta aaa aac atg act aga agg cta gtt gct			576
Asp Lys Ser Ile Lys Thr Leu Lys Thr Met Thr Arg Arg Leu Val Ala			
180	185	190	
aat aaa ttc ata agc tat gcc att atc gaa gtc ctt ata tta ttg att			624
Asn Lys Phe Ile Ser Tyr Ala Ile Ile Ala Val Leu Ile Leu Leu Ile			
195	200	205	
ttg cta gtt tgg ttc tca aag ttt aaa taa			654
Leu Leu Val Leu Phe Ser Lys Phe Lys			
210	215		
<210> 154			
<211> 217			
<212> FRT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 154			
Met Ser Ser Leu Leu Ile Ser Tyr Glu Ser Asp Phe Lys Thr Thr Leu			
1	5	10	15

Glu Gln Ala Lys Ala Ser Leu Ala Gln Ala Pro Ser Gln Pro Leu Ser
20 25 30

Gln Arg Asn Thr Thr Leu Lys His Val Glu Gln Gln Gln Asp Glu Leu
35 40 45

Phe Asp Leu Leu Asp Gln Met Asp Val Glu Val Asn Asn Ser Ile Gly
50 55 60

Asp Ala Ser Glu Arg Ala Thr Tyr Lys Ala Lys Leu Arg Glu Trp Lys
65 70 75 80

Lys Thr Ile Gln Ser Asp Ile Lys Arg Pro Leu Gln Ser Leu Val Asp
85 90 95

Ser Gly Asp Arg Asp Arg Leu Phe Gly Asp Asn Asn Ala Ser Asn Ile
100 105 110

Asp Asp Asp Gln Arg Gln Gln Leu Leu Ser Asn His Ala Ile Leu Gln
115 120 125

Lys Ser Gly Asp Arg Leu Lys Asp Ala Ser Arg His Ala Asn Glu Thr
130 135 140

Glu Gly Ile Gly Ser Gln Ile Met Met Asp Leu Arg Ser Gln Arg Glu
145 150 155 160

Thr Leu Glu Asn Ala Arg Gln Thr Leu Phe Gln Ala Asp Ser Tyr Val
165 170 175

Asp Lys Ser His Lys Thr Leu Lys Thr Met Val Arg Arg Leu Val Ala
180 185 190

Asn Lys Phe Ile Ser Tyr Ala Ile Ile Ala Val Leu Ile Leu Leu Ile
 195 200 205

Leu Leu Val Leu Phe Ser Lys Phe Lys
 210 215

<210> 155
 <211> 1863
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1863)

<400> 155
 atg agc gac tcc aat cag cga tca tta acg tgg acc aag cct ata gta 43
 Met Arg Asp Ser Asn His Arg Ser Leu Thr Ser Asn Lys Pro Ile Val
 1 5 10 15
 aca ata aca tct act gtc tat gac cga agc gca ttg gat atc acc tct 95
 Thr Ile Thr Ser Thr Val Tyr Asp Arg Arg Ala Leu Asp Ile Asn Ser
 20 25 30
 agt att cgg taa ata aac tcc cta aac tac tta aca tal cta acc tct 144
 Ser Ile Pro Leu Ile Asn Ser Leu Asn Tyr Leu Thr Tyr Leu Thr Ser
 35 40 45
 aat tca tca aaa gtt agc gaa acg gta gct aac gac ggt gct cta gaa 192
 Asn Ser Ser Lys Val Arg Glu Thr Val Ala Asn Asp Gly Ala Leu Glu
 50 55 60
 aga tca gtc tca ata ttg agc agt lgt cat tta agt ttg tct gag ttg 240
 Arg Leu Val Ser Ile Leu Arg Ser Cys His Leu Ser Leu Phe Glu Leu
 65 70 75 80
 cgg gat ttg gat tta gaa aat ttt aat gag cag gaa acc ata aag gat 288

Leu Asp Leu Asp Leu Glu Asn Phe Asn Glu His Glu Asn Ile Lys Asp			
85	90	95	
cta tgg aag gag aaa aga cta gca cta tgc gct tgg aat tgg act tta	336		
Leu Trp Lys Glu Lys Arg Leu Ala Leu Cys Ala Trp Lys Trp Thr Leu			
100	105	110	
aca ttt cag tgc tta gta ttg aca ggt act aga ggg aca gaa caa att	384		
Thr Phe Gln Cys Leu Val Leu Thr Gly Thr Arg Gly Thr Glu Glu Ile			
115	120	125	
agt aaa aca gtg gta arg tct ggg gtc cta tct gtg ctg gtc aca gta	432		
Arg Lys Lys Val Val Met Ser Gly Val Leu Ser Val Leu Val Thr Val			
130	135	140	
ttg gat aac tat tta cta tat cat aaa aat hac gac ttc atc aaa gat	480		
Leu Asp Asn Tyr Leu Leu Tyr His Lys Asn Tyr Asp Phe Phe Lys Asp			
145	150	155	160
caa aca atg acc ttt gac ttc aca ggg ata aca aca gag aca atg cat	528		
Gln Thr Met Thr Phe Asp Phe Lys Gly Ile Thr Thr Glu Thr Met Tyr			
165	170	175	
aaa ttc atg aga aaa gat gag aat gaa aca tat cag cag tat ata gag	576		
Lys Phe Met Arg Lys Asp Glu Asn Gln Thr Tyr Gln Gln Tyr Ile Glu			
180	185	190	
ttc att aca ggt cag gat aaa ttg aag ttg tca act gac aaa aat ttt	624		
Phe Ile Thr Gly Glu Asp Lys Leu Lys Leu Ser Thr Asp Lys Asn Glu			
195	200	205	
cna aac gaa aga tta gtg gca ccg tct atg aca att cca act gat ttt	672		
Leu Asn Glu Arg Leu Val Ala Pro Ser Met Thr Ile Pro Thr Asp Phe			
210	215	220	
agt gat ata tgg ggc cgg ttt gca gac cta ggt agc aat ttt gaa cat	720		
Ser Asp Ile Trp Gly Arg Phe Ala Asp Leu Ala Ser Asn Phe Glu Pro			
225	230	235	240
gac cag gaa aga aac gac gac gac att gat att gat agt gaa gta gaa	768		
Asp Glu Glu Arg His Asp Asp Asp Ile Asp Ile Asp Ser Glu Val Glu			
245	250	255	

agt gaa aat ttt gat gca cat aag aat ttc ttt tgg caa cca gac att	816
Ser Gly Asn Phe Asp Ala His Lys Asn Phe Phe Ser Gln Pro Arg Ile	
260 265 270	
aat aga cct acc att tcc aat cca cgt gaa ttt ttt ctc gga aga att	864
Asn Arg Pro Thr Ile Ser Thr Pro Arg Glu Phe Phe Leu Gly Arg Ile	
275 280 285	
gtc ccc aaa caa gac gac gtt ata tgg tgg ctt cag tta tta gct ttt	912
Val Pro Lys Gln Asp Asp Val Ile Trp Ser Leu Gln Leu Leu Ala Phe	
290 295 300	
gtt tgg aag tat aca tat atg aca tca acc ctt caa aat gtt gag atg	960
Val Ser Lys Tyr Thr Tyr Met Lys Ser Thr Leu Gln Asn Val Glu Leu	
305 310 315 320	
gtt gaa tcc cta tgg ttc aga agt atg gct tac aca att aca cag aga	1008
Val Glu Ser Leu Ser Phe Arg Ser Met Ala Tyr Lys Ile Lys Gln Arg	
325 330 335	
atc tca gaa gag aat gaa tca gaa gaa caa gaa ags gac gta act gta	1056
Ile Ser Glu Glu Asn Arg Leu Glu Glu Gln Glu Arg Asp Val Thr Val	
340 345 350	
aaa ttg tct tca tta tat cct tat tta tgg aaa aat cct gaa aac aat	1104
Lys Leu Ser Ser Leu Tyr Pro Tyr Leu Ser Lys Asn Pro Glu Asn Asn	
355 360 365	
tcc aaa gtt aag gca ata gat aot agc aaa atg gat cca ttt ttc aaa	1152
Ser Lys Val Lys Ala Leu Asp Thr Ser Lys Met Asp Pro Phe Phe Lys	
370 375 380	
gaa tta gaa gag ctc tca aac aga tgt caa caa gaa gaa caa aat gaa	1200
Glu Leu Glu Gly Leu Ser Asn Arg Cys Gln Gln Glu Glu Gln Asn Glu	
385 390 395 400	
ata tgt aat aac cac tgt ccc gll cll aat ttg ttt gag cgc tac cgt	1248
Ile Cys Asn Asn His Cys Pro Val Leu Asn Leu Phe Glu Arg Tyr Arg	
405 410 415	
gta ccg aca cct agc gac gac aat gcc tat ggc aca gac aag gaa aga	1296

Val Pro Lys Pro Ser Asp Asp Asn Ala Tyr Gly Lys Asp Lys Glu Arg	
420	425
430	
att aat tta agg aag gaa ata cct gat aac ttt gaa agg cgg tgg agc	1344
Ile Asn Leu Arg Lys Lys Ile Ser Asp Asn Phe Glu Arg Arg Trp Ser	
435	440
445	
tac gat aaa atg aaa aag gaa tta asa aat att gtt tac aaa aac aag	1392
Tyr Asp Lys Met Lys Lys Glu Leu Thr Asn Ile Val Tyr Lys Asn Lys	
450	455
460	
gta cta aca aat gtt gta aac atc ttc ccc tta gtc gaa aaa tat aca	1440
Val Leu Thr Asn Val Val Asn Ile Phe Pro Leu Val Glu Lys Tyr Thr	
465	470
475	480
gtg agt gaa aat aca cat gat gtt atn tat tgg agt tct gtc atc	1488
Val Ser Ala Glu Asn Thr His Asp Val Ile Tyr Trp Ser Ser Val Ile	
485	490
495	
atg aga aat tca tgt cga aca aat gag atc tta agt gtt cgt cag tgt	1536
Met Arg Asn Ser Cys Arg Lys Asn Glu Ile Leu Gly Val Arg Gln Cys	
500	505
510	
ggc aat ttt cag tgc gga aaa tgg gaa gtt ttt ccc agn aca ttt gca	1584
Ala Asn Phe Ser Cys Gly Lys Trp Glu Asp Phe Pro Arg Gln Phe Ala	
515	520
525	
aaa tgt cgt cga tgc aaa aga acg aaa tat tgc tca cga aag tgt gaa	1632
Lys Cys Arg Arg Cys Lys Arg Thr Lys Tyr Cys Ser Arg Lys Cys Gln	
530	535
540	
tta aaa gca tgg gga tat cat agg tat tgg tgc cac gaa gtt gga tca	1680
Leu Lys Ala Trp Gly Tyr His Arg Tyr Trp Cys His Glu Val Gly Ser	
545	550
555	560
agt cat atg aga tcc acg aat aet acc aca ggt gtc aat acg cca aat	1728
Ser His Met Arg Ser Thr Asn Thr Thr Thr Gly Val Asn Thr Pro Asn	
565	570
575	
gag cct agt tct tta aat gcc acc gct aat aca gca gct gat gtt cag	1776
Glu Pro Ser Ser Leu Asn Ala Thr Ala Thr Thr Ala Ala Asp Val Ser	
580	585
590	

aat tct acc agt aag ttg act cct aat ata tcc acc acc gta cct gat 1824
 Asn Ser Thr Ser Thr Phe Thr Pro Asp Ile Ser Thr Thr Val Pro Asp
 595 600 605

gaa ata agc aat agg gat gaa act agc ata cct gag taa 1863
 Glu Ile Ser Asn Arg Asp Glu Asn Ser Ile Pro Glu
 610 615 620

<210> 156

<211> 620

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 156

Met Arg Asp Ser Asn His Arg Ser Leu Thr Ser Asn Lys Pro Ile Val
 1 5 10 15

Thr Ile Thr Ser Thr Val Tyr Asp Arg Arg Ala Leu Asp Ile Asn Ser
 20 25 30

Ser Ile Pro Leu Ile Asn Ser Leu Asn Tyr Leu Thr Tyr Leu Thr Ser
 35 40 45

Asn Ser Ser Lys Val Arg Glu Thr Val Ala Asn Asp Gly Ala Leu Glu
 50 55 60

Arg Leu Val Ser Ile Leu Arg Ser Cys His Leu Ser Leu Phe Glu Leu
 65 70 75 80

Leu Asp Leu Asp Leu Glu Asn Phe Asn Glu His Glu Asn Ile Lys Asp
 85 90 95

Leu Tyr Lys Glu Lys Arg Leu Ala Leu Cys Ala Trp Lys Trp Thr Leu

100

105

110

Thr Phe Gln Cys Leu Val Leu Thr Gly Thr Arg Gly Thr Gln Ile
115 120 125

Arg Lys Lys Val Val Met Ser Gly Val Leu Ser Val Leu Val Thr Val
130 135 140

Leu Asp Asn Tyr Leu Leu Tyr His Lys Asn Tyr Asp Phe Ile Lys Asp
145 150 155 160

Gln Thr Met Thr Phe Asp Phe Lys Gly Ile Thr Thr Glu Thr Met Tyr
165 170 175

Lys Phe Met Arg Lys Asp Glu Asn Gln Thr Tyr Gln Gln Tyr Ile Glu
180 185 190

Phe Ile Thr Gly Gln Asp Lys Leu Lys Leu Ser Thr Asp Lys Asn Phe
195 200 205

Leu Asn Glu Arg Leu Val Ala Pro Ser Met Thr Ile Pro Thr Asp Phe
210 215 220

Ser Asp Ile Trp Gly Arg Phe Ala Asp Leu Ala Ser Asn Phe Glu Pro
225 230 235 240

Asp Gln Glu Arg His Asp Asp Asp Ile Asp Ile Asp Ser Glu Val Glu
245 250 255

Ser Glu Asn Phe Asp Ala His Lys Asn Phe Phe Ser Gln Pro Asp Ile
260 265 270

Asn Arg Pro Thr Ile Ser Thr Pro Arg Glu Phe Phe Leu Gly Arg Ile
275 283 285

Val Pro Lys Gln Asp Asp Val Ile Trp Ser Leu Gln Leu Leu Ala Phe
293 295 300

Val Ser Lys Tyr Thr Tyr Met Lys Ser Thr Leu Gln Asn Val Glu Leu
305 310 315 320

Val Glu Ser Leu Ser Phe Arg Ser Met Ala Tyr Lys Ile Lys Gln Arg
325 330 335

Ile Ser Glu Glu Asn Asp Leu Glu Glu Gln Glu Arg Asp Val Thr Val
340 345 350

Lys Leu Ser Ser Leu Tyr Pro Tyr Leu Ser Lys Asn Pro Glu Asn Asn
355 360 365

Ser Lys Val Lys Ala Leu Asp Thr Ser Lys Met Asp Pro Phe Phe Lys
370 375 380

Glu Leu Glu Glu Leu Ser Asn Arg Cys Gln Gln Glu Glu Gln Asn Glu
385 390 395 400

Ile Cys Asn Asn His Cys Pro Val Leu Asn Leu Phe Glu Arg Tyr Arg
405 410 415

Val Pro Lys Pro Ser Asp Asp Asn Ala Tyr Gly Lys Asp Lys Glu Arg
420 425 430

Ile Asn Leu Arg Lys Lys Ile Ser Asp Asn Phe Glu Arg Arg Trp Ser

435

440

445

Tyr Asp Lys Met Lys Lys Glu Leu Thr Asn Ile Val Tyr Lys Asn Lys
450 485 460

Val Leu Thr Asn Val Val Asn Ile Phe Pro Leu Val Glu Lys Tyr Thr
465 470 475 480

Val Ser Ala Glu Asn Thr His Asp Val Ile Tyr Trp Ser Ser Val Ile
485 490 495

Met Arg Asn Ser Cys Arg Lys Asn Glu Ile Leu Gly Val Arg Gln Cys
500 505 510

Ala Asn Phe Ser Cys Gly Lys Trp Glu Asp Phe Pro Arg Gln Phe Ala
515 520 525

Lys Cys Arg Arg Cys Lys Arg Thr Lys Tyr Cys Ser Arg Lys Cys Gln
530 535 540

Leu Lys Ala Trp Gly Tyr His Arg Tyr Trp Cys His Glu Val Gly Ser
545 550 555 560

Ser His Met Arg Ser Thr Asn Thr Thr Thr Gly Val Asn Thr Pro Asn
565 570 575

Glu Pro Ser Ser Leu Asn Ala Thr Ala Thr Thr Ala Ala Asp Val Ser
580 585 590

Asn Ser Thr Ser Thr Phe Thr Pro Asn Ile Ser Thr Thr Val Pro Asp
595 600 605

Glu Ile Ser Asn Arg Asp Glu Asn Ser Ile Pro Glu
 610 615 620

<210> 157
 <211> 1350
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 157
 atg cgt cta aaa gaa ttg tta cct aat ttt ttg att gtt cat caa gag 48
 Met Arg Leu Lys Glu Leu Ser Pro Asn Phe Leu Ile Val His Gln Glu
 1 5 10 15
 gtc cct gag gat cct att gca ttc aag tcc acc gat aac tgc gag aat 96
 Val Pro Glu Asp Pro Ile Ala Phe Lys Ser Thr Asp Lys Arg Glu Asn
 20 25 30
 gca aat aaa gag atc acc atc cct gag cta ata gat aat aac gtt cct 144
 Glu Asn Lys Glu Ile Thr Ile Pro Glu Leu Ile Asp Thr Lys Val Pro
 35 40 45
 gaa tta gct gaa ggt gct act gac act tta tat ggt tta cly gtc aat 192
 Glu Leu Ala Asp Gly Ala Thr Asp Thr Leu Tyr Gly Leu Leu Val Ser
 50 55 60
 ggu cat tta caa act gca tat ggt tcc ttt aga cac ttt gac aat ata 240
 Gly His Leu Gln Thr Ala Tyr Gly Ser Phe Arg His Phe Asp Asn Ile
 65 70 75 80
 taa aac gtt caa tat aac aga atg ata atc aaa taa cca cat ggg gga 288
 Tyr Lys Val Gln Tyr Lys Arg Met Ile Ile Lys Tyr Pro His Gly Gly
 85 90 95
 gaa ggg act gtc gat ttt gct gta aat ggt aga agt acc aaa aga aga 336
 Glu Gly Thr Val Asp Phe Ala Val Asn Gly Arg Ser Thr Lys Arg Arg

100	105	110	
aaa gtc gaa aaa gaa tac gtc cgc aca agt caa cgc gta ttt aac gga			304
Lys Val Glu Lys Glu Tyr Val Pro Thr Ser Glu Pro Val Phe Asn Gly			
115	120	125	
aac ttg aaa cga aga tat tgg tac tat tcc cct gat gat cct aca ttg			432
Asn Leu Lys Arg Arg Tyr Ser Tyr Tyr Ser Pro Asp Asp Pro Lys Leu			
130	135	140	
aac tca gac gat gct aag cct atg att att att ctc cat gga tta aca			460
Asn Ser Asp Asp Ala Lys Pro Met Leu Ile Ile Leu His Gly Leu Thr			
145	150	155	160
ggg ggt tgg agg gaa agc tac gtc agg gca ala gll cat gaa atc aac			528
Gly Gly Ser Arg Glu Ser Tyr Val Arg Asn Ile Val His Glu Ile Thr			
165	170	175	
acg aag tac gac ttt gaa gca tgc gtc ttt aat gct aga gga tgt tgt			576
Thr Gys Tyr Asp Phe Glu Ala Cys Val Phe Asn Ala Arg Gly Cys Cys			
180	185	190	
tat tct gca att aca acg cgc cca tta tac aac ggt ggt tgg aac aat			624
Tyr Ser Ala Ile Thr Thr Pro Leu Leu Tyr Asn Gly Gly Trp Thr Asn			
195	200	205	
gat ata aga tal tgl att aat gac ttg agg aca aga ttt cgc aat aga			672
Asp Ile Arg Tyr Cys Val Asn Asp Leu Arg Lys Arg Phe Pro Asn Arg			
210	215	220	
aag ttt tat atg atg gga ttt tgg lla ggc gcc tnn ata atg aca aat			720
Lys Phe Tyr Met Met Gly Phe Ser Leu Gly Ala Ser Ile Met Thr Asn			
225	230	235	240
tac ttg gga gaa gag tca gat cgt act aca aca gaa tgt gct att tcc			768
Tyr Leu Gly Glu Glu Ser Asp Arg Thr Lys Ile Glu Cys Ala Ile Ser			
245	250	255	
gtg agt aat cca ttt gac atg tac aac tct gca tat ttt att aac agt			816
Val Ser Asn Pro Phe Asp Leu Tyr Asn Ser Ala Tyr Phe Ile Asn Ser			
260	265	270	

360/762

aca cca atg ggg tca cga ttt tat tca cct gct ttg ggt cac aac tta	864
Thr Pro Met Gly Ser Arg Phe Tyr Ser Pro Ala Leu Gly His Asn Leu	
275 280 285	
cta cga atg gtt cga aac aat atc tct act ctg gaa gaa aac cct gat	912
Leu Arg Met Val Arg Asn His Leu Ser Thr Leu Glu Glu Asn Pro Asp	
290 295 300	
ttc aaa gat gtt atc gag aag cat tta aaa aag att cgc act gtc agg	960
Phe Lys Asp Val Ile Glu Lys His Leu Lys Lys Ile Arg Thr Val Arg	
305 310 315 320	
aaa ttt gat aac ttg ttg tca cca ggc cca atg ttt gga tat aaa aac tca	1008
Gln Phe Asp Asn Leu Leu Thr Gly Pro Met Phe Gly Tyr Lys Asn Ala	
325 330 335	
gag gag tat taa aag aat gct tca tca tat aaa aga ata ccc ggg aac	1056
Glu Glu Tyr Tyr Lys Ser Ala Ser Ser Tyr Lys Arg Ile Pro Gly Ile	
340 345 350	
aga aat cct ttt ata gct ttg cat gct cag gct gac cca att gtc gga	1104
Arg Thr Pro Phe Ile Ala Leu His Ala Glu Asp Asp Pro Ile Val Tyr	
355 360 365	
ggc gat ctt cct ata gac caa ata aaa tgc aat ccc tuc aat ttg att	1152
Gly Asp Leu Pro Ile Asp Glu Ile Lys Ser Asn Pro Tyr Thr Leu Leu	
370 375 380	
ata gaa aat tgc acg ggg ggg cat gtt gga tgg ttc aaa gac aga tcc	1200
Asn Glu Thr Ser Thr Gly Gly His Val Gly Trp Phe Lys Asp Arg Ser	
385 390 395 400	
ggc aga agg tgg taa gca gaa ccc tca tgc aga ttt ttg aaa ata ttt	1248
Gly Arg Arg Trp Tyr Ala Glu Pro Leu Cys Arg Phe Leu Lys Ile Phe	
405 410 415	
cac gac gaa att act gta aag tgc tta aaa cct gac ttg gaa aat gtt	1296
His Asp Glu Ile Thr Val Lys Gly Leu Lys Pro Asp Leu Glu Asn Val	
420 425 430	
caa ctc cca gat cct aat tgc gaa ccc ata gcc aca acc ttt cgc gag	1344
Gln Leu Pro Asp Pro Asn Cys Glu Pro Ile Ala Thr Thr Phe Arg Ala	

435

440

445

acc tag

1350

Asn

<210> 158

<211> 449

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 158

Met Arg Leu Lys Glu Leu Leu Pro Asn Phe Leu Ile Val His Gln Glu

1 5 10 15

Val Pro Glu Asp Pro Ile Ala Phe Lys Ser Thr Asp Lys Arg Gln Asn

20 25 30

Glu Asn Lys Glu Ile Thr Phe Pro Gln Leu Ile Asp Thr Lys Val Pro

35 40 45

Glu Leu Ala Asp Gly Ala Thr Asp Thr Leu Tyr Gly Leu Leu Val Asn

50 55 60

Gly His Leu Gln Thr Ala Tyr Gly Ser Phe Arg His Phe Asp Asn Ile

65 70 75 80

Tyr Lys Val Gln Tyr Lys Arg Met Ile Ile Lys Tyr Pro His Gly Gly

85 90 95

Glu Gly Thr Val Asp Phe Ala Val Asn Gly Arg Ser Thr Lys Arg Arg

100 105 110

Tyr Val Glu Lys Glu Tyr Val Pro Thr Ser Glu Pro Val Phe Asn Gly
 115 120 125

Asn Leu Lys Arg Arg Tyr Ser Tyr Tyr Ser Pro Asp Asp Pro Lys Leu
 130 135 140

Asn Ser Asp Asp Ala Lys Pro Met Leu Ile Ile Leu His Gly Leu Thr
 145 150 155 160

Gly Gly Ser Arg Glu Ser Tyr Val Arg Ala Ile Val His Glu Ile Thr
 165 170 175

Thr Lys Tyr Asp Phe Glu Ala Cys Val Phe Asn Ala Arg Gly Cys Cys
 180 185 190

Tyr Ser Ala Ile Thr Thr Pro Leu Leu Tyr Asn Gly Gly Trp Thr Asn
 195 200 205

Asp Ile Arg Tyr Cys Val Asn Asp Leu Arg Lys Arg Phe Pro Asn Tyr
 210 215 220

Tyr Phe Tyr Met Met Gly Phe Ser Leu Gly Ala Ser Ile Met Thr Asn
 225 230 235 240

Tyr Leu Gly Glu Glu Ser Asp Arg Thr Lys Ile Glu Cys Ala Ile Ser
 245 250 255

Val Ser Asn Pro Phe Asp Leu Tyr Asn Ser Ala Tyr Phe Trp Asn Ser
 260 265 270

Thr Pro Met Gly Ser Arg Phe Tyr Ser Pro Ala Leu Gly His Asn Leu
 275 280 285

Leu Arg Met Val Arg Asn His Leu Ser Thr Leu Glu Glu Asn Pro Asp
290 295 300

Phe Lys Asp Val Ile Glu Lys His Ser Lys Lys Ile Arg Thr Val Arg
305 310 315 320

Gln Phe Asp Asn Leu Leu Thr Gly Pro Met Phe Gly Tyr Lys Asn Ala
325 330 335

Glu Glu Tyr Tyr Lys Asn Ala Ser Ser Tyr Lys Arg Ile Pro Gly Ile
340 345 350

Arg Thr Pro Phe Ile Ala Leu His Ala Gln Asp Asp Pro Ile Val Gly
355 360 365

Gly Asp Leu Pro Ile Asp Gln Ile Lys Ser Asn Pro Tyr Thr Leu Leu
370 375 380

Leu Glu Thr Ser Thr Gly Gly His Val Gly Trp Phe Lys Asp Arg Ser
385 390 395 400

Gly Arg Arg Trp Tyr Ala Glu Pro Leu Cys Arg Phe Leu Lys Ile Phe
405 410 415

His Asp Glu Ile Thr Val Tyr Gly Leu Lys Pro Asp Leu Glu Asn Val
420 425 430

Gln Leu Pro Asp Pro Asn Cys Glu Pro Ile Ala Thr Thr Phe Arg Ala
435 440 445

ZFN

<210> 150

<211> 1.003

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1083)

<400> 150

atg	tcc	tat	cct	gag	aaa	ctt	gaa	ggc	atc	gct	att	caa	tca	aac	gaa	48
Met	Ser	Tyr	Pro	Glu	Lys	Phe	Glu	Gly	Ile	Ala	Ile	Gln	Ser	His	Glu	
1				5					10				15			

gat	tgg	aaa	aac	cca	aag	aag	acc	aag	tat	gac	cca	aaa	cca	ttt	tat	36
Asp	Trp	Lys	Asn	Pro	Lys	Lys	Thr	Lys	Tyr	Asp	Pro	Lys	Pro	Phe	Tyr	
			20					25					30			

gat	cat	gac	att	gac	att	aag	atc	gaa	gca	tgt	ggc	gtc	tgc	ggt	agc	144
Asp	His	Asp	Ile	Asp	Ile	Lys	Ile	Glu	Ala	Cys	Gly	Val	Cys	Gly	Ser	
		35				40						45				

gat	atc	cat	tgt	gca	gct	ggc	cat	tgg	ggc	aat	atg	aag	atg	ccg	cta	132
Asp	Ile	His	Cys	Ala	Ala	Gly	His	Trp	Gly	Asn	Met	Lys	Met	Pro	Leu	
		50				55					60					

gtc	gtc	ggt	cat	gaa	atc	ggt	ggc	aaa	ggt	gtc	aag	cta	ggg	ccc	aag	240
Val	Val	Gly	His	Glu	Ile	Val	Gly	Lys	Val	Val	Lys	Phe	Gly	Pro	Lys	
65					70					75				80		

tca	aac	agt	ggg	ttg	aaa	gtc	ggc	caa	ogt	gtt	ggt	gtc	ggt	gct	caa	288
Ser	Asn	Ser	Gly	Ileu	Lys	Val	Gly	Gln	Arg	Val	Gly	Val	Gly	Ala	Gly	
			85					90					95			

gtc	ttt	tca	tgc	ttg	gaa	tgt	gac	cgt	tgt	aag	aat	gat	aat	gaa	cca	336
Val	Phe	Ser	Cys	Leu	Glu	Cys	Asp	Arg	Cys	Lys	Asn	Asp	Asn	Glu	Pro	
				103				105					110			

Val Ser Ile Ser Ile Pro Glu Glu His Glu Met Leu Ser Leu Lys Pro
 275 280 285

tat ggc tta aag gct glt tcc att tct tac agt gct tta ggt tcc aic 912
 Tyr Gly Leu Lys Ala Val Ser Ile Ser Tyr Ser Ala Leu Gly Ser Ile
 290 295 300

aca gaa ttg aac caa ctc ttg aac tta gtc tat gaa aac gat atc aca 960
 Lys Glu Leu Asn Gln Leu Leu Lys Leu Val Ser Glu Lys Asp Ile Lys
 305 310 315 320

att tgg gtg gaa aca tta cct gtt ggt gaa gcc ggc gtc cat gaa gcc 1008
 Ile Trp Val Glu Thr Leu Pro Val Gly Glu Ala Gly Val His Glu Ala
 325 330 335

ttc gaa agg atg gaa aag ggt gac gtt aga tat aga ttt acc tta gtc 1056
 Phe Glu Arg Met Glu Lys Gly Asp Val Arg Tyr Arg Phe Thr Leu Val
 340 345 350

ggc tac gac aac gaa ttt tca gac tag 1088
 Gly Tyr Asp Lys Glu Phe Ser Asp
 355 360

<210> 160
 <211> 360
 <212> FRT
 <213> *Saccharomyces cerevisiae*
 <400> 160

Met Ser Tyr Pro Glu Lys Phe Glu Gly Ile Ala Ile Glu Ser His Glu
 1 5 10 15

Asp Trp Lys Asn Pro Lys Lys Thr Lys Tyr Asp Pro Lys Pro Phe Tyr
 20 25 30

Asp His Asp Ile Asp Ile Lys Ile Glu Ala Cys Gly Val Cys Gly Ser
 35 40 45

Asp Ile His Cys Ala Ala Gly His Trp Gly Asn Met Lys Met Pro Leu
50 55 60

Val Val Gly His Glu Ile Val Gly Lys Val Val Lys Leu Gly Pro Lys
65 70 75 80

Ser Asn Ser Gly Leu Lys Val Gly Gln Arg Val Gly Val Gly Ala Gln
85 90 95

Val Phe Ser Cys Leu Glu Cys Asp Arg Cys Lys Asn Asp Asn Glu Pro
100 105 110

Tyr Cys Thr Lys Phe Val Thr Thr Tyr Ser Gln Pro Tyr Glu Asp Gly
115 120 125

Tyr Val Ser Glu Gly Gly Tyr Ala Asn Tyr Val Arg Val His Glu His
130 135 140

Phe Val Val Pro Ile Pro Glu Asn Ile Pro Ser His Leu Ala Ala Pro
145 150 155 160

Leu Leu Cys Gly Gly Leu Thr Val Tyr Ser Pro Leu Val Arg Asn Gly
165 170 175

Cys Gly Pro Gly Lys Lys Val Gly Ile Val Gly Leu Gly Gly Ile Gly
180 185 190

Ser Met Gly Thr Leu Ile Ser Lys Ala Met Gly Ala Gln Thr Tyr Val
195 200 205

Ile Ser Arg Ser Ser Arg Lys Arg Glu Asp Ala Met Lys Met Cys Ala

210

215

220

Asp His Tyr Ile Ala Thr Leu Glu Glu Gly Asp Trp Gly Glu Lys Tyr
225 230 235 240

Phe Asp Thr Phe Asp Leu Ile Val Val Cys Ala Ser Ser Leu Thr Asp
245 250 255

Ile Asp Phe Asn Ile Met Pro Lys Ala Met Lys Val Gly Gly Arg Ile
260 265 270

Val Ser Ile Ser Ile Pro Glu Glu His Glu Met Leu Ser Leu Lys Pro
275 280 285

Tyr Gly Leu Lys Ala Val Ser Ile Ser Tyr Ser Ala Leu Gly Ser Ile
290 295 300

Lys Glu Leu Asn Gln Leu Leu Lys Leu Val Ser Glu Lys Asp Ile Lys
305 310 315 320

Ile Trp Val Glu Thr Leu Pro Val Gly Glu Ala Gly Val His Glu Ala
325 330 335

Phe Glu Arg Met Glu Lys Gly Asp Val Arg Tyr Arg Phe Thr Asn Val
340 345 350

Gly Tyr Asp Lys Glu Phe Ser Asp
355 360

<210> 161

<211> 858

<212> DNA

<213> *Saccharomyces cerevisiae*

<223>

<221> CDS

<222> (1)..(858)

<400> 161

atg	cgt	tct	tgg	gta	tat	agt	gag	aac	act	tac	aac	tgt	ata	cga	aca	48
Met	Arg	Ser	Ser	Val	Tyr	Ser	Glu	Asn	Thr	Tyr	Asn	Cys	Ile	Arg	Thr	
				5					10				15			

luc	aag	gag	cac	cta	aca	gaa	aga	agg	agg	gac	gac	atg	ccg	cca	atg	96
Ser	Tyr	Glu	His	Leu	Thr	Glu	Arg	Arg	Arg	Val	Ala	Met	Ala	Pro	Met	
		20					25					30				

ttc	caa	cac	luc	lta	aac	tta	tgc	gtg	gac	aaa	ttt	cct	gaa	luc	atc	144
Phe	Gln	His	Phe	Leu	Asn	Leu	Cys	Val	Glu	Lys	Phe	Pro	Glu	Ser	Ile	
	35					40					45					

gag	uuu	aag	gat	aca	gat	gga	aac	ggc	aac	ttc	acc	acc	gct	acc	tta	192
Glu	His	Lys	Asp	Thr	Asp	Gly	Asn	Gly	Asn	Phe	Thr	Thr	Ala	Ile	Leu	
	50					55				60						

gaa	agg	gag	att	atc	tac	atc	ccc	gaa	gat	gac	act	gac	agt	att	gac	240
Glu	Arg	Glu	Ile	Ile	Tyr	Ile	Pro	Glu	Asp	Asp	Thr	Asp	Ser	Ile	Asp	
65					70					75				80		

agc	ggt	gac	agc	ctc	aag	tgt	ata	aac	tac	aag	ctg	cac	aaa	tgt	cgc	288
Ser	Val	Asp	Phe	Leu	Lys	Cys	Ile	Asn	Tyr	Lys	Leu	His	Lys	Ser	Arg	
		85				90						95				

ggc	gac	caa	gtg	ctg	gac	gac	tgt	gtg	caa	tty	ata	gac	aag	cac	ctg	336
Gly	Asp	Gln	Val	Leu	Asp	Ala	Cys	Val	Gln	Leu	Ile	Asp	Lys	His	Leu	
		100					105					110				

ggc	gac	aag	tat	cgc	cgg	gac	tgg	cgc	att	atg	tac	ggc	aac	agg	aca	384
Gly	Ala	Lys	Tyr	Arg	Arg	Ala	Ser	Arg	Ile	Met	Tyr	Gly	Asn	Arg	Lys	
	115						120					125				

coa	tgg	aag	gca	aac	aaa	ctc	gca	gag	atg	aaa	agc	gac	ggc	ctt	gtg	432
Pro	Trp	Lys	Ala	Asn	Lys	Leu	Ala	Glu	Met	Lys	Ser	Ala	Gly	Leu	Val	

130	135	140	
tat gtc tgt tac tgg gac aac ggc gtg cta ggt gca ttt act tca ttc			480
Tyr Val Cys Tyr Trp Asp Asn Gly Val Leu Gly Ala Phe Thr Ser Phe			
145	150	155	160
alg ctt aca gag gag acg ggt ctc gtc gaa ggt gac gct tta cac gag			528
Met Leu Thr Glu Glu Thr Gly Leu Val Glu Gly Asp Ala Leu His Glu			
165	170	175	
gtt agc gtg ccc gtg ata tac ctt tac gaa gta cat gta gct agc gag			576
Val Ser Val Pro Val Ile Tyr Leu Tyr Gln Val His Val Ala Ser Ala			
180	185	190	
cac cgc ggg cal gga atc ggt cgg cgg cta ctg gag cat gca ctg tgc			624
His Arg Gly His Gly Ile Gly Arg Arg Leu Leu Glu His Ala Leu Cys			
195	200	205	
gat ggc gta gct cga cac aac cgc cgc atg tgg gac aal ttc ttc ggt			672
Asp Gly Val Ala Arg His Thr Arg Arg Met Cys Asp Asn Phe Phe Gly			
210	215	220	
gta gca ctc acc gta ttc agt gat aac act cgg gac cgg cga cta tat			720
Val Ala Leu Thr Val Phe Ser Asp Asn Thr Arg Ala Arg Arg Leu Tyr			
225	230	235	240
gag ggc ctt ggg ttc tac cgc gct cgg gga tca ccc gca cca gca tca			768
Glu Ala Leu Gly Phe Tyr Arg Ala Pro Gly Ser Pro Ala Pro Ala Ser			
245	250	255	
ccc aca aat cgt cac acg cga cat cgt ggg gga cgt gta gtc gtg ccc			816
Pro Thr Ile Arg His Thr Arg His Gly Gly Gly Arg Val Val Val Pro			
260	265	270	
tgc gat cgg ctc tat tac gta tat tgc ctt cac atg cag tga			868
Cys Asp Pro Leu Tyr Tyr Val Tyr Cys Leu His Met Pro			
275	280	285	

<210> 162

<211> 285

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 162

Met Arg Ser Ser Val Tyr Ser Gln Asn Thr Tyr Asn Cys Ile Arg Thr
1 5 10 15

Ser Lys Glu His Leu Thr Glu Arg Arg Arg Val Ala Met Ala Pro Met
20 25 30

Phe Gln His Phe Leu Asn Leu Cys Val Glu Lys Phe Pro Glu Ser Ile
35 40 45

Glu His Lys Asp Thr Asp Gly Asn Gly Asn Phe Thr Thr Ala Ile Leu
50 55 60

Gln Arg Glu Phe Ile Tyr Ile Pro Glu Asp Asp Thr Asp Ser Ile Asp
65 70 75 80

Met Val Asp Ser Ser Leu Lys Cys Ile Asn Tyr Lys Leu His Lys Ser Arg
85 90 95

Gly Asp Gln Val Leu Asp Ala Cys Val Gln Leu Ile Asp Lys His Leu
100 105 110

Gly Ala Lys Tyr Arg Arg Ala Ser Arg Ile Met Tyr Gly Asn Arg Lys
115 120 125

Pro Trp Lys Ala Asn Lys Leu Ala Gln Met Lys Ser Ala Gly Leu Val
130 135 140

Tyr Val Cys Tyr Trp Asp Asn Gly Val Leu Gly Ala Phe Thr Ser Phe
145 150 155 160

Met Leu Thr Glu Glu Thr Gly Leu Val Glu Gly Asp Ala Leu His Glu
165 170 175

Val Ser Val Pro Val Ile Tyr Leu Tyr Glu Val His Val Ala Ser Ala
180 185 190

His Arg Gly His Gly Ile Gly Arg Arg Leu Leu Glu His Ala Leu Cys
195 200 205

Asp Gly Val Ala Arg His Thr Arg Arg Met Cys Asp Asn Phe Phe Gly
210 215 220

Val Ala Leu Thr Val Phe Ser Asp Asn Thr Arg Ala Arg Arg Leu Tyr
225 230 235 240

Glu Ala Leu Gly Phe Tyr Arg Ala Pro Gly Ser Pro Ala Pro Ala Ser
245 250 255

Pro Thr Ile Arg His Thr Arg His Gly Gly Gly Arg Val Val Val Pro
260 265 270

Cys Asp Pro Leu Tyr Tyr Val Tyr Cys Leu His Met Pro
275 280 285

<210> 163

<211> 175E

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1755)

<400> 162

atg tog egg gag gca ttt gat gta cgg aat ala gyl aer aac aag ttt 48

Met Ser Arg Glu Ala Phe Asp Val Pro Asn Ile Gly Thr Asn Lys Phe

1 5 10 15

tta aaa gtc aca cct aat tta ttt acc cca gag cga ttg aat tta ttt 96

Leu Lys Val Thr Pro Asn Leu Phe Thr Pro Glu Arg Leu Asn Leu Phe

20 25 30

gat gat gtc gaa cta tat ctt acg tta ata aaa gca too aat tgt gtc 144

Asp Asp Val Glu Leu Tyr Leu Thr Leu Ile Lys Ala Ser Lys Cys Val

35 40 45

gag cag gga gaa agg ctg cac aat ata agl tgg aga att ctg aat aac 192

Glu Gln Gly Glu Arg Leu His Asn Ile Ser Trp Arg Ile Leu Asn Lys

50 55 60

gct gct cta aag gag cct aat att aat cga tct aaa aaa aga gac ggc 240

Ala Val Leu Lys Glu His Asn Ile Asn Arg Ser Lys Lys Arg Asp Gly

65 70 75 80

gtg aag aac ata tat tat gty tta aat cca aac aac aca aay aca ata 288

Val Lys Asn Ile Tyr Tyr Val Leu Asn Pro Asn Asn Lys Gln Pro Ile

85 90 95

aag cca aag aay gca gca gta aag cag cca cca tta cca aag gcc aat 336

Lys Pro Lys Gln Ala Ala Val Lys Gln Pro Pro Leu Gln Lys Ala Asn

100 105 110

ttg cct ccc aca aay gaa aaa cag aac gtt tta act cgg aca atg aca 384

Leu Pro Pro Thr Thr Ala Lys Gln Asn Val Leu Thr Arg Pro Met Thr

115 120 125

tca cca gct atc gca cag ggt gct cag gat aga tcc ttg gat aat cct 432

Ser Pro Ala Ile Ala Gln Gly Ala His Asp Arg Ser Leu Asp Asn Pro

130 135 140

aat tct cca aac act gat gtg aaa aat cag gtt gct cca aac aga caa 480

Asn Ser Thr Asn Asn Asp Val Lys Asn Asp Val Ala Pro Asn Arg Gln

145 150 155 160

tto tcc aaa tct act ccg tca ggg ttg ttt tca aat ttt gca gac aaa	528
Phe Ser Lys Ser Thr Thr Ser Gly Leu Phe Ser Asn Phe Ala Asp Lys	
155 170 175	
tat caa aaa atg aaa cat ggg aac cat gtt gct aat aag gaa gaa cca	576
Tyr Glu Lys Met Lys Asn Val Asn His Val Ala Asu Lys Glu Glu Pro	
160 183 190	
caa act att atc aat ggt ttt gat aca agc act gtt ata acc aag aat	624
Gln Thr Ile Ile Thr Gly Phe Asp Thr Ser Thr Val Ile Thr Lys Lys	
195 200 205	
act tta cca tcc aga cgc tca aga tca cct ttc cag cat ata gga gac	672
Pro Leu Gln Ser Arg Arg Ser Arg Ser Pro Phe Gln His Ile Gly Asp	
210 215 220	
atg aac atg aac tgc att gat aat gag act tcc aag agt acc agt cct	720
Met Asn Met Asn Cys Ile Asp Asn Glu Thr Ser Lys Ser Thr Ser Pro	
225 230 235 240	
act ttt gaa aat atg gga agt aga aaa tcc tct ttt cct cag ccg gaa	768
Thr Thr Gln Asn Met Gly Ser Arg Lys Ser Ser Phe Pro Gln Lys Glu	
245 250 255	
tct tta ttc gga cgg cca cgg cct tuc aag aat gac caa aat ggt caa	816
Ser Leu Phe Gly Arg Pro Arg Ser Tyr Lys Asn Asp Gln Asn Gly Gln	
260 265 270	
atg tca att tgg aaa tca tcc tct aga aaa gga aaa aac aag ata ttt	864
Leu Ser Leu Ser Lys Thr Ser Ser Arg Lys Gly Lys Asn Lys Ile Phe	
275 280 285	
tto agc agt gaa gat gaa gat tcc gat tgg gac agc gtt tgg aat gat	912
Phe Ser Ser Glu Asp Glu Asp Ser Asp Trp Asp Ser Val Ser Asn Arg	
290 295 300	
lua gaa ttc lau gcl gal gaa gac gat gaa gag tac gat gat tat aat	960
Ser Glu Phe Tyr Ala Asp Glu Asp Asp Gln Gln Tyr Asp Asp Tyr Asn	
305 310 315 320	
gag gaa gaa gca gat cag tac tat aga aga caa tgg gac aag cll tta	1008

Glu Glu Glu Ala Asp Gln Tyr Tyr Arg Arg Gln Trp Asp Lys Leu Leu			
325	330	335	
ttt gcc aaa aat caa cag aat ett gag tca acg aaa tca tct gtt tca	1036		
Phe Ala Lys Asn Gln Gln Asn Leu Arg Ser Thr Lys Ser Ser Val Ser			
340	345	350	
tca gag aac ada atc aac tca aac aca tcc cat gat ccc gta cga aaa	1104		
Ser Ala Asn Thr Ile Asn Ser Asn Thr Ser His Asp Pro Val Arg Lys			
355	360	365	
agt tta ctc agt gga cta ttc ctt agt gng gca aat agc aac agt aat	1152		
Scr Leu Leu Ser Gly Leu Phe Leu Ser Gln Ala Asn Ser Asn Ser Asn			
370	375	380	
aaa caa aat aat gcc cat agt gcc tac gct tct aaa caa gtt tgg cgg	1200		
Asn His Asn Thr Ala His Ser Gln Tyr Ala Ser Lys His Val Ser Pro			
385	390	395	400
act cct cag tcc tct cat ggt aat atc ggt cct caa cgg cag cca aat	1248		
Thr Pro Gln Ser Ser His Ser Asn Ile Gly Pro Gln Pro Gln Gln Asn			
405	410	415	
caa cgg agc gct aat ggt ata aaa caa caa aaa cct tct ttg aca aca	1296		
Pro Pro Ser Ala Asn Gly Ile Lys Gln Gln Lys Pro Ser Leu Lys Thr			
420	425	430	
agc aac gtg aca gct cta gcc tgg cta tct ccc cgg caa cca tcc aac	1344		
Ser Asn Val Thr Ala Leu Ala Ser Leu Ser Pro Pro Gln Pro Ser Asn			
435	440	445	
aat gag cgg tta tgg atg gat ata caa aag gac ttc aaa act gat aat	1392		
Asn Glu Arg Leu Ser Met Asp Ile Gln Lys Asp Phe Lys Thr Asp Asn			
450	455	460	
gag tcc aat cat tta tat gaa tct aat gct cgg cta act ggt caa act	1440		
Gln Ser Asn His Leu Tyr Gln Ser Asn Ala Pro Leu Thr Ala Gln Thr			
465	470	475	480
ata cgg ccc aac gcc tta tct act caa atg ttt ttt cca aat aat aat	1488		
Ile Leu Pro Thr Ala Leu Ser Thr His Met Phe Leu Pro Asn Asn Ile			
485	490	495	

cac caa caa cga atg gcg att gac act ggt agt aat acg cga cat cgt 1536
 His Gln Gln Arg Met Ala Ile Ala Thr Gly Ser Asn Thr Arg His Arg
 500 503 510

ttt tog agg cgg cag tog atg gat atc cca tcc aag aac agg aat act 1544
 Phe Ser Arg Arg Gln Ser Met Asp Tla Pro Ser Lys Asn Arg Asn Thr
 515 520 525

ggg ttt ttg aag aac aga atg gag atc tct gag gaa gaa aag atg gla 1632
 Gly Phe Leu Lys Thr Arg Met Glu Ile Ser Glu Glu Glu Lys Met Val
 530 535 540

cgt acc ata tca cgg ctt gac aat acg agt att gca aac agt aat gga 1680
 Arg Thr Ile Ser Arg Leu Asp Asn Thr Ser Ile Ala Asn Ser Asn Gly
 545 550 555 560

aat ggt aat gat gac aac tct aat cag aga acg gaa gaa ctg cgg cgt 1728
 Asn Gly Asn Asp Asp Thr Ser Asn Gln Arg Thr Glu Ala Leu Gly Arg
 565 570 575

aag aag cgt wcl gga ggg cga ata tga 1755
 Lys Thr Ser Asn Gly Gly Arg Ile
 580

<210> 164

<211> 584

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 166

Met Ser Arg Glu Ala Phe Asp Val Pro Asn Ile Gly Thr Asn Lys Phe
 1 5 10 15

Leu Lys Val Thr Pro Asn Leu Phe Thr Pro Glu Arg Leu Asn Leu Phe
 20 25 30

Asp Asp Val Glu Leu Tyr Leu Thr Leu Ile Lys Ala Ser Lys Cys Val

35

40

45

Glu Glu Gly Glu Arg Leu His Asn Ile Ser Trp Arg Ile Leu Asn Lys
50 55 60

Ala Val Leu Lys Glu His Asn Ile Asn Arg Ser Lys Lys Arg Asp Gly
65 70 75 80

Val Lys Asn Ile Tyr Tyr Val Leu Asn Pro Asn Asn Lys Gln Pro Ile
85 90 95

Lys Pro Lys Gln Ala Ala Val Lys Glu Pro Pro Leu Gln Lys Ala Asn
100 105 110

Leu Pro Pro Thr Thr Ala Lys Gln Asn Val Leu Thr Arg Pro Met Thr
115 120 125

Ser Pro Ala Ile Ala Gln Gly Ala His Asp Arg Ser Leu Asp Asn Pro
130 135 140

Asn Ser Thr Asn Asn Asp Val Lys Asn Asp Val Ala Pro Asn Arg Gln
145 150 155 160

Phe Ser Lys Ser Thr Thr Ser Gly Leu Phe Ser Asn Phe Ala Asp Lys
165 170 175

Tyr Gln Lys Met Lys Asn Val Asn His Val Ala Asn Lys Glu Glu Pro
180 185 190

Gln Thr Ile Ile Thr Gly Phe Asp Thr Ser Thr Val Ile Thr Lys Lys
195 200 205

Pro Leu Gln Ser Arg Arg Ser Arg Ser Pro Phe Gln His Ile Gly Asp
 210 215 220

Met Asn Met Asn Cys Ile Asp Asn Glu Thr Ser Lys Ser Thr Ser Pro
 225 230 235 240

Thr Val Glu Asn Met Gly Ser Arg Lys Ser Ser Phe Pro Gln Lys Glu
 245 250 255

Ser Val Phe Gly Arg Pro Arg Ser Tyr Lys Asn Asp Gln Asn Gly Gln
 260 265 270

Leu Ser Leu Ser Lys Thr Ser Ser Arg Lys Gly Lys Asn Lys Phe Phe
 275 280 285

Phe Ser Ser Glu Asp Glu Asp Ser Asp Trp Asp Ser Val Ser Asn Asp
 290 295 300

Ser Glu Phe Tyr Ala Asp Glu Asp Asp Glu Glu Tyr Asp Asp Tyr Asn
 305 310 315 320

Glu Glu Glu Ala Asp Gln Tyr Tyr Arg Arg Gln Trp Asp Lys Leu Leu
 325 330 335

Phe Ala Lys Asn Gln Gln Asn Leu Asp Ser Thr Lys Ser Ser Val Ser
 340 345 350

Ser Ala Asn Thr Ile Asn Ser Asn Thr Ser His Asp Pro Val Arg Lys
 355 360 365

Ser Leu Leu Ser Gly Leu Phe Leu Ser Glu Ala Asn Ser Asn Ser Asn

370.

375

380

Asn His Asn Thr Ala His Ser Glu Tyr Ala Ser Lys His Val Ser Pro
385 390 395 400

Thr Pro Gln Ser Ser His Ser Asn Ile Gly Pro Gln Pro Gln Glu Asn
405 410 415

Pro Pro Ser Ala Asn Gly Ile Lys Gln Gln Lys Pro Ser Leu Lys Thr
420 425 430

Ser Asn Val Thr Ala Leu Ala Ser Lys Ser Pro Pro Gln Pro Ser Asn
435 440 445

Asn Glu Arg Leu Ser Met Arg Ile Gln Lys Asp Phe Lys Thr Arg Asn
450 455 460

Glu Ser Asn His Leu Tyr Glu Ser Asn Ala Pro Leu Thr Ala Gln Thr
465 470 475 480

Ile Leu Pro Thr Ala Leu Ser Thr His Met Phe Leu Pro Asn Asn Ile
485 490 495

His Gln Gln Arg Met Ala Ile Ala Thr Gly Ser Asn Thr Arg His Arg
500 505 510

Phe Ser Arg Arg Gln Ser Met Arg Ile Pro Ser Lys Asn Arg Asn Thr
515 520 525

Gly Thr Leu Lys Thr Arg Met Glu Ile Ser Glu Glu Glu Lys Met Val
530 535 540

Arg Thr Ile Ser Arg Leu Asp Asn Thr Ser Ile Ala Asn Ser Asn Gly
 543 550 555 560

Asn Gly Asn Asp Asp Thr Ser Asn Gln Arg Thr Glu Ala Leu Gly Arg
 565 570 575

Lys Thr Ser Asn Gly Gly Arg Ile
 580

<210> 165
 <211> 741
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(741)

<400> 165
 atg gag agt ala ttt ggt ggg ttt gga gat cta gtt gtt cct agg cca 40
 Met Glu Ser Ile Phe Gly Gly Phe Gly Asp Ieu Val Val Pro Arg Pro
 1 5 10 15
 aaq gag cat ctc ggt caa aca gac ctt tcc ttc ggt gga aaa tta ttg 95
 Lys Glu His Leu Gly Gln Thr Asp Leu Ser Phe Gly Gly Lys Ieu Leu
 20 25 30
 cct gaa atg aaa att tgt gaa gal ggt ggt gaa agt ggt tgt ggc ggt 140
 Pro Ala Leu Lys Ile Cys Glu Asp Gly Gly Glu Ser Gly Cys Gly Gly
 35 40 45
 aaa gtc tgg atc got ggc gaa atg ttg tgc gag tac ata ctc gag aaa 195
 Lys Val Trp Ile Ala Gly Glu Leu Leu Cys Glu Tyr Ile Leu Glu Lys
 50 55 60
 tca gtt gac cat atg cta agt aag acg gtc aat ggt aag aaa cca ttt 240
 Ser Val Asp His Leu Leu Ser Lys Thr Val Asn Gly Thr Lys Gln Phe

65	70	75	80	
aaa aaa gtc tta gaa ttg ggt agt ggt aca ggt tta gtt gga ttg tgc				200
Lys Lys Val Leu Glu Leu Gly Ser Gly Thr Gly Leu Val Gly Leu Cys				
	85	90	95	
gtg ggg ttg ttg gaa aaa aac aca ttc cca gat ggc act aaa gta tat				336
Val Gly Leu Leu Glu Lys Asn Thr Phe His Asp Gly Thr Lys Val Tyr				
	100	105	110	
gtt acg gac att gac aag ttg ata cca cta ttg aaa aga aat ata gaa				384
Val Thr Asp Ile Asp Lys Leu Ile Pro Leu Leu Lys Arg Asn Ile Glu				
	115	120	125	
ctg gac gaa gtt cag tat gaa gll glt gag agg gaa ctt tgg tgg ggt				432
Leu Asp Glu Val Glu Tyr Glu Val Leu Ala Arg Glu Leu Trp Trp Gly				
	130	135	140	
gag cgg ctg tgg gca gat ttc tca cct caa gaa ggt gat atg caa gca				480
Glu Pro Leu Ser Ala Asp Phe Ser Pro Glu Glu Gly Ala Met Glu Ala				
	145	150	155	160
aat aac gtt gat cta gtt ttg gca gct gat tgt gtg tat ctc gag gaa				528
Asn Asn Val Asp Leu Val Leu Ala Ala Asp Cys Val Tyr Leu Glu Glu				
	165	170	175	
gct tll cca tta cta gaa aaa aca cta ctt gat ctc act cac tgc ata				576
Ala Phe Pro Leu Leu Glu Lys Thr Leu Leu Asp Leu Thr His Cys Ile				
	180	185	190	
aac cca cct gta atc ttg atg gct tuc aag aag aga aga aaa gct gat				624
Asn Pro Pro Val Ile Leu Met Ala Tyr Lys Lys Arg Arg Lys Ala Asp				
	195	200	205	
aaa tat ttt ttc aac aag att aua aga aat ttt gac gtt ctt gaa att				672
Lys His Phe Phe Asn Lys Ile Lys Arg Asn Phe Asp Val Leu Glu Ile				
	210	215	220	
aca gat ttt agt aaa ttt gaa cat tat ctt aag gaa aga aoc cac ttg				720
Thr Asp Phe Ser Lys Phe Glu His Tyr Leu Lys Glu Arg Thr His Leu				
	225	230	235	240

ttt caq ctt atc agg aag taa 741
 Phe Gln Leu Ile Arg Lys
 245

<210> 156
 <211> 246
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 156

Met Glu Ser Ile Val Gly Gly Phe Gly Asp Leu Val Val Pro Arg Pro
 1 5 10 15

Lys Glu Val Leu Gly Gln Thr Asp Leu Ser Phe Gly Gly Lys Leu Leu
 20 25 30

Pro Ala Leu Lys Ile Cys Glu Asp Gly Gly Glu Ser Gly Cys Gly Gly
 35 40 45

Lys Val Trp Ile Ala Gly Gln Leu Leu Cys Glu Tyr Ile Leu Glu Lys
 50 55 60

Ser Val Asp His Leu Leu Ser Lys Thr Val Asn Gly Thr Lys Gln Phe
 65 70 75 80

Lys Lys Val Leu Glu Leu Gly Ser Gly Thr Gly Leu Val Gly Leu Cys
 85 90 95

Val Gly Leu Leu Glu Tyr Asn Thr Phe His Asp Gly Thr Lys Val Tyr
 100 105 110

Val Thr Asp Ile Asp Lys Leu Ile Pro Leu Leu Tyr Arg Asn Ile Gln
 115 120 125

Leu Asp Glu Val Gln Tyr Glu Val Leu Ala Arg Glu Leu Trp Trp Gly
 130 135 140

Glu Pro Leu Ser Ala Asp Phe Ser Pro Gln Glu Gly Ala Met Gln Ala
 145 150 155 160

Asn Asn Val Asp Leu Val Leu Ala Ala Asp Cys Val Tyr Leu Glu Glu
 165 170 175

Ala Phe Pro Met Leu Glu Lys Thr Leu Leu Asp Leu Thr His Cys Ile
 180 185 190

Asn Pro Pro Val Ile Leu Met Ala Tyr Lys Lys Arg Arg Lys Ala Asp
 195 200 205

Lys His Phe Phe Asn Tyr Trp Lys Arg Asn Phe Asp Val Leu Glu Ile
 210 215 220

Thr Asp Phe Ser Lys Phe Glu His Tyr Leu Lys Glu Arg Thr His Leu
 225 230 235 240

Phe Gln Leu Ile Arg Lys
 245

<210> 167
 <211> 2022
 <212> DKA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS

<222> (1)..(2022)

<400> 167

atg tca aag aac tca aac gaa taa ttt tct ggt tct tcc gga atg gtc 48
Met Ser Thr His Ser Asn Asp Tyr Phe Ser Ala Ser Ser Gly Met Val

1 5 10 15

tct gag aca tgg tgg gag gtt tct tgg ata aac tct tca aag cct gta 96

Ser Glu Thr Ser Ser Glu Val Ser Ser Ile Asn Ser Ser Glu Pro Val

20 25 30

tca ttc tct aag gct tct att ggt gct ccg gtt cca tgc tct gat cta 144

Ser Phe Ser Ser Lys Ala Ser Ile Ala Ala Pro Val Pro Cys Ser Asp Leu

35 40 45

cac agc acc aag tgg aac gat gaa tgg aga aaa tgg tct att cgt agg 192

His Ser Thr Lys Ser Asn Asp Ala Ser Arg Lys Leu Ser Ile Ser Arg

50 55 60

agg tta uct aat cgg ctc aac gac att aaa aag gct gtc gat gac gac 240

Thr Leu Thr Asn Arg Leu Asn Asp Ile Lys Lys Ala Val Asp Asp Asp

65 70 75 80

cac tgg aag aag gaa gaa aat tcc gaa gac gtt aat aaa ata tta gaa 288

Asn Leu Gln Thr Glu Glu Asn Ser Ala Asp Val Asn Lys Thr Leu Glu

95 100 105 110 115

tct aga ttt gaa gtc gcc gat gcc att cgg cta ccg cac aat gag tca 336

Ser Arg Thr Asp Val Ala Asp Ala Ile Arg Leu Gln His Asn Glu Ser

120 125 130

gtc cag tca aag tta aac atc cca gtc aca cac aca aag act gaa gcc 384

Val Gln Ser Lys Leu Asn Ile Pro Val Thr His Thr Thr Thr Ala Gly

135 140 145 150 155 160

gcc tgg ttg tgg gaa cca tct tcc tct gct ttc tct gct tct tct att 432

Ala Ser Leu Ser Ala Pro Ser Ser Ser Ala Phe Ser Ala Ser Ser Ile

165 170 175 180 185 190

caa aat gat act aca gaa cat aaa gct tcc atg gac tcc aaa tta atg 480

Gln Asn Asp Thr Thr Glu His Lys Ala Ser Met Asp Ser Lys Leu Met

145 150 155 160 165 170

agg aat aga cta tat cag get too acy aak oac tcc ggt aay gat ctt	528
Arg Asn Arg Leu Tyr Pro Ala Ser Thr Tyr His Ser Gly Lys Asp Leu	
165 170 175	
gag gcc caa gga ata acc gaa ltc gag cct gat gaa cag act gta aaa	576
Glu Ala Gln Gly Ile Thr Glu Phe Glu Pro Asp Glu Pro Thr Val Lys	
180 185 190	
aaa gta ttc acc aac aag tct acc ggg cag ctg gaa ctg cdc ccc gac	624
Lys Val Phe Thr Asn Lys Ser Thr Gly Gln Leu Glu Leu Pro Pro Asp	
195 200 205	
ggg ggt ttt ggc tgg gtc gts aca ttc tgt ctg ttc ttg acc atg ttt	672
Gly Gly Tyr Gly Trp Val Val Thr Phe Cys Val Phe Leu Thr Met Phe	
210 215 220	
tcg aag tgg gcc tgc aac gca tcc ttc ggt gtc gac ctt gcc taa taa	720
Ser Thr Trp Gly Cys Asn Ala Ser Phe Gly Val Asp Leu Ala Tyr Tyr	
225 230 235 240	
ala aau caa gat act tac cct ggt gct tcy aag tcc gat tat gcc tta	768
Leu Asn His Asp Thr Tyr Pro Gly Ala Ser Lys Tyr Asp Tyr Ala Leu	
245 250 255	
att gct gcc cta aat gtc ttt ctg ggt caa ctg tta tcc cdc ctt gtc	816
Ile Ala Gly Leu Thr Val Phe Leu Gly Gln Leu Leu Ser Pro Leu Val	
260 265 270	
atg gaa ctg atg aga ata att ggt ctg cgg aac aca atg ctt ttt ggt	864
Met Ala Leu Met Arg Ile Ile Gly Leu Arg Thr Thr Met Leu Phe Gly	
275 280 285	
gat gcc gta atg ctt gcc gca tat ctg ttg gcc tcc ttt act acc aag	912
Asp Ala Val Met Leu Ala Ala Tyr Leu Leu Ala Ser Phe Thr Thr Lys	
290 295 300	
tta tgg caa lly lal gtu acc caa ggt ttt atg gtc ggt tgt tca ata	960
Leu Trp Gln Leu Tyr Val Thr Gln Gly Phe Met Val Gly Cys Ser Ile	
305 310 315 320	
tca ctg att ttc gtc caa gca aca acc gtc tta caa gga tgg ttc ttg	1008

Ser	Leu	Ile	Phe	Val	Pro	Ala	Thr	Thr	Val	Leu	Pro	Gly	Trp	Phe	Leu	
				325					330					335		
asa	aaa	aga	gcl	gto	gca	alg	ggt	gtc	tca	tta	ttg	ggt	acc	ggt	gac	1056
Lys	Lys	Arg	Ala	Val	Ala	Met	Gly	Val	Ser	Leu	Leu	Gly	Thr	Gly	Ala	
				340				345					350			
ggc	ggt	gtc	ggt	tac	ggt	ttg	gct	aca	aac	aaa	atg	ctt	tct	gac	ttt	1104
Gly	Gly	Val	Val	Tyr	Gly	Leu	Ala	Thr	Asn	Lys	Met	Leu	Ser	Asp	Phe	
				355			360					365				
gga	aat	acc	egg	lsg	tgc	ctt	cgt	atc	ata	ggc	atn	tgc	tgt	agc	ata	1152
Gly	Asn	Thr	Arg	Trp	Cys	Leu	Arg	Ile	Ile	Gly	Ile	Ser	Cys	Ser	Ile	
				370			375					380				
agt	gtt	cta	gtt	gct	att	gag	ctc	tta	aaa	gac	aga	aac	cct	aca	cct	1200
Ser	Val	Leu	Val	Ala	Ile	Ala	Leu	Leu	Lys	Glu	Arg	Asn	Pro	Thr	Pro	
				385			390				395			400		
gac	ata	gga	ttg	aaa	tgc	cct	egg	gac	atg	lil	gac	agc	ctc	aaa	gac	1248
Ala	Ile	Gly	Leu	Lys	Ser	Phe	Arg	Ala	Met	Phe	Glu	Gln	Leu	Lys	Ala	
				405				410					415			
arg	ttc	tca	tta	aag	gtt	ata	act	aag	cua	lil	gtg	gta	ctt	att	gac	1296
Met	Phe	Ser	Leu	Lys	Val	Ile	Thr	Lys	Pro	Phe	Val	Val	Leu	Ile	Ala	
				420				425					430			
tta	tgg	ttc	atg	ttn	gac	tta	ttt	gac	tac	aat	atg	atg	gtt	ttt	act	1344
Leu	Trp	Phe	Met	Phe	Ala	Leu	Phe	Ala	Tyr	Asn	Met	Met	Val	Phe	Thr	
				435				440					445			
tta	tcu	tca	tac	gca	atc	tgc	aaa	gga	tta	tca	tgc	cac	gac	gct	tcc	1392
Leu	Ser	Ser	Tyr	Ala	Ile	Ser	Lys	Gly	Leu	Ser	Ser	His	Asp	Ala	Ser	
				450				455				460				
aca	ttg	act	gac	att	ttg	aac	ggc	tgc	caa	tcc	atc	ggc	aga	cct	ctg	1440
Thr	Leu	Thr	Ala	Ile	Leu	Asn	Gly	Ser	Gln	Ser	Ile	Gly	Arg	Pro	Leu	
				465			470				475			480		
atg	ggt	tta	ggc	gga	gat	aag	ttt	ggt	agg	gca	aac	gla	agc	atc	gta	1488
Met	Gly	Leu	Ala	Gly	Asp	Lys	Phe	Gly	Arg	Ala	Asn	Val	Thr	Ile	Val	
				485					490					495		

ttt acc aat ttg tta aca ata tat atg ttt gag ttc tgg atc ccc gct.	1536
Leu Thr Thr Leu Leu Thr Ile Cys Met Phe Ala Phe Trp Val Pro Ala	
500 505 510	
cat aag ttt gtt caa ctc atc ttt ttt tca att cta gtt ggc tca tgc	1584
His Thr Phe Val Gln Leu Ile Phe Phe Ser Val Leu Val Gly Ser Cys	
515 520 525	
gtt ggt gtc gcc aac gtc atg aat acc gtt ctg att gcc gat atg gtt	1632
Val Gly Val Ala Asn Val Met Asn Thr Val Leu Ile Ala Asp Met Val	
530 535 540	
aaa cca gaa gag ttt ttg ccc gct tgg gcc ttc gtc aac tac tgt ggt	1680
Lys Pro Glu Glu Phe Leu Pro Ala Trp Ala Phe Val Asn Tyr Cys Gly	
545 550 555 560	
gag cct ttc tta ttg gtt tgc gag gtg att gcc cag cca ttg aag gtc	1728
Ala Pro Phe Leu Leu Val Cys Glu Val Ile Ala Glu Ala Leu Thr Val	
565 570 575	
gag aaa gat aag agc cat cct tac tta cat gca caa att ttt tgc agt	1776
Glu Lys Asp Lys Ser Asn Pro Tyr Leu His Ala Gln Ile Phe Cys Gly	
580 585 590	
tgc tgc ttt att gcc gca cta att tta att tct atc ctt cgt gaa tac	1824
Cys Cys Phe Ile Ala Ala Leu Ile Leu Ile Ser Ile Leu Arg Glu Tyr	
595 600 605	
tct atc agg atg aaa tta aag gaa aga gaa gct atg aca aac gag aag	1872
Ser Ile Arg Met Lys Leu Thr Glu Arg Gln Ala Met Thr Asn Glu Lys	
610 615 620	
tta aaa gaa tgg aag gaa agc gaa tac gat acc gat tct gcc gat gaa	1920
Leu Lys Glu Thr Lys Ala Ser Glu Tyr Asp Thr Asp Ser Ala Arg Glu	
625 630 635 640	
gat tgg ggt aaa tta aaa gaa aga aag act aaa tat gac ctt ctt cta	1968
Asp Trp Gly Lys Leu Lys Glu Arg Lys Thr Lys Tyr Asp Leu Leu Leu	
645 650 655	
ggt cag ggc att aaa aaa tac ttc cta aga atg gta tat cca atg aag	2016

Gly Pro Gly Ile Lys Lys Tyr Phe Leu Arg Met Val Tyr Pro Met Lys
 560 565 570

gta tag 2322
 Val

<213> 166
 <211> 473
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 168

Met Ser Thr His Ser Asn Asp Tyr Phe Ser Ala Ser Ser Gly Met Val
 1 5 10 15

Ser Glu Val Ser Ser Glu Val Ser Ser Ile Asn Ser Ser Gln Pro Val
 20 25 30

Ser Phe Ser Lys Ala Ser Ile Ala Ala Pro Val Pro Cys Ser Asp Leu
 35 40 45

His Ser Thr Lys Ser Asn Asp Ala Ser Asn Lys Leu Ser Ile Ser Arg
 50 55 60

Thr Leu Thr Asn Arg Leu Asn Asp Ile Lys Lys Ala Val Asp Asp Asp
 65 70 75 80

Asn Leu Gln Thr Glu Glu Asn Ser Ala Asp Val Asn Lys Ile Leu Glu
 85 90 95

Ser Arg Phe Asp Val Ala Asp Ala Ile Arg Leu Gln His Asn Glu Ser
 100 105 110

Val Glu Ser Lys Leu Asn Ile Pro Val Thr His Thr Thr Thr Ala Gly
115 120 125

Ala Ser Leu Ser Ala Pro Ser Ser Ser Ala Phe Ser Ala Ser Ser Ile
130 135 140

Gln Asn Asp Thr Thr Glu His Lys Ala Ser Met Asp Ser Lys Leu Met
145 150 155 160

Arg Asn Arg Leu Tyr Pro Ala Ser Thr Lys His Ser Gly Lys Asp Leu
165 170 175

Glu Ala Gln Gly Ile Thr Glu Phe Glu Pro Asp Glu Pro Thr Val Lys
180 185 190

Lys Val Phe Thr Asn Lys Ser Thr Gly Gln Leu Glu Leu Pro Pro Asp
195 200 205

Gly Gly Tyr Gly Trp Val Val Thr Phe Cys Val Phe Leu Thr Met Phe
210 215 220

Ser Thr Trp Gly Cys Asn Ala Ser Phe Gly Val Asp Leu Ala Tyr Tyr
225 230 235 240

Leu Asn His Asp Thr Tyr Pro Gly Ala Ser Lys Tyr Asp Tyr Ala Leu
245 250 255

Ile Ala Gly Leu Thr Val Phe Leu Gly Gln Leu Leu Ser Pro Leu Val
260 265 270

Met Ala Leu Met Arg Ile Ile Gly Leu Arg Thr Thr Met Leu Phe Gly

390/762

275

280

285

Asp Ala Val Met Leu Ala Ala Tyr Leu Leu Ala Ser Phe Thr Thr Lys
 290 295 300

Leu Trp Gln Leu Tyr Val Thr Gln Gly Phe Met Val Gly Cys Ser Ile
 305 310 315 320

Ser Leu Ile Phe Val Pro Ala Thr Thr Val Leu Pro Gly Trp Phe Leu
 325 330 335

Lys Lys Arg Ala Val Ala Met Gly Val Ser Leu Leu Gly Thr Gly Ala
 340 345 350

Gly Gly Val Val Tyr Gly Leu Ala Thr Asn Lys Met Leu Ser Asp Phe
 355 360 365

Gly Asn Thr Arg Trp Cys Leu Arg Ile Ile Gly Ile Ser Cys Ser Ile
 370 375 380

Ser Val Leu Val Ala Ile Ala Leu Leu Lys Gln Arg Asn Pro Thr Pro
 385 390 395 400

Ala Ile Gly Leu Lys Ser Pro Arg Ala Met Phe Gln Gln Leu Lys Ala
 405 410 415

Met Phe Ser Leu Lys Val Ile Thr Lys Pro Phe Val Val Leu Ile Ala
 420 425 430

Leu Trp Phe Met Phe Ala Leu Phe Ala Tyr Asn Met Met Val Phe Thr
 435 440 445

Leu Ser Ser Tyr Ala Ile Ser Lys Gly Leu Ser Ser His Asp Ala Ser
 450 455 460

Thr Leu Thr Ala Ile Leu Asn Gly Ser Gln Ser Ile Gly Arg Pro Leu
 465 470 475 480

Met Gly Leu Ala Gly Asp Lys Phe Gly Arg Ala Asn Val Thr Ile Val
 485 490 495

Leu Thr Thr Leu Leu Thr Ile Tyr Met Phe Ala Phe Trp Ile Pro Ala
 500 505 510

His Thr Phe Val Gln Leu Ile Phe Phe Ser Ile Leu Val Gly Ser Cys
 515 520 525

Val Gly Val Ala Asn Val Met Asn Thr Val Leu Ile Ala Asn Met Val
 530 535 540

Lys Pro Glu Glu Phe Leu Pro Ala Trp Ala Phe Val Asn Tyr Cys Gly
 545 550 555 560

Ala Pro Phe Leu Leu Val Cys Glu Val Ile Ala Gln Ala Leu Thr Val
 565 570 575

Glu Lys Asp Lys Ser Asn Pro Tyr Leu His Ala Gln Ile Phe Cys Gly
 580 585 590

Cys Cys Phe Ile Ala Ala Leu Ile Leu Ile Ser Ile Leu Arg Glu Tyr
 595 600 605

Ser Ile Arg Met Lys Leu Thr Glu Arg Gln Ala Met Thr Asn Glu Lys
 610

510

615

620

Leu Lys Glu Trp Lys Ala Ser Glu Tyr Asp Thr Asp Ser Ala Asp Glc
 625 630 635 640

Asp Trp Gly Lys Leu Lys Glu Arg Lys Thr Lys Tyr Asp Leu Leu Leu
 645 650 655

Gly Pro Gly Ile Lys Lys Tyr Phe Leu Arg Met Val Tyr Pro Met Lys
 660 665 670

Val

<210> 169

<211> 1569

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1569)

<400> 169

atg ttg cta ala aga aag aag ata aat gaa ttt ctg gga tgt atc cat 48

Met Leu Leu Ile Arg Arg Thr Ile Asn Ala Phe Leu Gly Cys Ile His

1

5

10

15

tgc aat ctt acg gag aag tgc atc ctg att gac ttc gtc ata aac aag 95

Cys Asn Leu Thr Ala Thr Cys Ile Leu Ile Ala Phe Val Ile Thr Met

20

25

30

tat gtg gta att gta tct gag cct gaa tcc gta gac gga aat atg gga 144

Tyr val val Leu Val Ser Glu Pro Ala Ser Val Asp Gly Thr Met Gly

35

40

45

aat ttt ctt cag ttt tcc aag atg gat ctt gag acg aag agy gac aga	192
Asn Phe Leu Pro Phe Ser Lys Met Asp Leu Ala Thr Lys Arg Asp Arg	
50 35 60	
ccc ttt tat tgg aat tgt gtg aat act cag gac tat ttg ttg aat cca	240
Pro Phe Tyr Ser Asn Cys Val Asn Thr Gln Asp Tyr Leu Leu Asn Pro	
65 70 75 80	
tgg taa atc aag cag aat gcc tgg ttt gtc atg cta aca agg aac ggg	288
Ser Tyr Ile Lys Gln Asn Ala Ser Phe Val Met Leu Thr Arg Asn Gly	
85 90 95	
gag cta gaa gat gtt atc aag act atc aac aat ata gaa gag cat ttc	336
Glu Leu Glu Asp Val Ile Lys Thr Ile Asn Ser Ile Glu Glu His Phe	
100 103 110	
aat cag tgg ttc cac tat cca tat gtg ttc tta aat gac cag cag ttt	384
Asn Gln Trp Phe His Tyr Pro Tyr Val Phe Leu Asn Asp Gln Pro Phe	
115 120 125	
gaa gag gac ttc aaa gca aac gta cgt gat gtt aca gtg ggc ggc atg	432
Glu Glu Asp Phe Lys Ala Lys Val Arg Asp Val Thr Val Gly Ala Leu	
130 135 140	
gtg gaa ttt ggc act atc gat gag atc tct tgg aat ttt cag agt gac	480
Val Glu Phe Gly Thr Ile Asp Glu Ile Ser Trp Asn Phe Pro Ser Asp	
145 150 155 160	
gta aag gat acg ttc gag ttc tac aac gca att gag gat aac ggt gat	528
Val Lys Asp Thr Phe Glu Phe Tyr Asn Ala Ile Glu Asp Gln Gly Asp	
165 170 175	
aga agc ata ctt tac gga aac tta gaa tca tat cal aag atg tgc cgg	576
Arg Ser Ile Leu Tyr Gly Asn Leu Glu Ser Tyr His Lys Met Cys Arg	
180 185 190	
ttt tat cca gga tta ttt taa aag caa cag ata gta cag aag taa gaa	624
Thr Tyr Ser Gly Leu Phe Tyr Lys His Pro Leu Val Gln Lys Tyr Glu	
195 200 205	
tgg tat tgg aga ttg gaa ccc gat gtt gag ttt ttc tgt gat atc aac	672
Trp Tyr Trp Arg Leu Glu Pro Asp Val Glu Phe Phe Cys Asp Ile Thr	

210	215	220	
taa gat ooc ttt ttg gag atg ctc cga act aat aag aaa tat gga ttt			720
Tyr Asp Pro Phe Leu Glu Met Leu Arg Thr Asn Lys Lys Tyr Gly Phe			
225	230	235	240
acg atc atc atc ooc gaa ttg tat tgg aca gtc cca aat ttg ttt aga			748
Thr Ile Ile Ile Pro Glu Leu Tyr Trp Thr Val Pro Asn Leu Phe Arg			
245	250	255	
cac act aaa agc ttt atc agt caa aaa ggc gtt acg ctt ggg tca tta			816
His Thr Lys Ser Phe Ile Asn Gln Lys Gly Val Thr Leu Gly Ser Leu			
260	265	270	
lys aaa cta ttt aca aag gat tac gac att ttt gaa tcc gat gat ccg			864
Trp Tyr Leu Phe Thr Lys Asp Tyr Asp Ile Phe Glu Ser Asp Asp Pro			
275	280	285	
gag tta cgg gac lys atc aac tat gat ttt cag gcc aag gct aag ata			912
Glu Leu Arg Asp Trp Ile Asn Tyr Asp Phe Gln Ala Lys Ala Lys Ile			
290	295	300	
tcc gaa aag ata gcc atc gag cag ctc ttg aaa aag ggt gat gat ttc			960
Ser Glu Lys Ile Ala Ile Glu Gln Leu Lys Lys Gly Asp Asp Phe			
305	310	315	320
caa cag ata aat gat gcc aaa gag gga ata atg aat ttg ata cat aag			1008
Gln Gln Ile Asn Asp Asp Lys Glu Gly Ile Met Asn Leu Ile His Lys			
325	330	335	
gat cga tct agg aag cat atc gta gaa gac aaa ttt ttc aat gaa gag			1056
Ala Arg Ser Arg Lys His Ile Val Glu Asp Lys Phe Phe Asn Glu Glu			
340	345	350	
taa aat cta tgc cat ttc tgg agt aat ttt gag att ggc cgg cca agc			1104
Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Gln Ile Ala Arg Leu Ser			
355	360	365	
gtg ttc gac aat gac att tac aac agt ttt ttt caa tat ttg gag aaa			1152
Val Phe Asp Asn Asp Ile Tyr Asn Ser Phe Phe Gln Tyr Leu Glu Lys			
370	375	380	

agt ggt gga ttt tgg aag gaa aga tgg ggg gac gct cct gtt caa tct 1200
 Ser Gly Gly Phe Trp Lys Glu Arg Trp Gly Asp Ala Pro Val His Ser
 385 390 395 400

att gga ttg tgg cka act atg gat ttg gac gat gta cac tat ttt aga 1245
 Ile Gly Leu Ser Leu Thr Leu Asp Leu Asp Asp Val His Tyr Phe Arg
 405 410 415

gac atc gga tat aga cac tcc aca ata cag cat tgt cca cat aat gcc 1295
 Asp Ile Gly Tyr Arg His Ser Thr Ile Gln His Cys Pro His Asn Ala
 420 425 430

atg ggg aat gag gaa ttc tcc tac tta gcc agt gac tca aaa ttc aaa 1344
 Met Gly Asn Glu Glu Thr Ser Tyr Leu Ala Ser Asp Ser Lys Phe Lys
 435 440 445

cgt aaa aac gcc gcc taa gcc gag gga agg gaa ttt ggg tgt gcc tgc 1392
 Arg Lys Asn Ala Ala Tyr Asp Glu Gly Arg Glu Phe Gly Cys Gly Cys
 450 455 460

agg tgc aga tct ccc aag aaa aag cgt gaa att gag gat tcc atg tgt 1440
 Arg Cys Arg Cys Pro Lys Lys Lys Arg Glu Ile Glu Asn Ser Met Gly
 465 470 475 480

ttc tgc gta aat att tgg gta aat ctg att aac caa cag agg gga taa 1488
 Phe Cys Val Asn Ile Trp Val Asn Leu Leu Asn Gln Gln Arg Gly His
 485 490 495

gaa cgc cac gtc gaa gca ctc aac gcc aat gaa atg gag gag caa ata 1536
 Glu Arg His Val Glu Ala Leu Asn Gly Asn Glu Met Glu Glu His Ile
 500 505 510

agg gaa gac tat cta aga cag ttc gga aac tag 1569
 Arg Glu Asp Tyr Leu Arg Gln Phe Gly Asn
 515 520

<210> 170

<211> 522

<212> DRT

<213> Saccharomyces cerevisiae

<400> 170

Met Leu Leu Ile Arg Arg Thr Ile Asn Ala Phe Leu Gly Cys Ile His
 1 5 10 15

Cys Asn Leu Thr Ala Thr Cys Ile Asn Ile Ala Phe Val Ile Thr Met
 20 25 30

Tyr Val Val Leu Val Ser Glu Pro Ala Ser Val Asp Gly Thr Met Gly
 35 40 45

Asn Phe Leu Pro Phe Ser Lys Met Asp Leu Ala Thr Lys Arg Asp Arg
 50 55 60

Pro Phe Tyr Ser Asn Cys Val Asn Thr Gln Asp Tyr Leu Leu Asn Pro
 65 70 75 80

Ser Tyr Ile Lys Gln Asn Ala Ser Phe Val Met Leu Thr Arg Asn Gly
 85 90 95

Glu Leu Glu Asp Val Ile Lys Thr Ile Asn Ser Ile Glu Glu His Phe
 100 105 110

Asn Gln Trp Phe His Tyr Pro Tyr Val Phe Leu Asn Asp Gln Pro Phe
 115 120 125

Glu Glu Asp Phe Lys Ala Lys Val Arg Asp Val Thr Val Gly Ala Leu
 130 135 140

Val Glu Phe Gly Thr Ile Asp Glu Ile Ser Trp Asn Phe Pro Ser Asp
 145 150 155 160

Val Lys Asp Thr Phe Glu Phe Tyr Asn Ala Ile Glu Asp Glu Gly Asp
 165 170 175

Arg Ser Ile Leu Tyr Gly Asn Leu Glu Ser Tyr His Lys Met Cys Arg
 180 185 190

Phe Tyr Ser Gly Leu Phe Tyr Lys His Pro Leu Val Gln Lys Tyr Glu
 195 200 205

Trp Tyr Trp Arg Leu Glu Pro Asp Val Glu Phe Phe Cys Asp Ile Thr
 210 215 220

Tyr Asp Pro Phe Leu Glu Met Leu Arg Thr Asn Lys Lys Tyr Gly Phe
 225 230 235 240

Thr Ile Ile Ile Pro Glu Leu Tyr Trp Trp Val Pro Asn Leu Phe Arg
 245 250 255

His Thr Lys Ser Phe Ile Ser Gln Lys Gly Val Thr Leu Gly Ser Leu
 260 265 270

Trp Lys Leu Phe Thr Lys Asp Tyr Asp Ile Phe Glu Ser Asp Asp Pro
 275 280 285

Glu Leu Arg Asp Trp Ile Asn Tyr Asp Phe Gln Ala Lys Ala Lys Ile
 290 295 300

Ser Glu Lys Ile Ala Ile Glu Gln Leu Leu Lys Lys Gly Asp Asp Phe
 305 310 315 320

Gln Glu Ile Asn Asp Asp Lys Glu Gly Ile Met Asn Leu Val His Lys
 325 330 335

Ala Arg Ser Arg Lys His Ile Val Glu Asp Lys Phe Phe Asn Glu Glu
340 345 350

Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile Ala Arg Leu Ser
355 360 365

Val Phe Asp Asn Asp Ile Tyr Asn Ser Phe Phe Gln Tyr Leu Glu Lys
370 375 380

Ser Gly Gly Phe Trp Lys Glu Arg Trp Gly Asp Ala Pro Val His Ser
385 390 395 400

Ile Gly Leu Ser Leu Thr Leu Asp Leu Asp Asp Val His Tyr Phe Arg
405 410 415

Asp Ile Gly Tyr Arg His Ser Thr Ile Gln His Cys Pro His Asn Ala
420 425 430

Met Gly Asn Glu Glu Phe Ser Tyr Leu Ala Ser Asp Ser Lys Phe Lys
435 440 445

Arg Lys Asn Ala Ala Tyr Asp Glu Gly Arg Glu Phe Gly Cys Gly Cys
450 455 460

Arg Cys Arg Cys Pro Lys Lys Lys Arg Glu Ile Glu Asp Ser Met Gly
465 470 475 480

Phe Cys Val Asn Ile Trp Val Asn Leu Leu Asn Gln Gln Arg Gly His
485 490 495

Glu Arg His Val Glu Ala Leu Asn Gly Asn Glu Met Glu Glu His Ile
 500 505 510

Arg Glu Asp Tyr Leu Arg Gln Phe Gly Asn
 515 520

<210> 171
 <211> 1506
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1506)

<400> 171
 atg ctt tta cca gga atg cgt tta tgg caa agn tta cat aag aga cat 48
 Met Leu Leu Gln Gly Met Arg Leu Ser Gln Arg Leu His Lys Arg His
 1 5 10 15
 cta ttt got tcc aag att ttc acg tgg act acg aau cct got cat ata 96
 Leu Phe Ala Ser Lys Ile Leu Thr Trp Thr Thr Asn Pro Ala His Ile
 20 25 30
 cgc cac cta cat gat ata agg ccg cct gca tca aac ttc aat acg caa 144
 Arg His Leu His Asp Ile Arg Pro Pro Ala Ser Asn Phe Asn Thr Gln
 35 40 45
 gaa ttg guu ccc ata ccg gag tct cca gca aao tca nca act cga cca 192
 Glu Ser Ala Pro Ile Pro Glu Ser Pro Ala Asn Ser Pro Thr Arg Pro
 50 55 60
 cag atg gca cct uaa ccc aat ttg aaa aaa aaa aat cgt cgt tta atg 240
 Gln Met Ala Pro Lys Pro Asn Leu Lys Tyr Lys Asn Arg Ser Leu Met
 65 70 75 80
 tat tct att att ggg gtt cou ata gta cgt tta tat ttt tgy ttt aaa 288
 Tyr Ser Ile Ile Gly Val Ser Ile Val Gly Leu Tyr Phe Trp Phe Lys
 85 90 95

agt aac tcc agg aaa caa aaa cta cct ctc tgg ggg caa aaa gtc tgg	316
Ser Asn Ser Arg Lys Gln Lys Leu Pro Leu Ser Ala Gln Tyr Val Trp	
103 106 110	
aag gaa gcc ata tgg caa gaa agt gat aaa atg gat ttt aat tac aaa	384
Lys Glu Ala Thr Trp Gln Glu Ser Asp Lys Met Asp Phe Asn Tyr Lys	
115 126 125	
gaa ggg cta agg cgg tat att gag ggg ttg gat gaa tgc gat cgc tct	432
Glu Ala Leu Arg Arg Tyr Ile Glu Ala Leu Asp Glu Cys Asp Arg Ser	
130 135 140	
cac gtc gat tta ttg tca gat gat tat acc aga ata gag ctg aaa att	480
His Val Asp Leu Leu Ser Asp Asp Tyr Thr Arg Ile Glu Leu Lys Ile	
145 150 155 160	
gct gaa atg tat gaa aag ctc aat atg ctt gaa gaa gcc caa aat ttg	528
Ala Glu Met Tyr Glu Lys Leu Asn Met Leu Glu Glu Ala Gln Asn Leu	
165 170 175	
tac caa gaa tta tta agt cgg ttt ttc gaa ggg ctg aat gtc cct ggc	576
Tyr Gln Glu Leu Leu Ser Arg Phe Phe Glu Ala Leu Asn Val Pro Gly	
180 185 190	
aaa gtc gat gag agt gaa aga gcc ggg gtt tta aga aaa gac ttg aga	624
Lys Val Asp Glu Ser Glu Arg Gly Glu Val Leu Arg Lys Asp Leu Arg	
195 200 205	
atc ttg att aac tcc tta gaa aca aat aag gac ata gaa agt ggc aag	672
Ile Leu Ile Lys Ser Leu Glu Thr Asn Lys Asp Ile Glu Ser Gly Lys	
210 215 220	
aga aaa ttg cta caa cat tta ctt tta gct caa gag gaa att tta agc	720
Arg Lys Leu Leu Gln His Leu Leu Leu Ala Gln Glu Glu Ile Leu Ser	
225 230 235 240	
aaa tgg cca gag ttg aag gaa ttt ttc gaa aac aga aaa aag aag ctc	768
Lys Ser Pro Glu Leu Lys Glu Phe Phe Glu Asn Arg Lys Lys Lys Leu	
245 250 255	
tgg atg gta aac gac atc aat aga gac cct aat gat gat ttt aaa aca	816

Ser Met Val Lys Asp Ile Asn Arg Asp Pro Asn Asp Asp Phe Lys Thr	
260	265
270	
ttt gtt agt gag gaa aat att aaq ttt gat gaq caa ggc tat atq att	864
Phe Val Ser Glu Glu Asn Ile Lys Phe Asp Glu Gln Gly Tyr Met Ile	
275	280
285	
ttg gat ctg gaa aag aat agc agc gct tgg gaa ccc ttt aag gaa gaa	912
Leu Asp Leu Glu Lys Asn Ser Ser Ala Trp Glu Pro Phe Lys Glu Glu	
290	295
300	
ttt ttt act gag aga gat tta tat aca gct tat tgt ctg tca tca aaa	960
Phe Phe Thr Ala Arg Asp Leu Tyr Thr Ala Tyr Cys Leu Ser Ser Lys	
305	310
315	320
gac ata gct gca gct cta agt tgc aag ata act agt gbg gaa tgg atg	1008
Asp Ile Ala Ala Ala Leu Ser Cys Lys Ile Thr Ser Val Glu Trp Met	
325	330
335	
gtt atg gca gac atg cca cca gga aag ata tgg cta tca cag gaa aat	1056
Val Met Ala Asp Met Pro Pro Gly Gln Ile Leu Leu Ser Gln Ala Asn	
340	345
350	
lly ggy lca lly lly lat att caa gca gaa aag cta gaa gct gac tta	1104
Leu Gly Ser Leu Phe Tyr Leu Gln Ala Gln Lys Leu Glu Ala Asp Leu	
355	360
365	
aat can tta gac caa aag aaa agt aaa gag tcc aac caa gag tta gat	1152
Asn Gln Leu Glu Gln Lys Lys Ser Lys Glu Ser Asn Glu Glu Leu Asp	
370	375
380	
atg gga acs kac ata aaa gcc gtt aga ttc gta cgc aaa aat cgt gac	1200
Met Gly Thr Tyr Ile Lys Ala Val Arg Phe Val Arg Lys Asn Arg Asp	
385	390
395	400
tta tgt ctg gaa aga gca caa aaa tgt taa gac agc gtt att gcg ttt	1248
Leu Cys Leu Glu Arg Ala Gln Lys Cys Tyr Asp Ser Val Ile Ala Phe	
405	410
415	
gcc aaa aga aac aga aaa att agg ttt cat gly aay gal uaa tly gat	1296
Ala Lys Arg Asn Arg Lys Ile Arg Phe His Val Tyr Arg Gln Trp Asp	
420	425
430	

ccr tca att gca cag toa att gat cta tct acc tat gga atg ggg gtt 1344
 Pro Ser Ile Ala Gln Ser Ile Ala Leu Ser Thr Tyr Gly Met Gly Val
 433 440 445

tta agc ctt cat gaa ggt gtt ttg gct aaa gct gaa aaa cta ttc aaa 1392
 Leu Ser Leu His Glu Gly Val Leu Ala Lys Ala Gln Lys Leu Phe Lys
 450 455 460

gat cag atc act atg ggc aag gag act gaa ttt aat gaa ctc ctt gca 1440
 Asp Ser Ile Thr Met Ala Lys Glu Thr Glu Phe Asn Glu Leu Leu Ala
 465 470 475 480

gaa gct gaa aag gaa cta gaa cag acg acc gtc tly aat gag gcc aaa 1488
 Glu Ala Glu Lys Glu Leu Glu Lys Thr Thr Val Leu Lys Ala Ala Lys
 485 490 495

aaa gag ggt tta aac taa 1506
 Lys Glu Gly Leu Asn
 500

<210> 172
 <211> 501
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 172

Met Leu Leu Gln Gly Met Arg Leu Ser Gln Arg Leu His Lys Arg His
 1 5 10 15

Leu Phe Ala Ser Lys Ile Leu Thr Trp Thr Thr Asn Pro Ala His Ile
 20 25 30

Arg His Leu His Asp Ile Arg Pro Pro Ala Ser Asn Phe Asn Thr Gln
 35 40 45

Glu Ser Ala Pro Ile Pro Glu Ser Pro Ala Asa Ser Pro Thr Arg Pro

"aa,"

50	55	60	
Gln Met Ala Pro Lys Pro Asn Leu Lys Lys Lys Asn Arg Ser Leu Met			
65	70	75	80
Tyr Ser Phe Ile Gly Val Ser Ile Val Gly Leu Tyr Phe Trp Phe Lys			
85	90	95	
Ser Asn Ser Arg Lys Gln Lys Leu Pro Leu Ser Ala Gln Lys Val Trp			
100	105	110	
Lys Gln Ala Phe Trp Gln Glu Ser Asp Lys Met Asp Phe Asn Tyr Lys			
115	120	125	
Glu Ala Leu Arg Arg Tyr Ile Glu Ala Leu Asp Glu Cys Asp Arg Ser			
130	135	140	
His Val Asp Leu Leu Ser Asp Asp Tyr Thr Arg Ile Glu Leu Lys Ile			
145	150	155	160
Ala Glu Met Tyr Glu Lys Leu Asn Met Leu Glu Glu Ala Gln Asn Leu			
165	170	175	
Tyr Gln Gln Leu Leu Ser Arg Phe Phe Glu Ala Leu Asn Val Pro Gly			
180	185	190	
Lys Val Asp Glu Ser Glu Arg Gly Glu Val Leu Arg Lys Asp Leu Arg			
195	200	205	
Ile Leu Ile Lys Ser Leu Glu Ile Asn Lys Asp Ile Glu Ser Gly Lys			
210	215	220	

Arg Lys Leu Leu Gln His Leu Leu Leu Ala Glu Glu Gln Ile Leu Ser
 225 230 235 240

Lys Ser Pro Gln Leu Lys Glu Phe Phe Glu Asn Arg Lys Lys Lys Leu
 245 250 255

Ser Met Val Lys Asp Ile Asn Arg Asp Pro Asn Asp Asp Phe Lys Thr
 260 265 270

Phe Val Ser Glu Glu Asn Ile Lys Phe Asp Glu Gln Gly Tyr Met Ile
 275 280 285

Leu Asp Leu Glu Lys Asn Ser Ser Ala Trp Glu Pro Phe Lys Glu Glu
 290 295 300

Phe Phe Thr Ala Arg Asp Leu Tyr Thr Ala Tyr Cys Leu Ser Ser Lys
 305 310 315 320

Asp Ile Ala Ala Ala Leu Ser Cys Lys Ile Thr Ser Val Glu Trp Met
 325 330 335

Val Met Ala Asp Met Pro Pro Gly Gln Ile Leu Leu Ser Gln Ala Asn
 340 345 350

Leu Gly Ser Leu Phe Tyr Leu Gln Ala Glu Lys Leu Glu Ala Asp Leu
 355 360 365

Asn Gln Leu Glu Gln Lys Lys Ser Lys Glu Ser Asn Gln Glu Leu Asp
 370 375 380

Met Gly Thr Tyr Ile Lys Ala Val Arg Phe Val Arg Lys Asn Arg Asp

385 390 395 400

Leu Cys Leu Glu Arg Ala Gln Lys Cys Tyr Asp Ser Val Ile Ala Phe
405 410 415

Ala Lys Arg Asn Arg Lys Ile Arg Phe His Val Lys Asp Gln Leu Asp
420 425 430

Pro Ser Ile Ala Gln Ser Ile Ala Leu Ser Thr Tyr Gly Met Gly Val
435 440 445

Leu Ser Leu His Glu Gly Val Asn Ala Lys Ala Glu Lys Leu Phe Lys
450 455 460

Asp Ser Ile Thr Met Ala Lys Glu Thr Glu Phe Asn Glu Leu Leu Ala
465 470 475 480

Glu Ala Glu Lys Glu Leu Glu Lys Thr Thr Val Leu Lys Ala Ala Lys
485 490 495

Lys Glu Gly Leu Asn
500

<210> 173
<211> 327
<212> DKA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(327)

<100> 173

atg tcc att gag aat atg aaa tca ttt gat cct ttc gcc gac aca gga 48
 Met Ser Ile Glu Asn Leu Lys Ser Phe Asp Pro Phe Ala Asp Thr Gly
 1 5 10 15

gac gac gaa acc gcc act tca aac tat att cat att cgt atc caa cag 96
 Asp Asp Glu Thr Ala Thr Ser Asn Tyr Ile His Ile Arg Ile Gln Gln
 20 25 30

aga aat ggt aga aac act tta act acg gtg caa ggt gtc cca gag gaa 144
 Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln Gly Val Pro Glu Glu
 35 40 45

tat gat tta aag aga att ctt aag gtc cta aag aag gac ttt gca tgc 192
 Tyr Asp Ileu Lys Arg Ile Ileu Lys Val Leu Lys Lys Asp Phe Ala Cys
 50 55 60

aat ggt aac att gtc aag gat cca gaa atg ggg gag att att cag ttg 240
 Asn Gly Asn Ile Val Lys Asp Pro Glu Met Gly Glu Ile Ile Gln Leu
 65 70 75 80

cag ggt gac caa aga gca aag gtt tgc gaa ttt atg atc tcc caa ctg 288
 Gln Gly Asp Gln Arg Ala Lys Val Cys Glu Phe Met Ile Ser Gln Leu
 85 90 95

gga ttg cca aag aag aac att aac att cat ggg ttt taa 327
 Gly Leu Gln Lys Lys Asn Ile Lys Ile His Gly Phe
 100 105

<210> 174

<211> 108

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 174

Met Ser Ile Glu Asn Leu Lys Ser Phe Asp Pro Phe Ala Asp Thr Gly
 1 5 10 15

Asp Asp Glu Thr Ala Thr Ser Asn Tyr Ile His Ile Arg Ile Gln Gln
 20 25 30

Protein Data Bank

Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln Gly Val Pro Glu Glu
35 40 45

Tyr Asp Leu Lys Arg Ile Leu Lys Val Leu Lys Lys Asp Phe Ala Cys
50 55 60

Asn Gly Asn Ile Val Lys Asp Pro Glu Met Gly Glu Ile Ile Gln Leu
65 70 75 80

Gln Gly Asp Gln Arg Ala Lys Val Cys Glu Phe Met Ile Ser Gln Leu
85 90 95

Gly Leu Gln Lys Lys Asn Ile Lys Ile His Gly Phe
100 105

<210> 175
<211> 669
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(669)

<400> 175
atg acc gtc gtt atc gga gtc ttg gca tta cag ggt gcg ttc att gaa 48
Met Thr Val Val Ile Gly Val Leu Ala Leu Gln Gly Ala Phe Xle Glu
1 5 10 15
cat gtc cga cad gta gaa aaa tgc atc gtc gaa aac agg gat ttc tat 96
His Val Arg His Val Glu Lys Cys Ile Val Glu Asn Arg Asp Phe Tyr
20 25 30
gaa aaa aaa cta tct gtc atg aca gtc aag gat aaa aat caa cta gct 144

Glu Lys Lys Leu Ser Val Met Thr Val Lys Asp Lys Asn Glu Leu Ala	
35 40 45	
caa tgt gat gca ttg atc ata cct ggg gga gag tgg act gca atg tgc	192
Gln Cys Asp Ala Leu Ile Ile Pro Gly Gly Glu Ser Thr Ala Met Ser	
50 55 60	
ctt att gca gaa aga cca gga ttt tac gac gat ctc tac gca ttc gta	240
Ile Ile Ala Glu Arg Thr Gly Phe Tyr Asp Asp Leu Tyr Ala Phe Val	
65 70 75 80	
cac aac cca agc aag gta acc tgg ggt act tgt gca ggt atg att tat	288
His Asn Pro Ser Lys Val Thr Thr Gly Thr Cys Ala Gly Met Ile Tyr	
85 90 95	
att taa caa caa tta tct aac gaa gaa aca ctg gtc aag acg ctg aat	336
Ile Ser Gln Glu Leu Ser Asn Glu Glu Lys Leu Val Lys Thr Leu Asn	
100 105 110	
tta cta aag gtt aaa gta aaa aga aat gca ttt ggg aga caa gct aag	384
Icu Leu Lys Val Lys Val Lys Arg Asn Ala Phe Gly Arg Gln Ala Gln	
115 120 125	
tct tct aca cgg aat Lys gac ttt tca aac ttt att cct cac tgc aat	432
Ser Ser Thr Arg Ile Cys Asp Phe Ser Asn Phe Ile Pro His Cys Asn	
130 135 140	
gat ttt cct gct act ttt ata aga gcc cca gta ata gaa gag ctg ctg	480
Asp Phe Pro Ala Thr Phe Ile Arg Ala Pro Val Ile Glu Glu Val Leu	
145 150 155 160	
gat cct gaa cat gtg cag gtc ctg taa aac tta gat ggg aag gat aat	528
Asp Pro Glu His Val Gln Val Leu Tyr Lys Leu Asp Gly Lys Asp Asn	
165 170 175	
ggt ggt caa gaa cta att gtt gcc gat aag caa aac aac aat att ctt	576
Gly Gly Gln Glu Leu Ile Val Ala Ala Lys Gln Lys Asn Asn Ile Leu	
180 185 190	
ggg aca tca ttt cat ccg gaa tgg gca gaa aac gat ala cgg ttt cac	624
Ala Thr Ser Phe His Pro Gln Leu Ala Glu Asn Arg Ile Arg Thr His	
195 200 205	

gaa tgg ttc atc aga gaa ttt gtt ctt aaa aac tac agt aaa taa 669
 asp trp phe ile arg glu phe val leu lys asn tyr ser lys
 210 215 220

<210> 176
 <211> 222
 <212> PRT
 <213> Saccharomyces cerevisiae
 <400> 176

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his val arg his val glu lys cys ile val glu asn arg asp phe tyr
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glu lys lys leu ser val met thr val lys asp lys asn gln leu ala
 35 40 45

gln cys asp ala leu ile ile pro gly gly glu ser thr ala met ser
 50 55 60

leu ile ala gln arg thr gly phe tyr asp asp leu tyr ala phe val
 65 70 75 80

his asn pro ser lys val thr trp gly thr cys ala gly met ile tyr
 85 90 95

ile ser gln gln leu ser asn glu gln lys leu val lys thr leu asn
 100 105 110

leu leu lys val lys val lys arg asn ala phe gly arg gln ala gln

Protein Data Bank

410/762

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Ser Ser Thr Arg Ile Cys Asp Phe Ser Asn Phe Ile Pro His Cys Asp
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Asp Phe Pro Ala Thr Phe Ile Arg Ala Pro Val Ile Glu Glu Val Leu
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Asp Pro Glu His Val Gln Val Leu Tyr Lys Leu Asp Gly Lys Asp Asn
165 170 175

Gly Gly Gln Glu Leu Xle Val Ala Ala Lys Glu Lys Asn Asn Ile Leu
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Leu Lys Gly Gly Ile Glu Gly Ala Leu Ala Gly Phe Ala Ile Ser Ala	
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ata att ttc aaa gtc cta cca aga agg tac cca aaa ttc aag cct tgg	144
...le Ile Phe Lys Val Leu Pro Arg Arg Tyr Pro Lys Phe Lys Pro Ser	
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act cta aca tgg tcc ata aaa acc gcc att tgg atc acc cct ccc aag	192
Thr Leu Thr Trp Ser Ile Lys Thr Ala Leu Trp ...le Thr Pro Pro Thr	
50 55 60	
gtc ttg act gct ata tct gag gag gag gcc tgg aac aat ttc gac gct	240
Val Leu Thr Ala Ile Cys Ala Glu Glu Ala Ser Asn Asn Phe Asp Ala	
65 70 75 80	
aca alg laa gga tcc ggt tcc tcc tgg gaa gac gca cta gat gag cac	288
Thr Met Tyr Gly Ser Gly Ser Ser Ser Glu Asp Ala Leu Asp Glu His	
85 90 95	
aga aga tgg aag agt ttg agt aca aag gac aag ttt gtc gaa ggt cta	336
Arg Arg Trp Lys Ser Leu Ser Thr Lys Asp Lys Phe Val Glu Gly Asp	
100 105 110	
tct aat aac aag tat aag atc atc acc ggt gcc tgg gcc gct tgg atg	384
Ser Asn Asn Lys Tyr Lys Ile Ile Thr Gly Ala Trp Ala Ala Ser Leu	
115 120 125	
tat ggg tgg tgg gta atc gtg aac aaa gac ccc atc atg acc aaa gct	432
Tyr Gly Ser Trp Val Ile Val Asn Lys Asp Pro Ile Met Thr Lys Ala	
130 135 140	
cag aag atc gtg cag gcc aga atg tac gct cca ttc att acc gtc ggg	480
Gln Lys Ile Val Gln Ala Arg Met Tyr Ala Gln Phe Ile Thr Val Gly	
145 150 155 160	
ctg ctg ctg gcc tcc gtt ggt ttg agc atg tac gag aat aag tta cct	528
Leu Leu Leu Ala Ser Val Gly Leu Ser Met Tyr Glu Asn Lys Leu His	
165 170 175	
cct aat aaa caa aag gtc aac gaa atg cgc tgc tgg gaa aac gca ctg	576
Pro Asn Lys Gln Lys Val Asn Glu Met Arg Arg Trp Cln Asn Ala Leu	

Protein 1: 180

185

190

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Arg Val Ala Glu Glu Glu Glu Arg Leu Glu Lys Glu Gly Arg Arg Thr
195 200 205

ggc laa gtt tct aac gaa gaa aga ata aac tcc aag atc ttc aag tcc 672
Gly Tyr Val Ser Asn Glu Glu Arg Ile Asn Ser Lys Ile Phe Lys Ser
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Ile Ile Phe Lys Val Leu Pro Arg Arg Tyr Pro Lys Phe Lys Pro Ser
35 40 45

Thr Leu Thr Trp Ser Ile Lys Thr Ala Leu Trp Ile Thr Pro Pro Thr
50 55 60

Val Leu Thr Ala Ile Cys Ala Glu Glu Ala Ser Asn Asn Phe Asp Ala
65 70 75 80

Thr Met Tyr Gly Ser Gly Ser Ser Ser Glu Arg Ala Leu Asp Glu His
85 90 95

FIG. 2 is a schematic diagram of the amino acid sequence of the protein.

Arg Arg Trp Lys Ser Leu Ser Thr Lys Asp Lys Phe Val Glu Gly Leu
100 105 110

Ser Asn Asn Lys Tyr Lys Ile Ile Thr Gly Ala Trp Ala Ala Ser Leu
115 120 125

Tyr Gly Ser Trp Val Ile Val Asn Lys Asp Pro Ile Met Thr Lys Ala
130 135 140

Gln Lys Ile Val Gln Ala Arg Met Tyr Ala Gln Phe Ile Thr Val Gly
145 150 155 160

Leu Leu Leu Ala Ser Val Gly Leu Ser Met Tyr Glu Asn Lys Leu His
165 170 175

Pro Asn Lys Glu Lys Val Asn Glu Met Arg Arg Trp Glu Asn Ala Leu
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Arg Val Ala Glu Glu Glu Glu Arg Leu Glu Lys Glu Gly Arg Arg Thr
195 200 205

Gly Tyr Val Ser Asn Glu Glu Arg Ile Asn Ser Tyr Ile Phe Lys Ser
210 215 220

<210> 179

<211> 1461

<212> DNA

<213> *Saccharomyces cerevisiae*

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1				5						10				15		

gag	atc	aag	gaa	act	aac	cca	tgg	ctc	aaa	cta	ggt	caa	ggg	cag	agg	96
Gln	Ile	Tyr	Glu	Thr	Asn	Pro	Leu	Leu	Lys	Leu	Val	Gln	Gly	Gln	Arg	
			20						25					30		

att	gtc	caa	gtt	cgg	gaa	cta	gtg	ctt	gag	tct	ggc	gtg	gtc	ata	aat	144
Ile	Val	Gln	Val	Pro	Glu	Asn	Val	Leu	Glu	Ser	Gly	Val	Val	Ile	Asn	
			25				40							45		

aat	ttc	cat	att	gct	tat	aag	atg	tgg	ggc	aca	ctg	aat	gaa	gct	ggc	192
Asn	Phe	Pro	Ile	Ala	Tyr	Lys	Thr	Trp	Gly	Thr	Leu	Asn	Glu	Ala	Gly	
			50				55					60				

cat	aat	gtc	ctg	gta	att	tgt	cat	gac	tty	aat	ggg	tac	gca	gat	gtt	240
Asp	Asn	Val	Leu	Val	Ile	Cys	His	Ala	Leu	Thr	Gly	Ser	Ala	Asp	Val	
65					70					75				80		

gct	gac	tgg	tty	gac	ucl	ucl	ctg	ggc	aac	gac	tta	gca	ttc	gac	cca	288
Ala	Asp	Trp	Trp	Gly	Pro	Leu	Leu	Gly	Asn	Asp	Leu	Ala	Phe	Asp	Pro	
				85					90					95		

tca	agg	ttt	ttt	ctc	ata	tgt	tta	aac	tct	atg	ggc	tct	cca	tat	ggg	336
Ser	Arg	Phe	Phe	Ile	Ile	Cys	Leu	Asn	Ser	Met	Gly	Ser	Pro	Tyr	Gly	
			100					105						110		

tct	ttc	tgg	cca	tta	acg	ata	aat	gag	gag	cgg	ggc	gtt	aga	tat	gga	384
Ser	Phe	Ser	Pro	Leu	Thr	Ile	Asn	Glu	Glu	Thr	Gly	Val	Arg	Tyr	Gly	
			115					120					125			

ccc	gaa	ttc	cca	tta	tgt	act	gtg	cgc	gat	gac	gtt	aga	gct	cac	aga	432
Pro	Glu	Phe	Pro	Leu	Cys	Thr	Val	Arg	Asp	Asp	Val	Arg	Ala	His	Arg	
	130						135					140				

att	gtt	ctg	gat	tct	ctg	gga	gta	aag	tca	ata	gac	tgt	gtt	ucl	ggt	480
Ile	Val	Leu	Asp	Ser	Leu	Gly	Val	Lys	Ser	Ile	Ala	Cys	Val	Trp	Gly	
145					150					155				160		

ggc tct atg ggg ggg atg atg agt ttg gaa tgg gct ggc atg tat ggt Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly 165 170 175	828
aag gaa tat gtg aag aat atg gct gct utg ggg aca tca gca aga cat Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His 180 185 190	876
tct gcc tgg tgc ata tgg tgg tct gag gct caa aga caa tgg att tac Ser Ala Thr Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr 195 200 205	924
tca gat ccc aac tac ttg gac ggg tac tat cgg gta gag gag caa cct Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro 210 215 220	972
gag gcc gga cta tgg gcl gca agt atg tct gca ttg tlg acg tac agg Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg 225 230 235 240	1020
aca gga aac agt ttc gag aac cca ttc tcc aga aga tct cct tca ata Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile 245 250 255	1068
gca caa cca caa cca gct caa agg gag gag aca cgc aca cca tct acg Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr 260 265 270	1116
gtc agc caa cac tcc cta caa atc cac aat gat ggg tat aca acc aac Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys 275 280 285	1164
ggc agc act gac atc gct ggc att tct ggg caa aaa ggt caa agc gtg Ala Ser Thr Ala Thr Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val 290 295 300	1212
gtg tcc acc gca tct tct tgg gat tca ttg aat tct tca aca tgg atg Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met 305 310 315 320	1260
act tgg gta ayt tct gta acg ggt gaa gtg aag gac ata aag cct gcy	1308

Thr Ser Val Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala	325	330	325
uay uay Lal Lbt tot gca caa agt tac ttg agg tac cag ggc aca aag			1056
G'n Thr Tyr Pha Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys	340	345	350
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aau			1104
Phe Ile Asn Arg Pha Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys	355	360	365
ctg gat aag cac gat ttg gca cga gac aga gta gat gac atc act gag			1152
Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu	370	375	380
gtc gtc tot aac atc caa caa cca tgc atg atc atc ggt atc caa tcc			1200
Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser	385	390	400
gat gga ctg ttc aca tat tca gaa caa gaa Lbt ttg gct gag cac ata			1248
Asp Gly Leu Thr Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile	405	410	415
cag aag tog caa tta gaa aac att gaa tct ccc gaa ggc cac gat gcc			1296
Pro Lys Ser Gln Leu Glu Lys Ile Gln Ser Pro Glu Gly His Asp Ala	420	425	430
ttc cta ttg gag ttt aag ctg ata aac aaa ctg ata gta caa ttt tta			1344
Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu	435	440	445
aaa acc aac tgc aag gcc att aac gat gcc gct cca aga gct tgg gga			1392
Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly	450	455	460
ggc gac gtl ggt aac gat gaa acg aag acg tat gtc ttt ggt gag gcc			1440
Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala	465	470	475
gaa gaa gtt acc aac tgg tag			1488
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Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
 35 40 45

Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
 50 55 60

Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
 65 70 75 80

Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
 85 90 95

Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
 100 105 110

Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
 115 120 125

Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg

FIG. 1 is a schematic diagram of the amino acid sequence of the protein.

130	135	140
Leu Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys val ile Gly		
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Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly		
165	170	175
Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His		
180	185	190
Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr		
195	200	205
Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro		
210	215	220
Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg		
225	230	235
		240
Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile		
245	250	255
Ala Gln Gln Gln Tyr Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr		
260	265	270
Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys		
275	280	285
Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Glu Lys Gly Gln Ser Val		
290	295	300

Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
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Thr Ser Val Ser Ser Val Thr Gly Glu Val Iys Asp Ile Lys Pro Ala
 325 330 335

Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
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Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
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Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
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Val Leu Ser Thr Ala Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser
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Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
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Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
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Phe Leu Leu Glu Phe Lys Leu Ile Asn Iys Leu Ile Val Gln Phe Leu
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Ile Ile Asn Asp Ser Ile Met Ser Tyr Ile Asp Arg Thr Lys Thr Leu

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cta agg atg att ggc tgc aag aac cag tac ata aac gca cgt atg aaa 144

Ile Arg Met Ile Gly Cys Lys Asn Gln Tyr Ile Lys Ala Arg Met Lys

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gat aag aac ttc ctg tat acg aag caa ttc cgt aca gcc aaa aac aaa 192

Asp Lys Thr Phe Phe Tyr Thr Lys Gln Phe Arg Thr Ala Lys Asn Lys

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ttt ttc ttt cat ctg tac cat tgg gag gcc act cat att aac gtt gac 240

Phe Phe Phe His Leu Tyr His Trp Glu Ala Thr His Ile Asn Val Asp

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cac tat ata tgt aca tgt cat ccc att ttt tgg ggc cct ata ggt cag 288

His Tyr Ile Cys Thr Cys His Pro Ile Phe Trp Gly Ser Ile Gly Gln

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<212> DNA

<213> *Saccharomyces cerevisiae*

€2205

<221> CDS

<222> (1) .. (1605)

470 183

atg agc tct gac gaa gaa gat ttc aac gac atc tac ggc gac gat aag 48
Met Ser Ser Asp Glu Glu Asp Phe Asn Arg Ile Tyr Gly Asp Asp Lys
1 5 10 15

GGT ACC ACT ACT GAA GAA GTC AAA AAA GAA GAA GAA CAA AAT AAG GGT 96
 Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Cln Asn Lys Ala
 20 25 30

ggc agt ggt acc tgg caa cta gat caa cta gcc gaa cta caa gcc tta 144
Gly Ser Gly Thr Ser Glu Leu Asp Glu Leu Ala Ala Leu Glu Ala Leu
35 40 45

tct tct agc trg aac asa cta aat aat' cca aat agt aac aac aat aat. 192
Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
50 55 60

agt gtt gat agt aac cca gac acc tct tct agt aag caa gat gcc act 240
 Ser Aan Aan Ser Aen Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr
 65 70 75 80

gcg aat gac aag gaa ggt tcn aat gaa gan act aag aat gaa aaa aaa 288
Ala Asn Asp Iys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
85 90 95

caa gaa agc gct aca tca gca aat gcc aat gcc aac gct agt tct gcc 336
Glu Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala
100 105 110

gga cct tct ggc tta cct tgg gaa caa ctt caa caa aoc atg tca caa 384
Gly Pro Ser Gly Leu Pro Trp Glu Glu Leu Glu Glu Thr Met Ser Glu
115 120 125

ttc cag caa cca tct tct caa tca cca cct caa cag caa gta act caa 412

FIG. 12. Amino acid sequence of the protein.

Phe	Gln	Gln	Pro	Ser	Ser	Gln	Ser	Pro	Pro	Gln	Gln	Gln	Val	Thr	Gln	
130							135						140			
acc	aaa	gag	gaa	ggt	log	aaa	gag	gat	tgg	tct	aaa	gaa	agt	tgc	aag	480
Thr	Lys	Glu	Glu	Arg	Ser	Lys	Ala	Asp	Leu	Ser	Lys	Glu	Ser	Cys	Lys	
145				150					155					160		
atg	ttc	att	ggt	ggt	ctg	aat	tgg	gac	act	acg	gaa	gal	aat	ctt	cgc	528
Met	Phe	Ile	Gly	Gly	Leu	Asn	Trp	Asp	Thr	Thr	Glu	Asp	Asn	Leu	Arg	
				165					170					175		
gaa	tat	ttt	ggt	aag	tat	ggt	acc	gtc	act	gat	tty	aaa	dlu	atg	aaa	576
Glu	Tyr	Phe	Gly	Lys	Tyr	Gly	Thr	Val	Thr	Asp	Leu	Lys	Phe	Met	Lys	
			180					185					190			
gac	cct	gca	aca	ggt	aga	tct	aga	ggg	ttc	ggt	ttc	tta	tct	llt	gaa	624
Asp	Pro	Ala	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Leu	Ser	Phe	Glu	
	195						200					205				
aaa	cct	tct	agt	gtt	gat	gaa	gtg	gta	aag	aca	caa	cat	atc	ctc	gat	672
Lys	Pro	Ser	Ser	Val	Asp	Glu	Val	Val	Lys	Thr	Gln	His	Ile	Leu	Asp	
	210					215					220					
ggt	aaa	gtt	atc	gac	cca	aaa	aga	gct	atc	cca	aga	gac	gag	caa	gat	720
Gly	Lys	Val	Ile	Asp	Pro	Lys	Arg	Ala	Ile	Pro	Arg	Asp	Glu	Gln	Asp	
225					230						235			240		
aaa	acc	ggt	aaa	atc	ttt	gtt	ggt	ggc	att	ggt	cct	gnt	gtg	aga	cca	768
Lys	Thr	Gly	Lys	Ile	Phe	Val	Gly	Gly	Ile	Gly	Pro	Asp	Val	Arg	Pro	
				245					250				255			
aag	gaa	ttt	gaa	gaa	ttt	ttt	tct	cag	agg	ggt	acg	att	atc	gat	gag	816
Lys	Glu	Phe	Glu	Glu	Phe	Phe	Ser	Gln	Trp	Gly	Thr	Ile	Ile	Asp	Ala	
			260					265				270				
caa	ctg	atg	tta	gat	aag	gat	acc	ggt	caa	tca	aga	ggt	tct	ggt	llt	864
Gln	Leu	Met	Leu	Asp	Lys	Asp	Thr	Gly	Gln	Ser	Arg	Gly	Phe	Gly	Phe	
			275				280					285				
gtg	acy	tat	gac	tcc	gct	gac	gcc	gtt	gac	aga	gtt	tgt	cag	aat	aaa	912
Val	Thr	Tyr	Asp	Ser	Ala	Asp	Ala	Val	Asp	Arg	Val	Cys	Gln	Asn	Lys	
	290					295						300				

ttc atc gat ttc aac gat cgc aag atc gaa ac cag aga gct gag cca	960
Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro	
305 310 315 320	
aga cat atg caa caa aaa tca tca aac aat ggt ggt aac aat ggt gga	1008
Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly	
325 330 335	
aac aac atg aat cgt cgt ggc ggt aac ttc ggt aac caa ggc gat ttc	1056
Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Glu Gly Asp Phe	
340 345 350	
acc cca atg tat caa aac cct atg atg ggc ggt tac aac cca atg atg	1104
Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met	
355 360 365	
aat ccg caa gca atg aca gat tac tat caa aag atg caa gaa tat tac	1152
Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr	
370 375 380	
caa caa atg caa aag caa cct cgt atg gat tat act caa atg tac caa	1200
Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Glu Met Tyr Gln	
385 390 395 400	
caa caa atg cag caa atg gca atg atg atg cca ggg ttt gcc atg cca	1248
Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro	
405 410 415	
cct aat gca atg act tta aac cca cca aag caa gat tca aat gcc act	1296
Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr	
420 425 430	
caa ggt tuc cca gca cct tct gat tcc gat aat aat aaa tcc aat gac	1344
Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp	
435 440 445	
gtc caa act att ggt aat aca tca aac act gac tct ggt tca ccg cca	1392
Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro	
450 455 460	
ttg aat tta cct aat ggt cca aag ggc cca tca caa tac aat gat gac	1440

425/762

Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
 465 470 475 480

 cac aat agc ggt tat ggc tac aac cgl gal cgc ggt gal cgt gtt cgt 1480
 His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asn Arg
 485 490 495

 aac gat cgt gac cgc gat tac aat cag cgt agt ggt gga aac cat aga 1536
 Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
 500 505 510

 aga aac ggc cgt ggt ggt cgc ggt gga tac aat aga cgt aac aat ggc 1584
 Arg Asn Gly Arg Gly Gly Arg Gly Tyr Asn Arg Arg Asn Asn Gly
 515 520 525

 tac cat cca tac aat agg taa 1605
 Tyr His Pro Tyr Asn Arg
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<210> 184

<211> 534

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 184

Met Ser Ser Asp Glu Glu Asp Phe Asn Asp Ile Tyr Gly Asp Asp Lys
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Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Glu Asn Lys Ala
 20 25 30

Gly Ser Gly Thr Ser Glu Leu Asp Gln Leu Ala Ala Leu Glu Ala Leu
 35 40 45

Ser Ser Ser Met Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
 50 55 60

Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr
 65 70 75 80

Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
 85 90 95

Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Ser Ser Ala
 100 105 110

Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Glu Thr Met Ser Gln
 115 120 125

Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Glu Gln Glu Val Thr Gln
 130 135 140

Thr Lys Glu Gln Arg Ser Lys Ala Asp Leu Ser Lys Gln Ser Lys Lys
 145 150 155 160

Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Met Arg
 165 170 175

Glu Tyr Phe Gly Lys Tyr Gly Thr Val Thr Asp Leu Lys Ile Met Lys
 180 185 190

Asp Pro Ala Thr Gly Arg Ser Arg Gly Phe Gly Phe Leu Ser Phe Glu
 195 200 205

Lys Pro Ser Ser Val Asp Glu Val Val Lys Thr Gln His Ile Leu Asp
 210 215 220

Gly Lys Val Ile Asp Pro Lys Arg Ala Ile Pro Arg Asp Glu Gln Asp

225	230	235	240
Lys Thr Gly Lys Ile Phe Val Gly Gly Ile Gly Pro Asp Val Asn Pro			
245	250	255	
Lys Glu Phe Glu Glu Phe Phe Ser Gln Trp Gly Thr Ile Ile Asp Ala			
260	265	270	
Gln Leu Met Leu Asp Lys Asp Thr Gly Cln Ser Arg Gly Phe Gly Phe			
275	280	285	
Val Thr Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Gln Asn Lys			
290	295	300	
Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro			
305	310	315	320
Arg His Met Gln Glu Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly			
325	330	335	
Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe			
340	345	350	
Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met			
355	360	365	
Asn Pro Glu Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr			
370	375	380	
Gln Gln Met Glu Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Glu			
385	390	395	400

Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro
 405 470 435

Pro Asp Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr
 420 435 439

Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp
 435 440 445

Val Gln Thr His Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro
 450 455 460

Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
 465 470 475 480

His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
 485 490 495

Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
 500 505 510

Arg Asn Gly Arg Gly Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
 515 520 525

Tyr His Pro Tyr Asn Arg
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<210> 185

<211> 321

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

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<400> 185

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Met	Ser	Thr	Leu	Leu	Lys	Ser	Ala	Lys	Ser	Ile	Val	Pro	Leu	Met	Asp	
1			5						10					15		

cgt	gtc	ctt	gtc	caa	aga	atc	aag	gca	caa	gca	aag	aca	gca	tcc	ggg	95
Arg	Val	Leu	Val	Gln	Arg	Ile	Lys	Ala	Gln	Ala	Lys	Thr	Ala	Ser	Gly	
			20					25					30			

tgg	tat	tta	cct	gaa	aag	aac	gtg	gaq	aag	tta	aac	caa	gct	gaa	gtt	144
Leu	Tyr	Leu	Pro	Glu	Lys	Asn	Val	Glu	Lys	Leu	Asn	Gln	Ala	Glu	Val	
			35				40						45			

gtt	gac	gta	ggc	cgc	ggc	ctt	act	gat	gct	cac	ggc	aat	aag	gtt	gtt	192
Val	Ala	Val	Gly	Pro	Gly	Phe	Thr	Asp	Ala	Asn	Gly	Asn	Lys	Val	Val	
			50				55				60					

cct	caa	gtt	aaa	gtt	ggc	gan	caa	gtt	tgg	ctt	cca	acg	tct	ggc	ggc	240
Pro	Glu	Val	Lys	Val	Gly	Asp	Gln	Val	Leu	Ile	Pro	Gln	Phe	Gly	Gly	
			65				70				75			80		

tct	acc	att	aaa	tgg	ggc	aac	gac	gat	gaa	glt	att	ctt	ttc	agg	gac	288
Ser	Thr	Ile	Lys	Leu	Gly	Asn	Asp	Asp	Glu	Val	Ile	Leu	Phe	Arg	Asp	
			85							90				95		

gct	gaa	atc	ctg	gct	aag	att	gac	aag	gac	taa						321
Ala	Glu	Ile	Leu	Ala	Lys	Ile	Ala	Lys	Asp							
				100					105							

<210> 166

<211> 106

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 166

Met Ser Thr Leu Leu Lys Ser Ala Lys Ser Ile Val Pro Leu Met Asp
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Arg Val Leu Val Gln Arg Ile Lys Ala Gln Ala Lys Thr Ala Ser Gly
 20 25 30

Leu Tyr Leu Pro Glu Lys Asn Val Gln Lys Ieu Asn Gln Ala Glu Val
 35 40 45

Val Ala Val Gly Pro Gly Phe Thr Asp Ala Asn Gly Asn Lys Val Val
 50 55 60

Pro Gln Val Lys Val Gly Asp Gln Val Leu Ile Pro Gln Phe Gly Gly
 65 70 75 80

Ser Thr Ile Lys Leu Gly Asn Asp Asp Glu Val Ile Leu Phe Arg Asp
 85 90 95

Ala Glu Ile Leu Ala Lys Ile Ala Lys Asp
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<210> 187

<211> 1149

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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 1 5 10 15

gct ata tta acc aac cgc gct gct cag ctg gaa agg cgt atg tct atg	96
Ala Ile Leu Thr Asn Arg Val Ala Glu Leu Glu Arg Arg Met Ser Met	
20 25 30	
ttt gag ggt ata ttt cac ggc tta agt aac cgt ctc gat att cac ttt	144
Phe Glu Gly Ile Phe His Ala Leu Ser Asn Arg Leu Asp Leu His Phe	
35 40 45	
aaa aaa tat gat gta gtg gta aac tcc caa cag caa cca atc aac gaa	192
Lys Lys Tyr Asp Val Val Val Asn Ser Gln Gln Gln Gln Ile Asn Glu	
50 55 60	
ctg acc ggc ttt tta tca acn ttg ctg aat gac caa cca cgc cac gct	240
Leu Thr Ala Phe Leu Ser Thr Leu Leu Asn Asp Gln Gln Arg His Ala	
65 70 75 80	
gaa att ctg agt gaa aaa tta agc gga aag ttg cat ggg gtg tca gct	288
Glu Ile Leu Ser Glu Lys Leu Ser Gly Thr Leu His Gly Val Ser Ala	
85 90 95	
acg tca ata tcc tta agc caa act ctg gac cca caa ggc ttc act gat	336
Thr Ser Ile Ser Leu Ser Gln Thr Leu Asp Pro Gln Gly Thr Thr Asp	
100 105 110	
ggc act aag gaa cca gga gct cct agg aat tat act tca gtc cgt atg	384
Gly Thr Thr Ala Pro Gly Ala Pro Arg Asn Tyr Thr Ser Val Pro Met	
115 120 125	
aat aat gat caa act gct cat ccg caa aat gaa gga gct gtt agt aat	432
Asn Asn Asp Gln Thr Ala His Pro Gln Asn Glu Gly Ala Val Ser Asn	
130 135 140	
gaa aca ctt ttt gag gac att ttg aat gga aat tca caa gaa aat gat	480
Glu Thr Leu Phe Glu Asp Ile Leu Asn Gly Asn Ser Gln Glu Asn Asp	
145 150 155 160	
aag agt cca cca cca cct aac agc tca aat tat ata agc cca gaa aat	528
Lys Ser Gln Gln Gln Thr Asn Ser Ser Asn Ser Ile Ser Gln Gln Asn	
165 170 175	
aat agc acc aac cct tca gtg gac act cgg ttc aac aag ccg caa aat	576

Asn Ser Thr Asn Pro Ser Val Asp Thr Arg Phe Asn Lys Pro Gln Asn	
180 185 190	
tat aat tcc aat tta gtc cca tcc ttg gaa gag tat tca gca aat cca	654
Tyr Asn Ser Asn Leu Val Pro Ser Leu Gln Gln Tyr Ser Ala Asn Pro	
195 200 205	
cct aac aat gat ggt ggc caa agt caa gga ctg tac ata agc agc aac	674
Pro Asn Asn Asp Gly Gly Gln Ser Gln Gly Leu Tyr Ile Ser Ser Asn	
210 215 220	
tct tct caa tca cgg cag tat cct aat ttc cag aaa gtt tct cct aac	720
Ser Ser Gln Ser Arg Gln Ser Pro Asn Leu Gln Lys Val Ser Pro Asn	
225 230 235 240	
cat gaa aat gcg gtt gaa tca aat gca caa gag agc ctg ccg aca ttt	762
His Gln Asn Ala Val Gln Ser Asn Ala Gln Gln Ser Val Pro Thr Phe	
245 250 255	
gag gag gaa cag tat gag aot aaa aca gga tta aac cag aaa cga ata	816
Gln Gln Gln Gln Tyr Gln Thr Lys Thr Gly Leu Lys Arg Lys Arg Ile	
260 265 270	
gtc tgc aca aga ccc ttc gaa ttt atc aag tca cca cac tct gtc atg	864
Val Lys Thr Arg Pro Phe Gln Phe Ile Lys Ser Pro His Ser Val Met	
275 280 285	
gag gtt tgg aag gag tat aca gaa ggt gtt aac ggg cag cct tct ata	912
Gln Val Trp Lys Gln Tyr Thr Gln Gly Val Asn Gly Gln Pro Ser Ile	
290 295 300	
agg aaa atg gaa gct ctt tat caa acg goa tgg agg cga gat cca gca	960
Arg Lys Met Gln Ala Leu Tyr Gln Thr Ala Trp Arg Arg Asp Pro Ala	
305 310 315 320	
gta aat aaa aga tat tcc aga aga aag gtt ctt tgg aaa ggc att caa	1008
Val Asn Lys Arg Tyr Ser Arg Arg Lys Val Leu Tip Lys Ala Ile Gln	
325 330 335	
act ggc ctt aat cgt ggg tat tca tta aac tat gtt gtt gaa ata tta	1056
Thr Gly Leu Asn Arg Gly Tyr Ser Leu Asn Tyr Val Val Gln Ile Leu	
340 345 350	

gaa aac tca aga tat gtt aat gat aaa gag aag gtt aaa caa cct att 1104
 Glu Asn Ser Arg Tyr Val Asn Asp Lys Gln Lys Val Lys Gln Pro Ile
 355 360 365

ggt tgg tta tgc aac agt tct cat att cca gag aat ttg aag tga 1149
 Gly Trp Leu Cys His Ser Ser His Ile Pro Glu Thr Leu Lys
 370 375 380

<210> 188

<211> 382

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 185

Met Ala Ser Asn Gln His His Gly Ala Ser Asn Leu Asn Glu Asn Glu
 1 5 10 15

Ala Ile Leu Thr Asn Arg Val His Glu Leu Glu Arg Arg Met Ser Met
 20 25 30

Phe Glu Gly Ile Phe His Ala Leu Ser Asn Arg Leu Asp Leu His Phe
 35 40 45

Lys Lys Tyr Asp Val Val Val Asn Ser Gln Gln Gln Gln Ile Asn Glu
 50 55 60

Leu Thr Ala Phe Leu Ser Thr Leu Leu Asn Asp Gln Gln Arg His Ala
 65 70 75 80

Glu Ile Leu Ser Glu Lys Leu Ser Gly Thr Ser His Gly Val Ser Ala
 85 90 95

Thr Ser Ile Ser Leu Ser Gln Thr Leu Asp Pro Gln Gly Phe Thr Asp

100

105

110

Gly Thr Thr Ala Pro Gly Ala Pro Arg Asn Tyr Thr Ser Val Pro Met
 115 120 125

Asn Asn Asp Gln Thr Ala His Pro Gln Asn Glu Gly Ala Val Ser Asn
 130 135 140

Glu Thr Leu Phe Glu Asp Ile Leu Asn Gly Asn Ser Gln Glu Asn Asp
 145 150 155 160

Lys Ser Gln Glu Gln Thr Asn Ser Ser Asn Ser Ile Ser Gln Glu Asn
 165 170 175

Asn Ser Thr Asn Pro Ser Val Asp Thr Arg Phe Asn Lys Pro Gln Asn
 180 185 190

Tyr Asn Ser Asn Leu Val Pro Ser Leu Gln Glu Tyr Ser Ala Asn Pro
 195 200 205

Pro Asn Asn Asp Gly Gly Gln Ser Gln Gly Leu Tyr Ile Ser Ser Asn
 210 215 220

Ser Ser Gln Ser Arg Glu Ser Pro Asn Leu Glu Lys Val Ser Pro Asn
 225 230 235 240

His Glu Asn Ala Val Glu Ser Asn Ala Gln Glu Ser Val Pro Thr Phe
 245 250 255

Glu Glu Glu Gln Tyr Glu Thr Lys Thr Gly Leu Lys Arg Lys Arg Ile
 260 265 270

Val Cys Thr Arg Pro Phe Glu Phe Ile Lys Ser Pro His Ser Val Met
275 280 285

Glu Val Trp Lys Glu Tyr Thr Glu Gly Val Asn Gly Gln Pro Ser Ile
290 295 300

Arg Lys Met Glu Ala Leu Tyr Gln Thr Ala Trp Arg Arg Asp Pro Ala
305 310 315 320

Val Asn Lys Arg Tyr Ser Arg Arg Lys Val Leu Trp Lys Ala Ile Gln
325 330 335

Thr Gly Leu Asn Arg Gly Tyr Ser Leu Asn Tyr Val Val Gln Ile Leu
340 345 350

Glu Asn Ser Arg Tyr Val Asn Asp Lys Gln Lys Val Lys Gln Pro Ile
355 360 365

Gly Trp Leu Cys His Ser Ser His Ile Pro Gln Thr Leu Lys
370 375 380

<210> 189

<211> 729

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(729)

<400> 109

atg ata aac aac tat ttg gga oga aga tgg ctc aat aat cct gaa att
Met Ile Lys Asn Tyr Leu Gly Arg Arg Trp Leu Asn Asn Pro Ala Ile

1	5	10	15	
caa gca tat gtg aaa caa aat gct gct gtc gcc cat tct acg gtg ttt				26
Gln Ala Tyr Val Leu Glu Asn Ala Lys Val Ala His Ser Thr Val Phe				
20	25	30		
caa gga aat ctt tat gaa tat acg gtg atg agg gag tta tct gag aaa				144
Gln Gly Asn Leu Tyr Glu Tyr Thr Val Met Arg Glu Leu Ser Glu Lys				
35	40	45		
cta cga atg aca aag ttg aga aaa acc ggt ggc gcc cat gal ggt ggc				192
Leu Arg Met Thr Lys Leu Arg Lys Thr Gly Gly Ala His Asp Gly Gly				
50	55	60		
gta gcc ata aag gga agt tgg cca gta gat gat att tat tgg aaa att				240
Val Asp Ile Lys Gly Ser Trp Pro Val Asp Asp Ile Tyr Trp Lys Phe				
65	70	75	80	
tca tgg tta atg acc aat ttg gaa atg gct agt acc ata aaa aga acg				288
Ser Ser Leu Met Pro Asn Leu Glu Met Ala Ser Asn Ile Lys Arg Thr				
85	90	95		
aaa tgg caa aat ggc tta gta ttg aaa cct tta aag tat agg ata atc				336
Asn Ser Gln Asn Gly Phe Val Leu Lys Pro Leu Lys Tyr Arg Ile Ile				
100	105	110		
gac cat act ttt gaa cca tlg aca gta cta gtc caa tgt aag gct ttc				384
Asp His Thr Phe Glu Pro Leu Lys Val Leu Val Gln Cys Lys Ala Phe				
115	120	125		
act aaa tca aaa tta tct cct aga gaa ttc cgt gag tta glu gga aca				432
Thr Lys Ser Lys Leu Ser Pro Arg Glu Phe Arg Glu Leu Val Gly Thr				
130	135	140		
tta acc tca cta gta tca cat agt caa cgc aac asa uca gta tgc att				480
Phe Thr Ser Leu Val Ser His Ser Glu Arg Asn Lys Thr Val Cys Ile				
145	150	155	160	
atg tgt tcc cct cat atg tta aca aaa gat acc tta aat ctt atc aat				528
Met Cys Ser Pro His Met Leu Thr Lys Asp Thr Leu Asn Leu Ile Asn				
165	170	175		

437/762

aac atc acg ctt cct ctg ata tat tta cgt gtc gag atg ctg aaa gag 576
 Asn Ile Thr Leu Pro Leu Ile Tyr Leu Arg Val Glu Met Leu Lys Glu
 130 185 190

aag act gac ggg cac ttt gac tta atc aat tca gga aaa cta att aat 624
 Lys Thr Asp Gly His Phe Asp Leu Ile Asn Ser Gly Lys Leu Ile Asn
 195 200 205

tat taa gag aat tca tac gcc tct acg tta atg caa gat tgc aag att 672
 Tyr Tyr Glu Asn Ser Tyr Ala Ser Thr Leu Met Gln Asp Cys Lys Ile
 210 215 220

tct gaa tgg ctg aag ttg aag lly tuc aaa aat agt gac ttt aat tgg 720
 Ser Glu Trp Leu Lys Leu Lys Leu Tyr Lys Asn Ser Asp Phe Asn Ser
 225 230 235 240

gaa aaa taa 723
 Glu Lys

<210> 150
 <211> 242
 <212> PPT
 <213> *Saccharomyces cerevisiae*
 <400> 190

Met Ile Lys Asn Tyr Leu Gly Arg Arg Trp Leu Asn Asn Pro Ala Ile
 1 5 10 15

Gln Ala Tyr Val Lys Glu Asn Ala Ala Val Ala His Ser Thr Val Phe
 20 25 30

Gln Gly Asn Leu Tyr Glu Tyr Thr Val Met Arg Glu Leu Ser Glu Lys
 35 40 45

Ile Arg Met Thr Lys Leu Arg Lys Thr Gly Gly Ala His Asp Gly Gly
 50 55 60

Val Asp Ile Lys Gly Ser Trp Pro Val Asp Asg Ile Tyr Trp Lys Ile
65 70 75 80

Ser Ser Leu Met Phe Asn Leu Glu Met Ala Ser Asn Ile Lys Arg Thr
85 90 95

Asn Ser Gln Asn Gly Phe Val Leu Lys Pro Leu Lys Tyr Arg Ile Ile
100 105 110

Asp His Thr Phe Glu Pro Leu Lys Val Leu Val Gln Cys Lys Ala Phe
115 120 125

Thr Lys Ser Lys Leu Ser Pro Arg Glu Phe Arg Glu Leu Val Gly Thr
130 135 140

Phe Thr Ser Leu Val Ser His Ser Gln Arg Asn Lys Thr Val Cys Ile
145 150 155 160

Met Cys Ser Pro His Met Leu Thr Lys Asp Thr Leu Asn Leu Ile Asn
165 170 175

Asn Ile Thr Leu Pro Leu Ile Tyr Leu Arg Val Glu Met Leu Lys Glu
180 185 190

Lys Thr Asp Gly His Phe Asp Leu Ile Asn Ser Gly Lys Leu Ile Asn
195 200 205

Tyr Tyr Glu Asn Ser Tyr Ala Ser Thr Leu Met Gln Asp Cys Lys Ile
210 215 220

Ser Glu Trp Leu Lys Leu Lys Leu Tyr Lys Asn Ser Asp Phe Asn Ser
 225 250 275 300

Glu Lys

<210> 191
 <211> 630
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(630)

<400> 191
 atg ata tca cca tca aaa aag aga acc att tta tca agc aag aat ata 48
 Met Ile Ser Pro Ser Lys Lys Arg Thr Ile Leu Ser Ser Lys Asn His
 1 5 10 15
 aac caa aaa cca cga gca gtg gta aaa ggc aal gaa att cgt tca cca 96
 Asn Glu Lys Pro Arg Ala Val Val Lys Gly Asn Glu Leu Arg Ser Pro
 20 25 30
 tca aag aga agg tca cca ata gcc aca gcc tat gca cta agg cga agt 144
 Ser Lys Arg Arg Ser Gln Ile Asp Thr Asp Tyr Ala Leu Arg Arg Ser
 35 40 45
 cca ata aag aca atc caa att tct aaa gct gca cca ttt atg ctg tac 192
 Pro Ile Lys Thr Ile Gln Ile Ser Lys Ala Ala Glu Phe Met Leu Tyr
 50 55 60
 gag gaa acg gct gaa gaa aga aac ata gct gtc cac aga cat cat gaa 240
 Glu Glu Thr Ala Glu Glu Arg Asn Ile Ala Val His Arg His Asn Glu
 65 70 75 80
 ata ttc aat aat aac aat tct gtg agc aat gag aat aat cct tcc caa 288
 Ile Tyr Asn Asn Asn Asn Ser Val Ser Asn Glu Asn Asn Pro Ser Gln
 85 90 95

gta aaa gaa aac ctt tca ccc gct aaa att tgc cct tat gaa aga gca 316
 Val Lys Glu Asn Leu Ser Pro Ala Lys Ile Cys Pro Tyr Glu Arg Ala
 136 105 110

ttt tta agg gaa gga ggn aga att gca ttg aag gac tta agt gtt gac 384
 Phe Leu Arg Glu Gly Gly Arg Ile Ala Leu Lys Asp Leu Ser Val Asp
 115 120 125

gaa ttc aaa ggt tac ata cag gat cct ctc acc gat gag aot ata cca 432
 Glu Phe Lys Gly Tyr Ile Gln Asp Pro Leu Thr Asp Glu Thr Ile Pro
 130 135 140

ctg acg ttg cca ctg ggt gat aaa aaa atc agc cta ccc agt ttt ata 480
 Leu Thr Leu Pro Leu Gly Asp Lys Lys Ile Ser Leu Pro Ser Phe Ile
 145 150 155 160

acg ccg cca aga aat tgg aag ata tct att ttc ttc act agt aaa cac 520
 Thr Pro Pro Arg Asn Ser Lys Ile Ser Ile Phe Phe Thr Ser Lys His
 165 170 175

caa ggc gag acc ccc gag acc cgg ata tcc dgt tct acc gct gac gtc 576
 Gln Gly Gln Asn Pro Glu Thr Lys Ile Ser Arg Ser Thr Asp Asp Val
 180 185 190

agt gaa aaa aaa gta gtg aga aaa ctg tcc ttc cac gtc tat gaa gat 624
 Ser Glu Lys Lys Val Val Arg Lys Leu Ser Phe His Val Tyr Glu Asp
 195 200 205

gag taa 630
 Glu

<210> 192
 <211> 209
 <212> PRT
 <213> Saccharomyces cerevisiae
 <400> 192

Met Ile Ser Pro Ser Lys Lys Arg Thr Ile Leu Ser Ser Lys Asn Ile

1 3 10 15

 Asn Glu Lys Pro Arg Ala Val Val Lys Gly Asn Glu Leu Arg Ser Pro
 20 25 30

 Ser Lys Arg Arg Ser Glu Ile Asp Thr Asp Tyr Ala Leu Arg Arg Ser
 35 40 45

 Pro Ile Lys Thr Ile Glu Ile Ser Lys Ala Ala Glu Phe Met Leu Tyr
 50 55 60

 Glu Glu Thr Ala Glu Glu Arg Asn Ile Ala Val His Arg His Asn Glu
 65 70 75 80

 Ile Tyr Asn Asn Asn Asn Ser Val Ser Asn Glu Asn Asn Pro Ser Glu
 85 90 95

 Val Lys Glu Asn Leu Ser Pro Ala Lys Ile Cys Pro Tyr Glu Arg Ala
 100 105 110

 Phe Leu Arg Glu Gly Gly Arg Ile Ala Leu Lys Asp Leu Ser Val Asp
 115 120 125

 Glu Phe Lys Gly Tyr Ile Glu Asp Pro Leu Thr Asp Glu Thr Ile Pro
 130 135 140

 Leu Thr Leu Pro Leu Gly Asp Lys Lys Ile Ser Leu Pro Ser Phe Ile
 145 150 155 160

 Thr Pro Pro Arg Asn Ser Lys Ile Ser Ile Phe Phe Thr Ser Lys His
 165 170 175

Gln Gly Gln Asn Pro Glu Thr Lys Ile Ser Asn Ser Thr Asp Asp Val
 182 185 190

Ser Glu Lys Lys Val Val Arg Lys Leu Ser Phe His Val Tyr Glu Asp
 195 200 205

Gln

<210> 191
 <211> 621
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(621)

<400> 193
 atg atg ccc tac aac acc cct cca aat atc cca gaa cct atg aac ttc 48
 Met Met Pro Tyr Asn Thr Pro Pro Asn Ile Gln Glu Pro Met Asn Phe
 1 5 10 15
 gca agc agc aac ccc ttt ggt att att cca gat ggc ctc agt ttc cag 96
 Ala Ser Ser Asn Pro His Gly Ile Ile Pro Asp Ala Leu Ser Phe Gln
 20 25 30
 aat ttc aaa tat gat cgt ctt cag cag cag caa cag cag cag caa cag 144
 Asn Thr Lys Tyr Asp Arg Leu Gln Gln Gln Gln Gln Gln Gln
 35 40 45
 cag caa caa aat agc act ggc tca tgg tta cag cag cag caa cag caa 192
 Gln Gln Gln Asn Arg Thr Ala Ser Ser Leu Gln Gln Pro Gln Gln Gln
 50 55 60
 caa cca ata agc cag cct ttg ttt tta gta ggg gcc ggt acc agc gaa 240
 Gln Pro Ile Ser Pro Pro Leu Phe Leu Val Gly Ala Gly Thr Ser Glu

65	70	75	80	
aac tca aac ctt aac aag aat gcc tcc acc agt act atc ccc cct tta				288
Asn Ser Asn Leu Asn Lys Asn Ala Asn Thr Ser Thr Ile Pro Pro Leu				
95		90	95	
ctc ttt agc aga tcc tot cag cat tat gtt gtc cca gat ata gcc tcc				336
Leu Phe Ser Arg Ser Ser Gln His Tyr Val Val Pro Asp Ile Asp His				
100	105	110		
ttc tcc ata ata tac aag aac aac atc tgc aua tot ttc aaa gat gac				384
Ser Ser Ile Ile Tyr Lys Asn Asn Ile Cys Lys Ser Thr Lys Asp Asp				
115	120	125		
tta ttt ttc tgt tca aga tct tta tct tct ttc gaa gaa caa caa gca				432
Tyr Thr Phe Cys Pro Arg Ser Asn Asn Ser Leu Glu Glu Gln Gln Ala				
130	135	140		
lyc gag aaa atg gat agg ctg acc gcc gaa caa atg tca ttg tat cat				480
Cys Glu Lys Met Asp Arg Leu Thr Ala Glu Gln Met Ser Ser Tyr His				
145	150	155	160	
cag aac aag caa tcc agt tct aat cct ggt tct atg tct tct tca cct				528
Gln Asn Thr Glu Ser Ser Ser Asn Pro Gly Ser Met Ser Ser Pro				
165	170	175		
cca cat tct gat tct tct ata ttc aac tct agg cag aag ttc aat cct				576
Pro Asn Ser Ala Ser Ser Ile Phe Asn Ser Arg Pro Lys Phe Asn Pro				
180	185	190		
tat aca tct caa agt ttt aat cat ttc gaa agt gtt caa gaa tga				624
Tyr Thr Ser Gln Ser Phe Asn Pro Leu Glu Ser Val Gln Glu				
195	200	205		
<210> 194				
<211> 206				
<212> PCT				
<213> Saccharomyces cerevisiae				
<400> 194				

Met Met Pro Tyr Asn Thr Pro Pro Arg Ile Gln Glu Pro Met Asn Phe
 1 5 10 15

Ala Ser Ser Asn Pro Phe Gly Ile Ile Pro Asp Ala Leu Ser Phe Gln
 20 25 30

Asn Phe Lys Tyr Asp Arg Leu Gln Gln Gln Gln Gln Gln Gln
 35 40 45

Gln Gln Gln Asn Arg Thr Ala Ser Ser Leu Gln Gln Pro Gln Gln Gln
 50 55 60

Gln Pro Ile Ser Pro Pro Leu Phe Leu Val Gly Ala Gly Thr Ser Glu
 65 70 75 80

Arg Ser Asn Leu Asn Lys Asn Ala Asn Thr Ser Thr Ile Pro Pro Leu
 85 90 95

Leu Phe Ser Arg Ser Ser Gln His Tyr Val Val Pro Arg Ile Asp His
 100 105 110

Ser Ser Ile Ile Tyr Lys Asn Asn Ile Cys Lys Ser Phe Lys Asp Asp
 115 120 125

Leu Phe Phe Cys Pro Arg Ser Leu Leu Ser Leu Glu Glu Gln Gln Ala
 130 135 140

Cys Gln Lys Met Asp Arg Leu Thr Ala Glu Gln Met Ser Asn Tyr His
 145 150 155 160

Gln Asn Thr Gln Ser Ser Ser Asn Pro Gly Ser Met Ser Ser Ser Pro
 165 170 175

Pro Asn Ser Ala Ser Ser Ile Phe Asn Ser Arg Pro Lys Phe Asn Pro
 180 185 190

Tyr Thr Ser Gln Ser Phe Asn Pro Leu Glu Ser Val Gln Glu
 195 200 205

<210> 195
 <211> 534
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(534)

<400> 195
 atg aac atg gcg aac gac atg aat gaa gat gaa ata ttt ctc aaa gaa 48
 Met Lys Leu Ala Gln Asp Met Asn Val Asp Glu Ile Phe Leu Lys Gln
 1 5 10 15

gcg gca gaa gct ata gcg gta atc tca tca agt ccc aat cat acg gac 96
 Ala Ala Glu Ala Ile Ala Val Ile Ser Ser Ser Pro Thr His Thr Asp
 20 25 30

ccc ata ata cga gag cta ctc gac aga att cga aac tcc agc cca tly 144
 Pro Ile Ile Arg Glu Leu Leu His Arg Ile Arg Gln Ser Ser Pro Leu
 35 40 45

agc gca gtt ata cca gca cca gaa aat gtt tta aag gct ggg gag cgg 192
 Ser Ala Val Ile Pro Ala Pro Glu Asn Val Leu Lys Ala Gly Glu Pro
 50 55 60

gaa aat atg gct aga cgt ctt ata agg att cca gaa aca caa aca aaa 240
 Glu Asn Met Ala Arg Gly Leu Ile Arg Ile Pro Glu Thr Gln Thr Lys
 65 70 75 80

aga aca gga ggt aac aac cat agc aag gca ggc gca cag ctc tcc agc 288

446/762

Arg Thr Gly Gly Asn Asn His Ser Iys Glu Gly Ala Gln Leu Tyr Ser
 85 90 95
 tgt ggg aaa tgt cag ttg aaa ttc agc aga agt tct gat atg aga aga 336
 Cys Ala Lys Cys Glu Leu Lys Phe Ser Arg Ser Ser Asp Ile Arg Arg
 100 105 110
 cat gaa aag gta cac tca ctc gtg ctg ccg cat att tgc tca aac tgt 344
 His Glu Lys Val His Ser Leu Val Leu Pro His Ile Cys Ser Asn Cys
 115 120 125
 ggc aaa ggg ttt gcc tgg aag gat gct cta aaa aga cat tct aac aca 432
 Gly Iys Gly Phe Ala Arg Lys Asp Ala Leu Lys Arg His Ser Asn Thr
 130 135 140
 ctg aac tgt caa aca aac aga aag aaa cta agt gaa ggc tca gaa gtt 480
 Val Thr Cys Gln Arg Asn Arg Lys Lys Leu Ser Glu Gly Ser Asp Val
 145 150 155 160
 gat gta gat gag ctc atc aag gat ggg ata aag aat ggt acc ggc ctg 528
 Asp Val Asp Glu Leu Ile Lys Asp Ala Ile Lys Asn Gly Thr Gly Leu
 165 170 175
 ttg taa 534
 Leu

<210> 196

<211> 177

<213> FRT

<214> *Saccharomyces cerevisiae*

<400> 196

Met Lys Leu Ala Gln Asp Met Asn Val Asp Glu Ile Phe Leu Lys Gln
 1 5 10 15

Ala Ala Glu Ala Ile Ala Val Ile Ser Ser Ser Pro Thr His Thr Asp
 20 25 30

Pro Ile Ile Arg Glu Leu Leu His Arg Ile Arg Gln Ser Ser Pro Leu
35 40 45

Ser Ala Val Ile Pro Ala Pro Glu Asn Val Leu Lys Ala Gly Gln Pro
50 55 60

Gln Asn Met Ala Arg Gly Leu Ile Arg Ile Pro Glu Thr Gln Thr Lys
65 70 75 80

Arg Thr Gly Gly Asn Asn His Ser Lys Glu Gly Ala Gln Asn Cys Ser
85 90 95

Cys Ala Lys Cys Gln Leu Lys Phe Ser Arg Ser Ser Asp Leu Arg Arg
100 105 110

His Glu Lys Val His Ser Leu Val Leu Pro His Ile Cys Ser Asn Cys
115 120 125

Gly Lys Gly Phe Ala Arg Lys Asp Ala Leu Lys Arg His Ser Asn Thr
130 135 140

Leu Thr Cys Gln Arg Asn Arg Lys Lys Asn Ser Gln Gly Ser Asp Val
145 150 155 160

Asp Val Asp Glu Leu Ile Lys Asp Ala Ile Lys Asn Gly Thr Gly Leu
165 170 175

Leu

<211> 1425

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1) .. (1425)

<400> 197

atg gag gta act tca atg ttt ctc aat aga atg arg aag acc egg act	48
Met Glu Val Thr Ser Met Phe Leu Asn Arg Met Met Lys Thr Arg Thr	
1 5 10 15	

ggc att tat cgc tta tat tca acc ctt aaa gtt coa cat gta gaa atc	96
Gly Met Tyr Arg Leu Tyr Ser Thr Leu Lys Val Pro His Val Glu Ile	
20 25 30	

aat ggc ata aaa tgc aag acc gac coa cag act acc aat gtt aca gat	144
Asn Gly Ile Lys Tyr Lys Thr Asp Pro Gln Thr Thr Asn Val Thr Asp	
35 40 45	

tca ata ata aag att acc gac aga tca tta cat ttg aag gaa tca gat	192
Ser Ile Ile Lys Leu Thr Asp Arg Ser Leu His Leu Lys Glu Ser His	
50 55 60	

cca gta ggc att att cgc gat cta att gaa aag aaa tta aac tca gtc	240
Pro Val Gly Ile Leu Arg Asp Leu Ile Glu Lys Lys Leu Asn Ser Val	
65 70 75 80	

gac aac aca ttt aag atc ttt aat aat ttc aag ccc gtg gta acc aca	288
Asp Asn Thr Phe Lys Ile Phe Asn Asn Phe Lys Pro Val Val Thr Thr	
85 90 95	

atg gaa aac ttc gat tct tta ggg ttt cct aag gat cat cct gga aga	336
Met Glu Asn Phe Asp Ser Leu Gly Phe Pro Lys Asp His Pro Gly Arg	
100 105 110	

tca aaa tct gac aca tat tat ata aat gag aag cag cta cty aga aca	384
Ser Lys Ser Asp Thr Tyr Tyr Ile Asn Glu Thr His Leu Leu Arg Thr	
115 120 125	

449/762

cat act tca gcc cac gaa tta gag tgc ttt caa aaa ata aga aac gat	432
His Thr Ser Ala His Glu Leu Glu Cys Phe Gln Lys Ile Arg Asn Asp	
130 135 140	
cca gat aat att aaa aqt gga ttt tta ata tct gca gat gtg tac aga	480
Ser Asp Asn Ile Lys Ser Gly Phe Leu Ile Ser Ala Asp Val Tyr Arg	
145 150 155 160	
aga gat gaa att gac aaa act cac tat ccg gta ttc cac caa atg gaa	528
Arg Asp Glu Ile Asp Lys Thr His Tyr Pro Val Phe His Gln Met Glu	
165 170 175	
gga gcc aca att tcc aaa cga acg aag gct gat gtg ggc gta aag gag	576
Gly Ala Thr Ile Trp Lys Arg Thr Lys Ala Asp Val Gly Val Lys Glu	
180 185 190	
cca atg tat atc gag aaa atc cgt gaa gat atc aga cag gta gag aac	624
Pro Met Tyr Ile Glu Lys Ile Arg Gln Asp Ile Arg Gln Val Glu Asn	
205 210 215	
ott tta aat aac gaa aat gaa aag att acg gtt gcc gat gat act ata	672
Leu Leu Asn Lys Glu Ser Val Lys Ile Thr Val Asp Asp Asp Thr Ile	
220 225 230	
oct lly aar gaa aat aat cct aaa caa gag tat atg tcc gat ctg gag	720
Pro Leu Lys Glu Asn Asn Pro Lys Gln Glu Tyr Met Ser Asp Leu Glu	
235 240 245 250	
att gat ttg tgc tct caa cat ttg aag agg lcc att gaa ctg ata gtt	768
Val Asp Leu Cys Ser Gln His Leu Lys Arg Ser Ile Glu Ilen Ile Val	
255 260 265	
tct gaa gtt ttt aac aca aaa ata tct agc atg atc aag aac aaa gcg	816
Ser Glu Val Phe Asn Lys Lys Ile Ser Ser Met Ile Lys Asn Lys Ala	
270 275 280 285	
aat aat aca ccc aaa gcg cta aca gtc cgt tgg att aac gct tac ttc	864
Asn Asn Thr Pro Lys Glu Leu Lys Val Arg Trp Ile Asn Ala Tyr Phe	
290 295 300	
ccc tgg aac gcg ccc tca tgg gaa ata gag gtt tgg tgg cag ggc gaa	912
Pro Trp Thr Ala Pro Ser Trp Glu Ile Glu Val Trp Trp Gln Gly Glu	

250	295	300	
tgg ctc gaa ctc tgc gga tgc gga ttg att cgt caa gat gtg cta ctc			960
Trp Leu Glu Leu Cys Gly Cys Gly Leu Ile Arg Gln Asp Val Leu Leu			
305	310	315	320
aga gcc gga tal aad uct tct gaa aca att ggg tgg got ttt ggc ttg			1005
Arg Ala Gly Tyr Lys Pro Ser Gln Thr Ile Gly Trp Ala Phe Gly Leu			
325	330	335	
ggc ttg gac cgc att gct atg ctt ctt ttt gau att cca gat att aga			1056
Gly Leu Asp Arg Ile Ala Met Leu Leu Phe Glu Ile Pro Asp Ile Arg			
340	345	350	
ctg ctt tgg agt cgt gat gaa aga ttt tca aga aua ttt tcc aag gga			1104
Leu Leu Trp Ser Arg Asp Glu Arg Phe Ser Arg Gln Phe Ser Tyr Gly			
355	360	365	
tta att aot tcc ttc cca cct tat tca aaa cac cgg gga tca ttt aag			1152
Leu Ile Thr Ser Phe Lys Pro Tyr Ser Lys His Pro Gly Ser Phe Arg			
370	375	380	
gat gtt ggg ttt tgg tta cca gaa gat aaa cca gat att cat caa gct			1200
Asp Val Ala Phe Trp Leu Pro Glu Asp Lys Pro Arg Ile His Glu Val			
385	390	395	400
uac gaa aat gat ttg atg gaa att atc aga aat ata got ggc got ttg			1248
His Glu Asn Asp Leu Met Glu Ile Ile Arg Asn Ile Ala Gly Asp Leu			
405	410	415	
gta gag agt gtc aag cta gtc gat agu ttt aag aat ccg aua act ggg			1296
Val Glu Ser Val Lys Leu Val Asp Ser Phe Thr His Pro Lys Thr Gly			
420	425	430	
aga aaa tct atg tgc tac agg atc aad tat cuu tca atg gac aga aat			1344
Arg Lys Ser Met Cys Tyr Arg Ile Asn Tyr Gln Ser Met Asp Arg Asn			
435	440	445	
ttg aca aac gcc gaa gtt aac aot ttg caa gac atg gtg tgt tct aaa			1392
Leu Thr Asn Ala Glu Val Asn Thr Leu Gln Asp Met Val Cys Ser Lys			
450	455	460	

ttg gta aad gac tac agc gca gaa ctg aga tag 1425
 Leu Val Lys Glu Tyr Ser Val Glu Leu Arg
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<210> 198
 <211> 474
 <212> PRT
 <213> Saccharomyces cerevisiae

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Gly Leu Tyr Arg Leu Tyr Ser Thr Leu Lys Val Pro His Val Glu Ile
 20 25 30

Asn Gly Ile Lys Tyr Lys Thr Asp Pro Glu Thr Thr Asn Val Thr Asp
 35 40 45

Ser Ile Ile Lys Leu Thr Asp Arg Ser Leu His Leu Lys Glu Ser His
 50 55 60

Pro Val Gly Ile Leu Arg Asp Leu Ile Glu Lys Lys Leu Asn Ser Val
 65 70 75 80

Asp Asn Thr Phe Lys Ile Phe Asn Asn Phe Lys Pro Val Val Thr Thr
 85 90 95

Met Glu Asn Phe Asp Ser Leu Gly Phe Pro Lys Asp His Pro Gly Arg
 100 105 110

Ser Lys Ser Asp Thr Tyr Tyr Ile Asn Glu Thr His Leu Leu Arg Thr
 115 120 125

His Thr Ser Ala His Glu Leu Glu Cys Phe Glu Lys Ile Arg Asn Asp
 130 135 140

Ser Asp Asn Ile Lys Ser Gly Phe Leu Ile Ser Ala Asp Val Tyr Arg
 145 150 155 160

Arg Asp Glu Ile Asp Lys Thr His Tyr Pro Val Phe His Glu Met Glu
 165 170 175

Gly Ala Thr Ile Trp Lys Arg Thr Lys Ala Asp Val Gly Val Lys Glu
 180 185 190

Pro Met Tyr Ile Glu Lys Ile Arg Glu Asp Ile Arg Glu Val Glu Asn
 195 200 205

Leu Met Asn Tyr Glu Arg Val Lys Ile Thr Val Asp Asp Asp Thr His
 210 215 220

Pro Leu Lys Glu Asn Asn Pro Lys Glu Glu Tyr Met Ser Asp Leu Glu
 225 230 235 240

Val Asp Leu Cys Ser Glu His Leu Lys Arg Ser Ile Glu Leu Ile Val
 245 250 255

Ser Glu Val Phe Asn Lys Lys Ile Ser Ser Met Ile Lys Asn Lys Ala
 260 265 270

Asn Asn Thr Pro Lys Glu Leu Tyr Val Arg Trp Ile Asn Ala Tyr Phe
 275 280 285

Pro Trp Thr Ala Pro Ser Trp Glu Ile Glu Val Trp Trp Gln Gly Glu
290 335 380

Trp Leu Glu Leu Cys Gly Cys Gly Leu Ile Arg Gln Asp Val Leu Leu
305 310 315 320

Arg Ala Gly Tyr Lys Pro Ser Glu Thr Ile Gly Trp Ala Phe Gly Leu
325 330 335

Gly Leu Asp Arg Ile Ala Met Leu Leu Phe Glu Ile Pro Asp Ile Arg
340 345 350

Leu Leu Trp Ser Arg Asp Glu Arg Phe Ser Arg Gln Phe Ser Lys Gly
355 360 365

Leu Ile Thr Ser Phe Lys Pro Tyr Ser Lys His Pro Gly Ser Phe Arg
370 375 380

Asp Val Ala Phe Trp Leu Pro Glu Asp Lys Pro Asp Ile His Gln Val
385 390 395 400

His Glu Asn Asp Leu Met Glu Ile Ile Arg Asn Ile Ala Gly Asp Leu
405 410 415

Val Glu Ser Val Lys Leu Val Asp Ser Phe Thr His Pro Lys Thr Gly
420 425 430

Arg Lys Ser Met Cys Tyr Arg Ile Asn Tyr Gln Ser Met Asp Arg Asn
435 440 445

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Leu Val Lys Glu Tyr Ser Val Glu Leu Arg

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470

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<211> 1062

<212> DNA

<213> *Saccharomyces cerevisiae*

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5

10

15

ctc caa cta ttg aag gca caa gga llt gac agg gca agg cdc agt ctg 80

Leu Gln Leu Leu Lys Ala Gln Gly Phe Asp Arg Ala Arg Pro Ser Leu

20

25

30

gtg gct gtc atg acc gat ctc tat gca aat ttc ttg agt ttg tta gca 120

Val Asp Val Met Thr Asp Leu Tyr Ala Lys Phe Leu Ser Leu Leu Ala

35

40

45

tca gag gtc agt tct atc gct cag gca aga tgt gat cag gac gal aca 160

Ser Glu Val Ser Ser Ile Ala Gln Ala Arg Cys Asp Glu Asp Asp Thr

50

55

60

att gct tta caa gat ala acn ctg got ctg gaa aat cta ggt att gtt 200

Ile Ala Leu Gln Asp Ile Thr Leu Ala Leu Glu Asn Leu Gly Ile Val

65

70

75

80

aag cct acg aac gtt ctg gat gtc tal gal gaa aac tcc gaa tta tca 240

Lys Pro Thr Asn Val Leu Asp Val Tyr Asp Gln Asn Ser Glu Leu Ser

85

90

95

agt tca cga gga atg gaa aag ttc aag gac tgg tgt att tat agt act 330

Ser Ser Arg Gly Met Glu Lys Phe Lys Asp Trp Cys Ile Tyr Ser Thr	
100	105
110	
caa tbg acc gac gag cga ata act gac lta enc aga gla gaa tca cta	384
Gln Leu Thr Asp Ala Arg Ile Thr Ala Leu Pro Thr Val Glu Leu Leu	
115	120
125	
caa agt gag gaa aaa gaa tot gat cct ttg tca gca ata act gac tat	432
Gln Ser Glu Glu Lys Glu Ser Asp Pro Leu Ser Ala Ile Pro Asp Tyr	
130	135
140	
ctc aat cca tta ctg caa aac aag ggc ggc aaa cag aaa ttc gna aca	480
Leu Asn Gln Leu Leu Gln Asn Lys Gly Ala Lys Gln Lys Leu Glu Thr	
145	150
155	160
aag aat aga aaa acc gac ttg ata gaa gat cta ata aat aat act gga	528
Lys Asn Arg Lys Thr Glu Leu Ile Glu Asp Leu Ile Asn Asn Asn Gly	
165	170
175	
tta gat gat tgg atc aaa tta gtc att gct aga caa cgt ata aac ctg	576
Leu Asp Asp Trp Ile Lys Leu Val Ile Ala Arg Gln Arg Ile Asn Met	
180	185
190	
att gaa aga gct tcc aua aua gaa tot caa aat gta cag gac tta cca	624
Ile Glu Arg Ala Ser Lys Lys Glu Ser Gln Asn Val Pro Ala Leu Pro	
195	200
205	
cat att gaa ggc tat aaa tct tcc att cta aga cgc cat cac cac act	672
His Ile Ala Gly Tyr Lys Ser Ser Ile Leu Ser Arg His His His Thr	
210	215
220	
acc ata aca aac gaa gat agg atg cct tgg gog atg acc cca aga gat	720
Thr Ile Thr Asn Glu Asp Arg Met Pro Ser Ala Met Thr Pro Arg Asp	
225	230
235	240
gag gat gcc tta aca gag atc caa gaa aat cca ttt gta act agc aac	768
Glu Asp Ala Leu Thr Glu Ile Gln Glu Asn Pro Phe Val Thr Ser Lys	
245	250
255	
ctg ccg ata atg aga aaa gaa aat agg tta gaa eat ata act ccl leu	816
Leu Pro Ile Met Arg Lys Glu Asn Arg Leu Glu Asn Ile Thr Leu Ser	
260	265
270	

ttt gag gat gag gag ctt gaa tca ctt ggu gaa gtg gaa ggu cct aac 854
 Phe Glu Asp Gln Gln Leu Glu Ser Leu Gly Gln Val Glu Gly Pro Asn
 275 280 285

cac aag tct cca gaa aat aac aat gag gaa agt ttt aaa gag aac aat 912
 Gln Lys Ser Gln Glu Asn Asn Asn Glu Glu Ser Phe Lys Gln Asn Asn
 290 295 300

aaa agt tta aca gag tct cct cat ggt gat gac cgt gac ata tca atg 960
 Lys Ser Leu Thr Glu Ser Pro His Gly Asp Asp Arg Asp Ile Ser Met
 305 310 315 320

tll cca ttc gac tca cat gtt gat act aac tgg gca gag cag gaa gat 1008
 Phe Gln Phe Asp Ser Asn Val Asp Thr Lys Trp Ala Glu Gln Glu Asp
 325 330 335

atg gac ago aca ttt cca cgt cga acc tca cta gat tat ggg ggt tac 1055
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 340 345 350

ttt taa 1062
 Phe

<210> 100
 <211> 353
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 200

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 20 25 30

Val Asp Val Met Thr Asp Leu Tyr Ala Lys Phe Leu Ser Leu Ile Ala

35

40

45

Ser Glu Val Ser Ser Ile Ala Gln Ala Arg Cys Asp Gln Asp Asp Thr
50 55 60

Ile Ala Leu Gln Asp Ile Thr Leu Ala Leu Glu Asn Leu Gly Ile Val
65 70 75 80

Lys Pro Thr Asn Val Leu Asp Val Tyr Asp Glu Asn Ser Glu Leu Ser
85 90 95

Ser Ser Arg Gly Met Glu Lys Phe Lys Asp Trp Cys Ile Tyr Ser Thr
100 105 110

Gln Leu Thr Asp Ala Arg Ile Thr Ala Leu Pro Thr Val Glu Leu Leu
115 120 125

Gln Ser Glu Glu Lys Glu Ser Asp Pro Leu Ser Ala Ile Pro Asp Tyr
130 135 140

Leu Asn Gln Leu Leu Gln Asn Tyr Gly Ala Lys Gln Lys Leu Glu Thr
145 150 155 160

Lys Asn Arg Lys Thr Glu Leu Ile Glu Asp Leu Ile Asn Asn Asn Gly
165 170 175

Leu Asp Asp Trp Ile Lys Leu Val Ile Ala Arg Gln Arg Ile Asn Met
180 185 190

Ile Glu Arg Ala Ser Lys Lys Glu Ser Gln Asn Val Pro Ala Leu Pro
195 200 205

His Ile Ala Gly Tyr Lys Ser Ser Ile Leu Ser Arg His His His Thr
 210 215 330

Thr Ile Thr Asn Glu Asp Arg Met Pro Ser Ala Met Thr Pro Arg Asp
 225 240 340

Glu Asp Ala Jou Thr Glu Ile Gln Glu Asn Pro Phe Val Thr Ser Lys
 245 255 255

Leu Pro Ile Met Arg Val Lys Glu Asn Arg Leu Glu Asn Ile Thr Leu Ser
 260 265 270

Phe Glu Asp Glu Glu Leu Glu Ser Leu Gly Glu Val Glu Gly Pro Asn
 275 280 285

Glu Lys Ser Glu Glu Asn Asn Asn Asn Glu Glu Ser Phe Lys Glu Asn Asn
 290 295 300

Lys Ser Leu Thr Glu Ser Pro His Gly Asp Asp Arg Asp Ile Ser Met
 305 310 315 320

Phe Gln Phe Asp Ser Asn Val Asp Thr Lys Trp Ala Glu Gln Glu Asp
 325 330 335

Met Asp Ser Thr Phe Gln Arg Arg Thr Ser Leu Asp Tyr Gly Gly Tyr
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Phe

<210> 201

<211> 1308

<212> DNA

<213> *Saccharomyces cerevisiae*

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<222> (1)..(1308)

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att	gac	acc	gct	gct	cac	aag	acc	caa	gac	aat	lly	aac	aat	gca	tta	96
Ile	Ala	Thr	Ala	Ala	His	Lys	Thr	Gln	Asp	Thr	Leu	Asn	Asn	Ala	Leu	
			20					25					30			

gca	aat	gca	aat	gta	aac	cta	aat	gac	act	caa	aca	aga	cta	tca	atc	144
Ala	Asn	Ala	Asp	Val	Asn	Leu	Asn	Asp	Pro	Gln	Thr	Arg	Leu	Ser	Ile	
			35					40					45			

aaa	tgg	cga	act	aga	ttt	ggt	cag	gaa	tca	ttg	ggt	act	gta	tca	gat	192
Lys	Ser	Arg	Thr	Arg	Phe	Val	Gln	Glu	Ser	Leu	Gly	Thr	Val	Ser	Asp	
			50				55					60				

ata	agt	aaa	tta	cca	cca	cag	tac	caa	ttc	ttg	gag	aaa	aaa	agt	gat	240
Ile	Ser	Lys	Leu	Pro	Pro	Gln	Tyr	Gln	Phe	Leu	Glu	Lys	Lys	Ser	Asp	
65						70				75					80	

ccc	tta	gag	aag	gta	tgt	aaa	agg	att	cta	ctg	gtg	tcc	aaa	acg	ttc	288
Ser	Leu	Glu	Lys	Val	Cys	Lys	Arg	Ile	Leu	Leu	Val	Ser	Lys	Thr	Phe	
					85					90				95		

gaa	gta	gag	ggc	tac	gac	tat	cca	cca	aat	tta	atg	gag	agt	att	tgg	346
Glu	Val	Glu	Gly	Tyr	Asp	Tyr	Pro	Pro	Asn	Leu	Thr	Glu	Ser	Ile	Ser	
			100							105				110		

gat	tgg	tgg	tct	ctc	aat	aaa	gat	ggc	tgg	tct	ggc	tcc	aaa	aaa	tcc	394
Arg	Trp	Trp	Ser	Leu	Asn	Lys	Asp	Gly	Trp	Phe	Gly	Ser	Lys	Lys	Ser	
			115							120				125		

gaa agl ttc act aaa aaa aag gaa tca aac cat gac gaa got ttt ttg	432
Glu Ser Ser Thr Lys Lys Lys Gly Ser Asn His Asp Asp Ala Phe Leu	
130 135 140	
caa agg tct ttt gct caa gaa ala tca aaa ggc gct gtt gac tgc gaa	480
Pro Arg Ser Phe Ala Gln Ala Ile Ser Lys Ala Ala Val Asp Cys Glu	
145 150 155 160	
tgt gaa ttt caa aat tta gaa cac aac gaa aag gaa gaa cta aag aag	528
Cys Glu Phe Gln Asn Leu Glu His Asn Glu Lys Ala Glu Leu Lys Lys	
165 170 175	
aaa aag gag tct atc aaa act gca aag aca aag gaa got cag ggt gcc	576
Lys Lys Gln Ser Ile Lys Thr Ala Glu Thr Thr Glu Ala Gln Gly Ala	
180 185 190	
gac cat aat gaa gaa gaa gag gaa gat gaa gaa gaa gaa gat gat	624
Asp His Asn Glu Glu Asp Glu Glu Asp Glu Glu Asp Asp	
195 200 205	
gaa gat tly tct nnt tgg atc aaa gtt ttc gcl tgg tgg tog aca tgc	672
Glu Asp Leu Ser Asn Ile Lys Val Phe Asp Ser Tyr Phe Thr Cys	
210 215 220	
tat aaa aat atc gat gaa ggg aag gca gag atg gat tct atg atg gtc	720
Tyr Lys Asn Ile Asp Gln Gly Lys Ala Glu Met Asp Ser Met Met Val	
225 230 235 240	
aag gaa ttc aac aaa aaa tta gaa aca tta ata aac caa gac ttc aag	768
Lys Glu Phe Asn Lys Lys Leu Glu Thr Asn Ile Asn Gln Asp Phe Lys	
245 250 255	
aag gtc cat gac ctg cgc aaa aaa ggg gaa gaa tca aga ctc aca ttc	816
Lys Val His Asp Leu Arg Lys Lys Val Glu Glu Ser Arg Leu Lys Phe	
260 265 270	
gat aca atg cgt tat gaa gtc aaa gca aaa gaa gca gag tta gag ggg	864
Asp Thr Met Arg Tyr Gln Val Lys Ala Lys Glu Ala Glu Leu Glu Ala	
275 280 285	
aaa aaa got gaa gac aca gga gaa gaa cat aac aag gat gtt aca gca	912
Lys Lys Ala Glu Ala Thr Gly Glu Ala His Ser Lys Asp Val Ser Ala	

290	295	300	
aag gag att ago gaa aac act acc acc tct ttt gac gaa aag ctt tct			960
Lys Asp Ile Ser Ala Asn Thr Thr Thr Ser Phe Asp Glu Thr Pro Ser			
305	310	315	320
acc gag gat gaa aag cca asa tca gag ggt gcc gaa gag gaa tca aag			1008
Thr Glu Asp Glu Lys Pro Lys Ser Glu Gly Ala Glu Glu Glu Ser Lys			
325	330	335	
aaa gaa gcg aat gag cct act gtt gat gac gtt gct gat aga aaa gaa			1056
Lys Glu Ala Asn Glu Pro Thr Val Asp Asp Val Ala Asp Arg Lys Glu			
340	345	350	
gat tta aag agt aac aaa gta aat gat gag cca cag ctt gaa gaa tct			1104
Asp Leu Lys Ser Asn Lys Val Asn Asp Glu Pro Pro Ile Glu Glu Ser			
355	360	365	
gag gat aat aca tta ctg gac aaa ctg gag gat gaa ttt gtt tcc aat			1152
Glu Asp Asn Lys Leu Leu Glu Lys Leu Glu Asp Glu Phe Val Ser Asn			
370	375	380	
act aca gca gaa gta aca atg gaa gaa atc act gac agt tct gaa			1200
Thr Thr Ala Ala Val Glu Thr Met Glu Glu Ile Thr Asp Ser Ser Glu			
385	390	395	400
att ctg ggc ttg ata aaa ctg ttc cag aat ttc cag ttg gtt taa ttt			1248
Ile Leu Gly Leu Ile Lys Leu Phe Gln Asn Phe Glu Leu Val Tyr Phe			
405	410	415	
aga caa tgt gtc caa gaa gtg gag gca aac ctt aaa gtt cta act ggt			1296
Arg Gln Cys Val Gln Glu Val Glu Ala Asn Leu Lys Val Leu Asn Gly			
420	425	430	
ttg gaa att ttg			1308
Leu Glu Ile			
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«213» *Saccharomyces cerevisiae*

400 202

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20 25 30

Ala Asn Ala Asn Val Asn Leu Asn Arg Pro Gln Thr Arg Leu Ser Ile
35 40 45

Lys Ser Arg Thr Arg Phe Val Gln Glu Ser Leu Gly Thr Val Ser Asp
50 55 60

Ile Ser Lys Leu Pro Pro Gln Tyr Gln Phe Leu Glu Lys Lys Met Asp
65 70 75 80

Ser Leu Glu Lys Val Cys Lys Arg Ile Leu Leu Val Ser Lys Thr Phe
85 90 95

Glu Val Glu Gly Tyr Asp Tyr Pro Pro Asn Leu Thr Glu Ser Ile Ser
100 105 110

Asp Trp Trp Ser Leu Asn Lys Asp Gly Trp Phe Gly Ser Lys Lys Ser
115 120 125

Glu Ser Ser Thr Iys Lys Lys Gly Ser Asn His Asp Asp Ala Phe Leu
131 135 140

Pro Arg Ser Phe Ala Gln Ala Ile Ser Tyr Ala Ala Val Asp Cys Glu
145 150 155 160

Cys Glu Phe Gly Asn Leu Glu His Asp Glu Lys Ala Glu Leu Lys Lys
 165 176 175

Lys Lys Glu Ser Ile Lys Thr Ala Glu Thr Thr Glu Ala Glu Gly Ala
 180 185 190

Asp His Asn Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Asp Asp
 195 200 205

Glu Asp Leu Ser Asn Leu Ile Lys Val Phe Asp Ser Trp Ser Thr Cys
 210 215 220

Tyr Lys Asn Ile Asp Glu Gly Lys Ala Glu Met Asp Ser Met Met Val
 225 230 235 240

Lys Glu Phe Asn Lys Lys Leu Glu Thr Leu Ile Asn Glu Asp Phe Lys
 245 250 255

Lys Val His Asp Leu Arg Lys Lys Val Glu Glu Ser Arg Leu Lys Phe
 260 265 270

Asp Thr Met Arg Tyr Glu Val Lys Ala Lys Glu Ala Glu Leu Glu Ala
 275 280 285

Lys Lys Ala Glu Ala Thr Gly Glu Ala His Ser Lys Asp Val Ser Ala
 290 295 300

Lys Asp Ile Ser Ala Asn Thr Thr Thr Ser Phe Asp Glu Thr Pro Ser
 305 310 315 320

Thr Glu Asp Glu Lys Pro Lys Ser Glu Gly Ala Glu Glu Glu Ser Lys
325 339 335

Lys Glu Ala Asn Glu Pro Thr Val Asp Asp Val Ala Asp Arg Lys Glu
340 345 350

Asp Leu Lys Ser Asn Lys Val Asn Asp Glu Pro Pro Ile Glu Glu Ser
355 360 365

Glu Asp Asn Lys Leu Leu Glu Lys Leu Glu Asp Glu Phe Val Ser Asn
370 375 380

Thr Thr Ala Ala Val Glu Thr Met Glu Glu Ile Thr Asp Ser Ser Glu
385 390 395 400

Ile Leu Gly Leu Ile Lys Leu Phe Glu Asn Phe Glu Leu Val Tyr Phe
405 410 415

Arg Glu Cys Val Glu Glu Val Glu Ala Asn Leu Lys Val Leu Asn Gly
420 425 430

Leu Glu Ile
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<310> 203
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agt cgt ctc tcc cat ttc ttt ccc tgg tac act aat agc agt ggt atg      95
Ser Arg Leu Ser His Phe Phe Pro Ser Tyr Thr Asn Ser Ser Gly Met
          20          25          30

ggg gcc gcc tca act gat caa tct tct aag cag gga gaa gaa ctg cac      144
Gly Ala Ala Ser Thr Asp Gln Ser Ser Thr Gln Gly Glu Glu Leu His
          35          40          45

cat agg aag cac tgt gaa gaa gac aat gat ggt caa aaa cgg aaa aag      192
His Arg Lys His Cys Glu Gln Asp Asn Asp Gly Gln Lys Pro Lys Lys
          50          55          60

tct ccc gta tcc acc tct aca atg caa ata aaa tct aga cag gat gag      240
Ser Pro Val Ser Thr Ser Thr Met Glu Ile Lys Ser Arg Gln Asp Glu
65          70          75          80

gac gag gat gac ggt cga att gtc att aaa ccc ggt aac gat gaa gat      288
Asp Glu Asp Asp Gly Arg Ile Val Ile Lys Pro Val Asn Asp Glu Asp
          85          90          95

gat aca tca gta att ata act ttc aat cag tca aia tcc cct ttt att      336
Asp Thr Ser Val Ile Ile Thr Phe Asn Glu Ser Ile Ser Pro Phe Ile
          100          105          110

att aca tgg aca ttc gtt gcg tcc att tct ggg ttc atg ttt ggt tat      384
Ile Thr Leu Thr Phe Val Ala Ser Ile Ser Gly Phe Met Phe Gly Tyr
          115          120          125

gat act ggt tac ata tgg agt gcg cta att tct atc aat aga gat tta      432
Asp Glu Gly Tyr Ile Ser Ser Ala Leu Ile Ser Ile Asn Arg Asp Leu
          130          135          140

gac aac aaa ggt tta act tat gga gaa aaa gaa tta att aag gcc gcc      480
Asp Asn Lys Val Leu Thr Tyr Gly Glu Lys Glu Leu Ile Thr Ala Ala
          145          150          155          160

aca lea tgg gcc ggt tgg att aca agt gtg gcc gct ggt act gcc gct      528

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Thr Ser Leu Gly Ala Leu Ile Thr Ser Val Gly Ala Gly Thr Ala Ala	
165	175
gat gtg ttt gga aga aga cca tgt tta atg ctc ccc aat atg atg ttt	576
Asp Val Phe Gly Arg Arg Pro Cys Leu Met Phe Ser Asn Leu Met Phe	
180	195
10g atc gga gca att tta caa att acc gcg cac aag ttt tgg cca atg	624
Leu Ile Gly Ala Ile Leu Gln Ile Thr Ala His Lys Phe Trp Gln Met	
195	200
gag gcc ggt aga atg att atg ggt tta ggt gtc ggt att ggt tct ttg	672
Ala Ala Gly Arg Leu Ile Met Gly Phe Gly Val Gly Ile Gly Ser Leu	
210	215
att tct cct ctt ttt att agt gaa att gct cct aag atg atc agg ggt	720
Ile Ser Pro Leu Phe Ile Ser Glu Ile Ala Pro Lys Met Ile Asn Gly	
225	230
agg ttc acc gtt ata aat tcc cta tgg ctg acc ggt ggt cca ttg att	750
Arg Leu Thr Val Ile Asn Ser Leu Trp Leu Thr Gly Gly Gln Leu Ile	
245	250
gct tac ggt tgt ggt gcg ggc ctg aac cac gtc aaa aac ggt tgg aga	816
Ala Tyr Gly Cys Gly Ala Gly Leu Asn His Val Lys Asn Gly Trp Arg	
260	265
atc lta gtt ggt itg ccc ttg ata cct aat gtt ttg cag ttt tct ttt	864
Ile Leu Val Gly Leu Ser Leu Ile Pro Thr Val Leu Gln Phe Ser Phe	
275	280
ltd tgt ttt ttg ccg gat acc cca aga tac tac gta atg aaa ggc gat	912
Phe Cys Phe Leu Pro Asp Thr Pro Arg Tyr Tyr Val Met Lys Gly Asp	
290	295
tta aag aga gca aaa atg gtt ctc aaa cga agt tac gta aac act gaa	960
Leu Lys Arg Ala Lys Met Val Leu Lys Arg Ser Tyr Val Asn Thr Glu	
305	310
gat gaa ata att gat cca aaa gtt gca gaa tta tct agc tta aat cca	1008
Asp Glu Ile Ile Asp Gln Lys Val Glu Glu Leu Ser Ser Leu Asn Gln	
325	330

tcg ata cca gga aaa aat cca ata aca aaa ttc ttg aat aig ctc aag	1056
Ser Ile Pro Gly Tyr Asn Pro Ile Thr Lys Phe Trp Asn Met Val Lys	
340 345 350	
gaa ttg cac act gtg cct tca aat ttc aga ggc ttg att att ggt tgt	1104
Glu Leu His Thr Val Pro Ser Asn Phe Arg Ala Leu Ile Ile Gly Cys	
355 360 365	
ggc cta caa gcc att caa caa ttc tca ggt tgg aat tcc tta atg tac	1152
Gly Leu Gln Ala Ile Gln Gln Phe Thr Gly Trp Asn Ser Leu Met Tyr	
370 375 380	
ttc tcc ggt aca ata ttt gaa act gtt gga ttc aaa aat tct tct gcc	1200
Phe Ser Gly Thr Ile Phe Glu Thr Val Gly Phe Lys Asn Ser Ser Ala	
385 390 395 400	
gtt tct att att gtc tca ggt act aat ttt gtg ttc aca tta ata gca	1248
Val Ser Ile Ile Val Ser Gly Thr Asn Phe Val Phe Thr Leu Ile Ala	
405 410 415	
ttt ttc tgt att gat aaa acg gcc cgt cgg taa att tta ctg att gga	1296
Phe Phe Cys Ile Asp Lys Ile Gly Arg Arg Tyr Ile Leu Leu Ile Gly	
420 425 430	
cta cct ggt atg act gtg gcg ctg gtt ata tgt gct ata gcg ttc ctt	1344
Leu Pro Gly Met Thr Val Ala Leu Val Ile Cys Ala Ile Ala Phe His	
435 440 445	
ttc cta ggt att aag ttt aac ggt gct gat gca gta gtg gca tct gat	1392
Phe Leu Gly Ile Lys Thr Asn Gly Ala Asp Ala Val Val Ala Ser Asp	
450 455 460	
gga ttt tca tct tgg gcc att gtc att acc gta ttt att att gtg tat	1440
Gly Phe Ser Ser Trp Gly Ile Val Ile Ile Val Phe Ile Ile Val Tyr	
465 470 475 480	
gca gcc ttt tat gcc ctg ggt atc gcc act gtt cca tgg caa caa tgg	1488
Ala Ala Phe Tyr Ala Leu Gly Ile Gly Thr Val Pro Trp Gln Gln Ser	
485 490 495	
gaa tta ttt cca caa acc gtc aga ggt gta ggg aca tcc tac gct act	1536

468/762

Glu	Leu	Phe	Pro	Gln	Asn	Val	Arg	Gly	Val	Gly	Thr	Ser	Tyr	Ala	Thr	
500							505				510					
gcc	acc	aat	tgg	gca	ggc	tct	tta	gac	att	geg	tct	acg	ttc	tty	act	1534
Ala	Thr	Asn	Trp	Ala	Gly	Ser	Leu	Val	Ile	Ala	Ser	Thr	Phe	Leu	Thr	
515							520				525					
atg	tta	caa	aat	att	aca	cca	acg	ggt	aca	ttt	tca	tcc	ttt	gcc	ggt	1632
Met	Leu	Gln	Asn	Ile	Thr	Pro	Thr	Gly	Thr	Phe	Ser	Phe	Phe	Ala	Gly	
530							535				540					
gta	gca	tgt	tta	tca	acc	att	ttt	tgt	tac	ttt	tgt	tat	cca	gaa	cta	1680
Val	Ala	Cys	Leu	Ser	Thr	Ile	Phe	Cys	Tyr	Phe	Cys	Tyr	Pro	Glu	Leu	
545							550				555					560
tca	gga	tty	gag	tta	gag	gaa	gtt	caa	cca	att	tta	aag	gaa	gga	ttc	1728
Ser	Gly	Leu	Glu	Leu	Glu	Glu	Val	Gln	Thr	Ile	Leu	Lys	Asp	Gly	Phe	
565							570				575					
aat	ctc	aaa	gac	tct	aaa	gct	cta	gct	aaa	aag	agg	aaa	caa	cag	gtg	1776
Asn	Ile	Lys	Ala	Ser	Lys	Ala	Leu	Ala	Lys	Lys	Arg	Lys	Gln	Gln	Val	
580							585				590					
gcc	gaa	ggt	gct	gcc	cat	cat	aaa	ctc	aaa	ttc	gaa	cct	aca	cag	gaa	1824
Ala	Glu	Gly	Ala	Ala	His	His	Lys	Leu	Lys	Phe	Glu	Pro	Thr	Gln	Glu	
595							600				605					
att	gta	gaa	agt	tag												1839
Ile	Val	Glu	Ser													
610																

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<212> FRT
<213> Saccharomyces cerevisiae
<400> 204
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20 25 30

Gly Ala Ala Ser Thr Asp Gln Ser Ser Thr Gln Gly Glu Glu Leu His
35 40 45

His Arg Lys His Cys Glu Glu Asp Asn Asp Gly Gln Lys Pro Lys Lys
50 55 60

Ser Pro Val Ser Thr Ser Thr Met Gln Ile Lys Ser Arg Gln Asp Glu
65 70 75 80

Asp Glu Asp Asp Gly Arg Ile Val Ile Lys Pro Val Asn Asp Glu Asp
85 90 95

Asp Thr Ser Val Ile Ile Thr Phe Asn Gln Ser Ile Ser Pro Phe Ile
100 105 110

Ile Thr Leu Thr Phe Val Ala Ser Ile Ser Gly Phe Met Phe Gly Tyr
115 120 125

Asp Thr Gly Tyr Ile Ser Ser Ala Leu Ile Ser Ile Asn Arg Asp Leu
130 135 140

Asp Asn Lys Val Leu Thr Tyr Gly Glu Lys Glu Leu Ile Thr Ala Ala
145 150 155 160

Thr Ser Leu Gly Ala Leu Ile Thr Ser Val Gly Ala Gly Thr Ala Ala
165 170 175

Asp Val Phe Gly Arg Arg Pro Cys Leu Met Phe Ser Asn Leu Met Phe

130

185

190

Leu Ile Gly Ala Ile Leu Gln Ala Thr Ala His Lys Phe Trp Gln Met
195 200 205

Ala Ala Gly Arg Leu Ile Met Gly Phe Gly Val Gly Ile Gly Ser Leu
210 215 220

Ile Ser Pro Leu Phe Ile Ser Glu Ile Asn Pro Lys Met Ile Arg Gly
225 230 235 240

Arg Leu Thr Val Ile Asn Ser Leu Trp Leu Thr Gly Gly Gln Leu Phe
245 250 255

Ala Tyr Gly Cys Gly Ala Gly Leu Asn His Val Lys Asn Gly Trp Arg
260 265 270

Ile Leu Val Gly Leu Ser Leu Ile Pro Thr Val Leu Gln Phe Ser Phe
275 280 285

Phe Cys Phe Leu Pro Asp Thr Pro Arg Tyr Tyr Val Met Lys Gly Asp
290 295 300

Leu Lys Arg Ala Lys Met Val Leu Lys Arg Ser Tyr Val Asn Thr Gln
305 310 315 320

Asp Glu Ile Ile Asp Gln Lys Val Glu Glu Leu Ser Ser Leu Asn Gln
325 330 335

Ser Ile Pro Gly Lys Asn Pro Ile Thr Lys Phe Trp Asn Met Val Lys
340 345 350

Glu Leu His Thr Val Pro Ser Asn Phe Arg Ala Leu Ile Ile Gly Cys
 355 360 365

Gly Leu Gln Ala Ile Glu Gln Phe Thr Gly Trp Asn Ser Leu Met Tyr
 370 375 380

Phe Ser Gly Thr Ile Phe Glu Thr Val Gly Phe Lys Asn Ser Ser Ala
 385 390 395 400

Val Ser Ile Ile Val Ser Gly Thr Asn Phe Val Phe Thr Leu Ile Ala
 405 410 415

Phe Phe Cys Ile Asp Lys Ile Gly Arg Arg Tyr Ile Leu Leu Ile Gly
 420 425 430

Leu Pro Gly Met Thr Val Ala Leu Val Ile Cys Ala Ile Ala Phe His
 435 440 445

Phe Leu Gly Ile Lys Phe Asn Gly Ala Asp Ala Val Val Ala Ser Asp
 450 455 460

Gly Phe Ser Ser Trp Gly Ile Val Ile Ile Val Phe Ile Ile Val Tyr
 465 470 475 480

Ala Ala Phe Tyr Ala Leu Gly Ile Gly Thr Val Pro Trp Gln Gln Ser
 485 490 495

Glu Leu Phe Pro Gln Asn Val Arg Gly Val Gly Thr Ser Tyr Ala Thr
 500 505 510

Ala Thr Asn Trp Ala Gly Ser Leu Val Ile Ala Ser Thr Phe Leu Thr

472/762

515

520

525

Met Leu Gln Asn Ile Thr Pro Thr Gly Thr Phe Ser Phe Phe Ala Gly
 530 535 540

Val Ala Cys Leu Ser Thr Ile Phe Cys Tyr Phe Cys Tyr Pro Glu Leu
 545 550 555 560

Ser Gly Leu Glu Leu Glu Glu Val Glu Thr Ile Leu Lys Asp Gly Phe
 565 570 575

Asn Ile Lys Ala Ser Lys Ala Leu Ala Lys Lys Arg Lys Gln Gln Val
 580 585 590

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 595 600 605

Ile Val Glu Ser
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 <213> *Saccharomyces cerevisiae*

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aca cat gca ttc tcc tct aat tat gct cct gta ggc ata tca tta cct	96
Thr His Ala Phe Ser Ser Asn Tyr Ala Pro Val Gly Ile Ser Leu Pro	
20 25 30	
gct ttt acc aac gaa tgt ctt tac tat gat tta tcc tct gat aaa gat	164
Ala Phe Thr Lys Glu Cys Leu Tyr Tyr Asp Leu Ser Ser Asp Lys Asp	
35 40 45	
gtc ctt gtg gtc agt tau caa gtt ttg aca ggt ggg aat ttc gag ata	192
Val Leu Val Val Ser Tyr Glu Val Leu Thr Gly Gly Asn Phe Glu Ile	
50 55 60	
gac ttc gat att aou guc uat gal ygc lcl yll xlc glu act gaa aga	240
Asp Phe Asp Ile Thr Ala Pro Asp Gly Ser Val Ile Val Thr Glu Arg	
65 70 75 80	
caa aag aag cat tct gat ttt cta ctg aag tgg ttt ggt ata ggt aag	288
Gln Lys Lys His Ser Asp Phe Leu Leu Lys Ser Phe Gly Ile Gly Lys	
85 90 95	
tac aat llo lg. lly agt aat aac tac ggc act tcc cca aag aaa gtt	336
Tyr Thr Phe Cys Leu Ser Asn Asn Tyr Gly Ile Ser Pro Lys Lys Val	
100 105 110	
gaa ttc acc ctc gaa aag gaa aag gaa att gtt tct tcc cat gaa agc	384
Glu Ile Thr Leu Glu Lys Glu Lys Glu Ile Val Ser Ser His Glu Ser	
115 120 125	
aaa gag gac ata atc gca aac aac ggc ttc yag gaa all gat agg aac	432
Lys Glu Asp Ile Ile Ala Asn Asn Ala Ile Glu Glu Ile Asn Arg Asn	
130 135 140	
ctg aat aag atc acc aaa aca atg gat tat tta agg gct aga gaa tgg	480
Leu Asn Lys Ile Thr Lys Thr Met Asp Tyr Val Arg Ala Arg Ser Trp	
145 150 155 160	
aga aac atg tat act gtg agt tct act gag tca aga tta aca tgg ctc	528
Arg Asn Met Tyr Thr Val Ser Ser Thr Glu Ser Arg Leu Thr Trp Leu	
165 170 175	
tca tta cta att atg ggg gta atg gtc ggt atc aat ata qta caq gca	576
Ser Leu Leu Ile Met Gly Val Met Val Gly Ile Ser Ile Val Glu Ala	

180	185	190	
tta att att cag ttc ttt ttt acc agt cgc cca aaa aac tac gta tag			624
Leu Ile Ile Gln Phe Phe Phe Thr Ser Arg Gln Lys Asn Tyr Val			
195	200	205	
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<212> PRT			
<213> <i>Saccharomyces cerevisiae</i>			
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1	5	10	15
Thr His Ala Phe Ser Ser Asn Tyr Ala Pro Val Gly Ile Ser Leu Pro			
20	25	30	
Ala Phe Thr Lys Glu Cys Leu Tyr Tyr Asp Leu Ser Ser Asp Lys Asp			
35	40	45	
Val Leu Val Val Ser Tyr Gln Val Leu Thr Gly Gly Asn Phe Glu Ile			
50	55	60	
Asp Phe Asp Ile Thr Ala Pro Asp Gly Ser Val Ile Val Thr Glu Arg			
65	70	75	80
Gln Lys Lys His Ser Asp Phe Leu Leu Lys Ser Phe Gly Ile Gly Lys			
85	90	95	
Tyr Thr Phe Cys Leu Ser Asn Asn Tyr Gly Thr Ser Pro Lys Lys Val			
100	105	110	

Glu Ile Thr Leu Glu Lys Glu Lys Glu Ile Val Ser Ser His Glu Ser
115 120 125

Lys Glu Asp Ile Leu Ala Asn Asn Ala Ile Glu Glu Ile Asp Arg Asn
130 135 140

Leu Asn Lys Ile Thr Lys Thr Met Asp Tyr Leu Arg Ala Arg Glu Trp
145 150 155 160

Arg Asn Met Tyr Thr Val Ser Ser Thr Glu Ser Arg Leu Thr Trp Leu
165 170 175

Ser Leu Leu Ile Met Gly Val Met Val Gly Ile Ser Ile Val Gln Ala
180 185 190

Leu Ile Ile Gln Phe Phe Phe Thr Ser Arg Gln Lys Asn Tyr Val
195 200 205

<210> 207

<211> 483

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

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cgt gac ttc aga aag cat ggt gcc gtt cac atg tcc acc tac ttg aag 96
Arg Asp Phe Arg Lys His Gly Ala Val His Met Ser Thr Leu Lys
20 25 30

atc tac aag gtt ggt gac att gtc gac aic aua ggc aat ggt tct aic	144
Ile Tyr Lys Val Gly Asp Ile Val Asp Ile Lys Ala Asn Gly Ser Ile	
35 40 45	
caa aag ggt atg cca cca aag ttc tac caa ggt aag aac ggt gtc gtc	192
Gln Lys Gly Met Pro His Lys Phe Tyr Gln Gly Lys Thr Gly Val Val	
50 55 60	
tac aac gtt aac aag tcc tct gtt ggt gtt atc atc aac aag atg gtc	240
Tyr Asn Val Thr Lys Ser Ser Val Gly Val Ile Ile Asn Lys Met Val	
65 70 75 80	
ggt aac aga tac ttg gaa aag aga ttc aac ttc aga gtt gaa aac aic	288
Gly Asn Arg Tyr Leu Gln Lys Arg Leu Asn Leu Arg Val Gln His Ile	
85 90 95	
aag aac tct aaa tgt aga caa gaa ttt ttc gaa aga gtt aag gcc aac	336
Lys His Ser Lys Cys Arg Gln Glu Phe Iou Glu Arg Val Lys Ala Asn	
100 105 110	
gct gct aag tct gct gaa gcc aag gcc caa ggt gtt gct gtc caa ttg	384
Ala Ala Lys Arg Ala Glu Ala Lys Ala Gln Gly Val Ala Val Glu Leu	
115 120 125	
aag aga caa cca gct cca cca aga gaa tcc cgt att gtc tct aat gaa	432
Lys Arg Gln Pro Ala Glu Pro Arg Glu Ser Arg Ile Val Ser Thr Glu	
130 135 140	
ggt aac gtt ccc caa act tta gct cca gtt cca tac gaa aac ttc att	480
Gly Asn Val Pro Gln Thr Leu Ala Pro Val Pro Tyr Glu Thr Phe Ile	
145 150 155 160	
taa	463

<210> 208

<211> 160

<212> PRT

<213> Saccharomyces cerevisiae

<400> 208

Met Gly Lys Ser His Gly Tyr Arg Ser Arg Thr Arg Tyr Met Phe Gln
 1 5 10 15

Arg Asp Phe Arg Lys His Gly Ala Val His Met Ser Thr Tyr Leu Lys
 20 25 30

Ile Tyr Lys Val Gly Asp Ile Val Asp Ile Lys Ala Asn Gly Ser Ile
 35 40 45

Gln Lys Gly Met Pro His Lys Phe Tyr Gln Gly Lys Thr Gly Val Val
 50 55 60

Tyr Asn Val Thr Lys Ser Ser Val Gly Val Ile Ile Asn Lys Met Val
 65 70 75 80

Gly Asn Arg Tyr Leu Glu Lys Arg Leu Asn Leu Arg Val Glu His Ile
 85 90 95

Lys His Ser Lys Cys Arg Gln Glu Phe Leu Glu Arg Val Lys Ala Asn
 100 105 110

Ala Ala Lys Arg Ala Glu Ala Lys Ala Gln Gly Val Ala Val Gln Lys
 115 120 125

Lys Arg Gln Pro Ala Gln Pro Arg Gln Ser Arg Ile Val Ser Thr Glu
 130 135 140

Gly Asn Val Pro Gln Thr Leu Ala Pro Val Pro Tyr Glu Thr Phe Ile
 145 150 155 160

<210> 209

<211> 1737

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1737)

<400> 209

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Met	Ser	Ile	Gln	Ala	Phe	Val	Phe	Cys	Gly	Lys	Gly	Ser	Asn	Leu	Ala	
1			5					10				15				

ccc	ttc	acc	cag	cca	gat	ttt	cca	ttc	caa	acg	cag	aac	aaa	gac	agt	76
Pro	Phe	Thr	Gln	Pro	Asp	Phe	Pro	Phe	Gln	Thr	Gln	Asn	Lys	Asp	Ser	
			20					25				30				

aca	gct	gcc	acg	agc	ggt	gac	aaa	ctt	aat	gag	ttg	gtc	act	agc	gac	144
Thr	Ala	Ala	Thr	Ser	Gly	Asp	Lys	Leu	Asn	Gly	Asn	Val	Asn	Ser	Ala	
	35					40						45				

ctc	gat	tca	act	gtc	ata	aat	gag	ttc	atg	caa	cat	tca	acg	cgc	tgg	152
Ile	Asp	Ser	Thr	Val	Ile	Asn	Glu	Phe	Met	Gln	Ile	Ser	Thr	Arg	Leu	
	50					55					60					

ccc	aag	gac	glt	ttg	ccc	atc	ggt	aat	aga	cct	atg	att	gaa	tac	gtc	240
Pro	Lys	Ala	Leu	Leu	Pro	Ile	Gly	Asn	Arg	Pro	Met	Ile	Glu	Tyr	Val	
65			70						75				80			

ttg	gat	tgg	tgt	gat	cag	gca	gat	ttc	aaa	gaa	atc	agt	gtg	gtc	gca	288
Leu	Asp	Tyr	Cys	Asp	Gln	Ala	Asp	Phe	Lys	Glu	Ile	Ser	Val	Val	Ala	
			85					90				95				

ccc	gtt	gac	gaa	atc	gaa	tta	att	gaa	agt	gga	ctg	act	tgg	ttt	ttg	336
Pro	Val	Asp	Glu	Ile	Glu	Leu	Ile	Glu	Ser	Gly	Leu	Thr	Ser	Phe	Leu	
	100							105				110				

tac	cta	aga	aag	caa	caa	ttt	gaa	cta	ata	tac	aag	gct	ttg	tca	aat	384
Ser	Leu	Arg	Lys	Gln	Gln	Phe	Glu	Leu	Ile	Tyr	Lys	Ala	Leu	Ser	Asn	
	115							120				125				

<p> toc aac cac agt cat cac ttg caa gat cct aag aaa att aat ttc atc Ser Asn His Ser His His Leu Gln Arg Pro Lys Lys Ile Asn Phe Ile 130 135 140 </p>	432
<p> cct tgg aag gca aat tct acg ggc gag tcc ttg caa aaa gag ctt ttg Pro Ser Lys Ala Asn Ser Thr Gly Glu Ser Leu Gln Lys Glu Leu Leu 145 150 155 160 </p>	480
<p> cct aga atc aat ggc gat ttt gta atc ttg ccc tgt gat ttt gtc aca Pro Arg Ile Asn Gly Asp Phe Val Ile Leu Pro Cys Asp Phe Val Thr 165 170 175 </p>	528
<p> gat ata cct cca caa gtc ttg gtc gat caa ttt agg cat agg gat gat Arg Ile Pro Pro Gln Val Leu Val Arg Gln Phe Arg Asn Arg Asp Asp 180 185 190 </p>	576
<p> aal aac cta gca atg aat atc tac tat aag aac tct tta gat agt agt Asn Asn Leu Ala Met Thr Ile Tyr Tyr Lys Asn Ser Leu Asp Ser Ser 195 200 205 </p>	624
<p> atc gat aaa aag caa cag caa aag caa aca caa cag caa ttt ttc aat Ile Arg Lys Lys Gln Gln Gln Lys Glu Lys Gln Gln Cln Phe Phe Thr 210 215 220 </p>	672
<p> gtt tat tca gaa aac gaa gac tca gag agg cag caa ata ctt ttg gac Val Tyr Ser Glu Asn Glu Asp Ser Glu Arg Gln Pro Ile Leu Leu Asp 225 230 235 240 </p>	720
<p> gtt tat tct caa agg gac gtc aca aaq aca aaa tat cta cag atc aca Val Tyr Ser Glu Arg Asp Val Thr Lys Thr Lys Tyr Leu Gln Ile Arg 245 250 255 </p>	768
<p> tct cat tta tta tgg aac tct cca aat tta aca gta tcc aat aag tta Ser His Leu Leu Trp Asn Tyr Pro Asn Leu Thr Val Ser Thr Lys Leu 260 265 270 </p>	816
<p> ctg aac taa ttc atc tgc tt. tgt tcc ttt gaa ctt tgc aag ttg tta Leu Asn Ser Phe Ile Tyr Phe Cys Ser Phe Glu Leu Cys Gln Leu Leu 275 280 285 </p>	864
<p> aaa tta gga cct caa tca atg tca aga caa gct tca ttc aaa gat cca Lys Leu Gly Pro Gln Ser Met Ser Arg Gln Ala Ser Phe Lys Asp Pro 290 295 </p>	912

290	295	300	
ttt act gga aac caa caa cag caa aac cct cct act act gat gat gat			960
Phe Thr Gly Asn Gln Gln Gln Gln Asn Pro Pro Thr Thr Asp Asp Asp			
305	310	315	320
gaa gat cgc aat cat gat gat gac gat gat taa aaa cct tgg gtt acc			1008
Glu Asp Arg Asn His Asp Asp Asp Asp Asp Tyr Lys Pro Ser Ala Thr			
325	330	335	
tct atc cag cct acc tac ttc aaa aaa aag aat gat ctc atc ttg gac			1056
Ser Ile Gln Pro Thr Tyr Phe Lys Lys Lys Asn Asp Leu Ile Leu Asp			
340	345	350	
cca ata aac tgt aat aaa tca ttg agt aag gtt ttt aga gat tta tct			1104
Pro Ile Asn Cys Asn Lys Ser Leu Ser Lys Val Phe Arg Asp Leu Ser			
355	360	365	
cgt cgt tgg tgg caa cat tgg aac cag agg gaa cca ata ggt att ttt			1152
Arg Arg Ser Trp Gln His Ser Lys Pro Arg Gln Pro Ile Gly Ile Phe			
370	375	380	
att tta cca aac gaa acc ttg ttc atc aga gcc aat acc ttg aat gct			1200
Ile Leu Pro Asn Glu Thr Leu Phe Ile Arg Ala Asn Asn Leu Asn Ala			
385	390	395	400
tao atg gac gcc aat aga ttt gta cta aag ata aaa tca caa acg atg			1248
Tyr Met Asp Ala Asn Arg Phe Val Leu Lys Ile Lys Ser Gln Thr Met			
405	410	415	
ttc aag aaa aat ata cag att caa tct gcc gct atc ggt gct gat gcc			1296
Phe Thr Lys Asn Ile Gln Ile Gln Ser Ala Ala Ile Gly Ala Asp Ala			
420	425	430	
ata gta gat ccc aaa tgc caa atc tct ggt cat agt aat gtc aag atg			1344
Ile Val Asp Pro Lys Cys Gln Ile Ser Ala His Ser Asn Val Lys Met			
435	440	445	
tct gtt ctc ggt act cag gcc act att ggt tcc aga tgt agt gtt gcc			1392
Ser Val Leu Gly Thr Gln Ala Asn Ile Gly Ser Arg Cys Arg Val Ala			
450	455	460	

ggg tct ctc tta ttt cct gga gtc cat ctt ggt gac gaa gta atc ctg 1440
 Gly Ser Leu Leu Phe Pro Gly Val His Leu Gly Asp Glu Val Ile Leu
 465 470 475 480

gaa aat tgt att att gga cct atg gca aaa atc ggt tca aag tgt aaa 1488
 Glu Asn Cys Ile Ile Gly Pro Met Ala Lys Ile Gly Ser Lys Cys Lys
 485 490 495

ctc agc aal tgt tat atc gaa ggc cat tat gtt gtg gag cct aaa aal 1536
 Leu Ser Asn Cys Tyr Ile Glu Gly His Tyr Val Val Glu Pro Lys Asn
 500 505 510

aau tct aaa gg- gaa aca ctg ggc aac gtt tat ttg gat gaa gat gag 1584
 Asn Phe Lys Gly Glu Thr Leu Ala Asn Val Tyr Leu Asp Glu Asp Glu
 515 520 525

gag gac gag tta ata tat gat gat agt gtt ctt gct gga gaa agt gaa 1632
 Glu Asp Glu Leu Ile Tyr Asp Asp Ser Val Ile Ala Gly Glu Ser Glu
 530 535 540

atc ggc gaa gaa act gac agt gat gat aga agc gat gaa gat tct gat 1680
 Ile Ala Glu Glu Thr Asp Ser Asp Asp Arg Ser Asp Glu Asp Ser Asp
 545 550 555 560

gat agt gaa tat acc gac gag tac gag tac gaa gat gat gga tta tct 1728
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 565 570 575

gag cgt taa 1737
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<211> 578

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 210

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Pro Phe Thr Glu Pro Asp Phe Pro Phe Glu Thr Glu Asn Lys Asp Ser
 20 25 30

Thr Ala Ala Thr Ser Gly Asp Lys Leu Asn Glu Leu Val Asn Ser Ala
 35 40 45

Leu Asp Ser Thr Val Ile Asn Glu Phe Met Glu His Ser Thr Arg Leu
 50 55 60

Pro Lys Ala Leu Leu Pro Ile Gly Asn Arg Pro Met Ile Glu Tyr Val
 65 70 75 80

Leu Asp Thr Cys Asp Gln Ala Asp Phe Lys Glu Ile Ser Val Val Ala
 85 90 95

Pro Val Asp Glu Ile Glu Leu Ile Glu Ser Gly Leu Thr Ser Phe Leu
 100 105 110

Ser Leu Arg Lys Gln Gln Phe Glu Leu Ile Tyr Lys Ala Leu Ser Asn
 115 120 125

Ser Asn His Ser His His Leu Gln Asp Pro Lys Lys Ile Asn Phe Thr
 130 135 140

Pro Ser Lys Ala Asn Ser Thr Gly Gln Ser Leu Gln Lys Glu Leu Leu
 145 150 155 160

Pro Arg Ile Asn Gly Asp Phe Val Ile Leu Pro Cys Asp Phe Val Thr
 165 170 175

Asp Ile Pro Pro Gln Val Leu Val Asp Gln Phe Arg Asn Arg Asp Asp
180 185 190

Asn Asn Leu Ala Met Thr Ile Tyr Tyr Lys Asn Ser Leu Asp Ser Ser
195 200 205

Ile Asp Lys Lys Gln Gln Gln Lys Gln Lys Gln Gln Gln Phe Phe Thr
210 215 220

Val Tyr Ser Glu Asn Glu Asp Ser Glu Arg Gln Pro Ile Leu Leu Asp
225 230 235 240

Val Tyr Ser Gln Arg Asp Val Thr Lys Thr Lys Tyr Leu Gln Ile Arg
245 250 255

Ser His Leu Leu Trp Asn Tyr Pro Asn Leu Thr Val Ser Thr Lys Leu
260 265 270

Leu Asn Ser Phe Ile Tyr Phe Cys Ser Phe Glu Leu Cys Gln Leu Leu
275 280 285

Lys Leu Gly Pro Gln Ser Met Ser Arg Gln Ala Ser Phe Lys Asp Pro
290 295 300

Phe Thr Gly Asn Gln Gln Gln Gln Asn Pro Pro Thr Thr Asp Asp Asp
305 310 315 320

Glu Arg Arg Asn His Asp Asp Asp Asp Asp Tyr Lys Pro Ser Ala Thr
325 330 335

Ser Ile Gln Pro Thr Tyr Phe Lys Lys Lys Asn Asp Leu Ile Leu Asp
340 345 350

Pro Ile Asn Cys Asn Lys Ser Leu Ser Lys Val Phe Arg Asp Leu Ser
355 360 365

Arg Arg Ser Trp Gln His Ser Lys Pro Arg Glu Pro Ile Gly Ile Phe
370 375 380

Ile Leu Pro Asn Glu Thr Leu Phe Ile Arg Ala Asn Asn Leu Asn Ala
385 390 395 400

Cys Met Asp Ala Asn Arg Phe Val Gln Lys Ile Lys Ser Gln Thr Met
405 410 415

Phe Thr Lys Asn Ile Gln Ile Gln Ser Ala Ala Ile Gly Ala Asp Ala
420 425 430

Ile Val Asp Pro Lys Cys Gln Ile Ser Ala His Ser Asn Val Tyr Met
435 440 445

Ser Val Leu Gly Thr Gln Ala Asn Ile Gly Ser Arg Cys Arg Val Ala
450 455 460

Gly Ser Leu Leu Phe Pro Gly Val His Leu Gly Asp Glu Val Ile Leu
465 470 475 480

Glu Asn Cys Ile Ala Gly Pro Met Ala Lys Ile Gly Ser Lys Cys Lys
485 490 495

Leu Ser Asn Cys Tyr Ile Glu Gly His Tyr Val Val Glu Pro Lys Asn
500 505 510

Asn Phe Lys Gly Glu Thr Leu Ala Asn Val Tyr Leu Asp Glu Asp Glu
 515 520 525

Glu Asp Glu Leu Phe Tyr Asp Asp Ser Val Ile Ala Gly Gln Ser Glu
 530 535 540

Ile Ala Glu Glu Thr Asp Ser Asp Asp Arg Ser Asp Glu Asp Ser Asp
 545 550 555 560

Asp Ser Glu Tyr Thr Asp Glu Tyr Glu Tyr Glu Asp Asp Gly Leu Phe
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Glu Arg

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 <213> *Saccharomyces cerevisiae*

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 Met Ser Thr Leu Phe Leu Ile Gly Ile His Glu Ile Glu Lys Ser Glu
 1 5 10 15
 aca att gta cag aat gaa cac tat ttt gat aga gtg att gag ctt oaa 96
 Thr Ile Val Glu Asn Gln His Tyr Phe Asp Arg Val Ile Glu Leu Glu
 20 25 30
 ggt ttg gat tct ctg atg gta gca ttg tat aag gac aga gtt tgg cct 144
 Asp Leu Asp Ser Leu Met Val Ala Leu Tyr Lys Asp Arg Val Ser Pro
 35 40 45

tct cca aac gtc cat aac ttt cca acg qqc gta tct ata gcc ott tat	192
Phe Pro Asn Val His Asn Phe Glu Thr Gly Val Ser Ile Val Leu Tyr	
50 55 60	
gac cct taa aaa ttt cca tta tct gtg cga caa ktg gal gct cta ttc	240
Asp Pro Ser Lys Phe Gln Leu Ser Val Arg Gln Leu Asp Val Leu Phe	
65 70 75 80	
aag cga ttt ttc cca tct ttc aat att tct gag ata gat cat aca cga	288
Lys Arg Phe Phe Pro Ser Phe Asn Ile Ser Ala Ile Asp His Thr Arg	
85 90 95	
gag gaa aac atg caa cgt ctt gaa tgt gtt gag cgt gaa aat agc atc	336
Glu Gln Asn Leu Gln Arg Leu Glu Cys Val Glu Arg Glu Asn Ser Ile	
100 105 110	
tgt cgt aat aga ata acg aga att aac caa kgg atg tat cac cat cat	384
Cys Arg Asn Arg Ile Thr Arg Ile Asn His Tyr Met Tyr His His His	
115 120 125	
gal gal aat cca gaa ggt att aac aca aac agt tat ggt act gta aat	432
Asp Asp Thr Pro Asp Gly Tyr Asn Lys Asn Ser Tyr Gly Thr Val Asn	
130 135 140	
ggg aat tct gtc ccc act caa gca tgt gaa gca aac att taa act tta	480
Gly Asn Ser Val Pro Thr Gln Ala Cys Glu Ala Asn Ile Tyr Thr Leu	
145 150 155 160	
tta tbg cat ttg aat gat tcc aag gca caa cat tta cga aag gca tca	528
Leu Leu His Leu Asn Asp Ser Lys Ala Gln His Leu Arg Lys Ala Ser	
165 170 175	
gtg cca agg cta att cgc aac atc gag ttt atg tct ttt ttg tca gat	576
Val Pro Arg Leu Ile Arg Asn Ile Glu Phe Met Ser Phe Leu Ser Asp	
180 185 190	
cca ata gaa aaa att tct caa gag gga taa caa tat tgg aac att cta	624
Pro Ile Glu Lys Ile Ser Gln Glu Gly Ser His Tyr Trp Asn Ile Leu	
195 200 205	
tca act tgg gac ttt tgt gct tta tca tta agc act caa gaa ttg att	672

Ser Thr Trp Asp Phe Cys Ala Leu Ser Leu Ser Thr Glu Gln Trp Ile	
210	215 220
tgq tgc ggg ttc aag ctt atc aaa aay lla tcl nag cat gca aaa gln	720
Trp Cys Gly Phe Thr Leu Ile Lys Lys Leu Ser Lys Asp Ala Lys Val	
225	230 235 240
ctc att gca gat aat nag lla ctg cta cta cta ttt act tta gaa tca	768
Leu Ile Ala Asp Asn Lys Leu Leu Leu Leu Phe Thr Leu Glu Ser	
245	250 255
tcg tat cat cca gtt aac aaa ttt cag aat ttt agy cat ggc aic gat	816
Ser Tyr His Glu Val Asn Lys Phe His Asn Phe Arg His Ala Ile Asp	
260	265 270
gtc atg cca gcc aca tgg cga ttg tgt aca tat ctt ctt aaa gat aat	864
Val Met Glu Ala Thr Trp Arg Leu Cys Thr Tyr Leu Leu Lys Arg Asn	
275	280 285
acc gta cca aca tta ctg ttg tgt atg gct gcc ata ggt cat gat gtc	912
Pro Val Glu Thr Leu Leu Leu Cys Met Ala Ala Ile Gly His Asp Val	
290	295 300
ggc cat cct ggg act aac aat cca cta ttg tgc aac tgt gaa tca gag	960
Gly His Pro Gly Thr Asn Asn Glu Leu Leu Cys Asn Cys Glu Ser Glu	
305	310 315 320
gtc gct cca aal lla aua aat gtc tct atc ttg gag aat ttt cag agg	1008
Val Ala Glu Asn Phe Lys Asn Val Ser Leu Glu Asn Phe His Arg	
325	330 335
gaa tta tll cca cca ttg cta tca gag cat tgg cct cca ttg cta tct	1056
Glu Leu Phe Glu Leu Leu Ser Glu His Trp Pro Glu Leu Leu Ser	
340	345 350
atc tcc aan aca aat ttt gat ttt att tcc gag gct att ctg gcc aca	1104
Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala Thr	
355	360 365
gat atg gca ttg cat tct cag tat gag gat aga tta atg cat gaa aac	1152
Asp Met Ala Leu His Ser Glu Tyr Glu Asp Arg Leu Met His Glu Asn	
370	375 380

cca atg aaa caa atc acc ttg ata tct cta att att aaa gct gca gac 1200
 Pro Met Lys Gln Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala Asp
 385 390 395 400

atc tct aat gtg aag aga acc ttg tca ata tca gaa cgt tgg gca tac 1248
 Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala Tyr
 405 410 415

ctc att act ctc gaa ttt aat gat tgg gct cct ttg gaa aca ttt cct 1296
 Leu Ile Thr Leu Glu Phe Asn Asp Cys Ala Leu Leu Glu Thr Phe His
 420 425 430

aaa gct cac cgc cca gaa caa gac tgt ttt ggc gat tca tac aag aat 1344
 Lys Ala His Arg Pro Glu Gln Asp Cys Phe Gly Asp Ser Tyr Lys Asn
 435 440 445

gtt gat tct cgg aaa gaa gat ttg gaa tca att caa aat att ttg gtg 1392
 Val Asp Ser Pro Lys Glu Asp Leu Glu Ser Ile Gln Asn Ile Leu Val
 450 455 460

aac gaa aca gaa cca gct gct att att aac gaa val cgg val att cca 1440
 Asn Val Thr Asp Pro Asp Asp Ile Ile Lys Asp His Pro His Ile Pro
 465 470 475 480

aac ggt caa ata ttt ttc att aat acg ttt gct gaa gta ttt ttc aac 1488
 Asn Gly Gln Ile Phe Phe Ile Asn Thr Phe Ala Glu Val Phe Phe Asn
 485 490 495

gaa tta agt caa aaa ttc tca gga tta aaa ttt tta agc gat aat gtc 1536
 Ala Leu Ser Gln Lys Phe Ser Gly Leu Lys Phe Leu Ser Asp Asn Val
 500 505 510

aaa atc aat aaa gaa tac tgg atg aaa cac aag aaa caa caa tag 1584
 Lys Ile Asn Lys Glu Tyr Trp Met Lys His Lys Lys Pro Gln
 515 520 525

<210> 212

<211> 526

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 212

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Thr Ile Val Gln Asn Glu His Tyr Phe Asp Arg Val Ile Glu Leu Glu
 20 25 30

Asp Leu Asp Ser Leu Met Val Ala Leu Tyr Lys Asp Arg Val Ser Pro
 35 40 45

Phe Pro Asn Val His Asn Phe Glu Thr Gly Val Ser Ile Val Leu Tyr
 50 55 60

Asp Pro Ser Lys Phe Gln Leu Ser Val Arg Glu Leu Asp Val Leu Phe
 65 70 75 80

Lys Arg Phe Phe Pro Ser Thr Asn Ile Ser Ala Ile Asp His Thr Arg
 85 90 95

Glu Glu Asn Leu Gln Arg Leu Glu Cys Val Glu Arg Glu Asn Ser Ile
 100 105 110

Cys Arg Asn Arg Ile Thr Arg Ile Asn His Trp Met Tyr His His His
 115 120 125

Asp Asp Thr Pro Asp Gly Ile Asn Lys Asn Ser Tyr Gly Thr Val Asn
 130 135 140

Gly Asn Ser Val Pro Thr Glu Ala Cys Glu Ala Asn Ile Tyr Thr Leu
 145 150 155 160

Leu Leu His Leu Asn Asp Ser Lys Ala Gln His Leu Arg Lys Ala Ser
165 170 175

Val Pro Arg Leu Ile Arg Asn Ile Glu Phe Met Ser Phe Leu Ser Asp
180 185 190

Pro Ile Glu Lys Ile Ser Gln Glu Gly Ser His Tyr Trp Asn Ile Leu
195 200 205

Ser Thr Trp Asp Phe Cys Ala Leu Ser Leu Ser Thr Gln Gln Leu Ile
210 215 220

Trp Cys Gly Phe Thr Leu Ile Lys Lys Leu Ser Lys Asp Ala Lys Val
225 230 235 240

Leu Ile Ala Arg Asn Lys Leu Leu Ser Leu Leu Phe Thr Leu Glu Ser
245 250 255

Ser Tyr His Gln Val Asn Lys Phe His Asn Phe Arg His Ala Ile Asp
260 265 270

Val Met Gln Ala Thr Trp Arg Leu Cys Thr Tyr Leu Leu Lys Asp Asn
275 280 285

Pro Val Gln Thr Leu Leu Leu Cys Met Ala Ala Ile Gly His Asp Val
290 295 300

Gly His Pro Gly Thr Asn Asn Gln Leu Leu Cys Asn Cys Glu Ser Glu
305 310 315 320

Val Ala Gln Asn Phe Lys Asn Val Ser Ile Leu Glu Asn Phe His Arg

325

330

335

Glu Leu Phe Glu Gln Leu Leu Ser Glu His Trp Pro Gln Leu Leu Ser
 340 345 350

Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala Thr
 355 360 365

Asp Met Ala Leu His Ser Gln Tyr Glu Asp Arg Leu Met His Glu Asn
 370 375 380

Pro Met Lys Glu Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala Asp
 385 390 395 400

Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala Tyr
 405 410 415

Leu Ile Thr Leu Glu Phe Asn Asp Cys Ala Leu Leu Glu Thr Phe His
 420 425 430

Lys Ala His Arg Pro Glu Gln Asp Cys Phe Gly Asp Ser Tyr Lys Asn
 435 440 445

Val Asp Ser Pro Lys Glu Asp Leu Glu Ser Ile Gln Asn Ile Leu Val
 450 455 460

Asn Val Thr Asp Pro Asp Asp Ile Ile Lys Asp His Pro His Ile Pro
 465 470 475 480

Asn Gly Gln Ile Phe Phe Ile Asn Thr Phe Ala Glu Val Phe Phe Asn
 485 490 495

Alu Leu Ser Gln Lys Thr Ser Gly Leu Lys Phe Leu Ser Asp Asn Val
 500 505 510

Lys Ile Asn Lys Glu Tyr Trp Met Lys His Lys Lys Pro Gln
 515 520 525

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 <222> (1)..(2367)

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 tac aaa tcc aaa cat gct tct aaa ggc gct ttg aaa aga tra tcc aag 96
 Tyr Lys Ser Lys His Ala Ser Lys Gly Ala Leu Lys Arg Leu Tyr Lys
 20 25 30
 ggg aaa gtg gaa aaa gaa ccc gtg ggc aat ggc aaa cca gac aaa aaa 144
 Gly Lys Val Glu Lys Glu Pro Val Gly Thr Gly Lys Pro Asp Lys Gln
 35 40 45
 gll tca aaa ttg caa cgt aaa aac aag gca aaa caa tta agg gcc caa 192
 Val Ser Lys Leu Gln Arg Lys Asn Lys Ala Lys Gln Asn Arg Ala Gln
 50 55 60
 agy atc ttg gat tcc att gaa aac agg aaa tta ttc gaa gga aaa aat 240
 Arg Ile Asn Asp Ser Ile Glu Asn Arg Lys Leu Phe Glu Gly Lys Asn
 65 70 75 80
 ggc gct gcc aaa atc att acg att gtc ccg tta atg aat gat tta gac 288
 Gly Ala Ala Lys Ile Ile Thr Ile Val Pro Leu Val Asn Asp Leu Asp

85	90	95	
cca ttg gac atc ctt tac aag cta tta aag tgg gca gat gat gaa gga			336
Pro Leu Asp Ile Leu Tyr Lys Leu Leu Lys Cys Ala Asp Asp Glu Gly			
130	105	110	
acc atg gtg cag gaa gta gac tca aaa cgt ata ttt aat gtt cat ata			384
Glu Met Val Gln Glu Val Asp Ser Lys Arg Ile Phe Asn Val His Ile			
115	120	125	
acg aag lll auu ugc aat ctt aaa atc ata att cca gac atg acc aat			432
Lys Lys Phe Lys Ser Asn Leu Lys Ile Ile Ile Pro Asp Met Thr Asn			
130	135	140	
ttt ttg aac att tta gat tgc gct aaa gta gca gac ttt gtt gtg ttt			480
Phe Leu Asn Ile Leu Asp Cys Ala Lys Val Ala Asp Phe Val Val Phe			
145	150	155	160
ggg ctc agt ggt gtc caa gaa gtc gat gaa gaa ttt ggt gag cag acc			528
Gly Leu Ser Gly Val Gln Glu Val Asp Glu Gln Phe Gly Glu Gln Ile			
165	170	175	
atc cgt gcg tta gaa cta caa ggt att gct tca tat atc ggt gtc tta			576
Ile Arg Ala Leu Glu Leu Gln Gly Ile Ala Ser Tyr Ile Gly Val Ile			
180	185	190	
agc aac ctc tca gca gtc cat gaa aag gag aaa ttc caa ttg gat gtc			624
Ser Asn Leu Ser Ala Val His Glu Lys Glu Lys Phe Gln Leu Asp Val			
195	200	205	
acg caa tcc tta gaa agt tat ttc aag cac ttt ttc cca agt gaa gaa			672
Lys Gln Ser Leu Glu Ser Tyr Phe Lys His Phe Phe Pro Ser Glu Glu			
210	215	220	
cgt gtt tat aat ttg gaa aaa aac tca gac gct tta aat gtc ttg aga			720
Arg Val Tyr Asn Leu Glu Lys Asn Ser Asp Ala Leu Asn Val Leu Arg			
225	230	235	240
aca ttg tgg gag aag cta cca aga tca atc aat tgg aga gac aat aga			768
Thr Leu Cys Gln Arg Leu Pro Arg Ser Ile Asn Trp Arg Asp Asn Arg			
245	250	255	

ggc tac gta glt gct gac ttt gtt gat ttc gtt gaa acc tot ccc gat Gly Tyr Val Val Ala Asp Phe val Asp phe Val Glu Thr Ser Pro Asp 260 265 270	815
tct ggt gac ctg gta att gag ggg acc gtc cgt ggt att ggc ttc aac Ser Gly Asp Leu Val Ile Glu Gly Thr Val Arg Gly Ile Gly Phe Asn 275 280 285	866
gcc aat aga ctg gtc cat att cct gat ttt ggt gac ttc caa ctg aat Ala Asn Arg Leu Val His Ile Pro Asp Phe Gly Asp Phe Gln Leu Asn 290 295 300	912
aag ata gaa aaa atc agt gaa tct ccg cag aaa agg aaa ala ala aag Lys Ile Glu Lys Ile Ser Glu Ser Ser Gln Lys Arg Lys Ile Ile Tyr 305 310 315 320	960
gaa aaa gct aca gat agt ctg agc tta gag ctg gat tta caa aca gct Glu Lys Ala Thr Asp Ser Leu Ser Leu Glu Leu Asp Leu Gln Thr Val 325 330 335	1000
ttc gaa agt aat atg aat aga gat act atg gag gaa tat ggc cca gaa Phe Glu Ser Asn Met Asn Arg Asp Thr Leu Asp Glu Tyr Ala Pro Glu 340 345 350	1055
ggc acc gaa gat tgg tca gat tat gac gag gat ttt gag tac gac ggt Gly Thr Glu Asp Trp Ser Asp Tyr Asp Glu Asn Phe Glu Tyr Asp Gly 355 360 365	1104
ttg aca acc gcg aga tac gac gac aat ggc ttc tly cca ggg agg gaa Leu Thr Thr Ala Arg Tyr Asp Asp His Gly Phe Leu Pro Gly Arg Gln 370 375 380	1152
caa aca tca aaa aag gcg gcu gtc cct aag gga act tct gac tat caa Glu Thr Ser Lys Lys Ala Ala Val Pro Lys Gly Thr Ser Asp Tyr Gln 385 390 395 400	1200
gcg aag tgg tac ttg gat gac gtc att gac gca aat gag gaa gaa gag Ala Lys Trp Tyr Leu Asp Asp Val Ile Asp Ala Asn Glu Glu Glu Glu 405 410 415	1248
gca gaa ccg acc aat gga aag gat cag aca atg atg gaa att gat gat Ala Glu Gln Thr Asn Gly Lys Asp Glu Thr Met Met Glu Ile Asp Asp 1296	

430	435	440	
gaa atg atg gtg gag caa gac aat gaa gag gta gca ggc gac gaa gaa			1244
Glu Met Met Val Glu Glu Asp Asn Glu Glu Val Ala Gly Asp Glu Glu			
435	440	445	
tat gac ata gag gat aat gaa gga ttt gaa gag ctt tca ccc gaa gaa			1292
Tyr Asp Ile Glu Asp Asn Glu Gly Phe Glu Glu Leu Ser Pro Glu Glu			
450	455	460	
gaa gaa cgt cca ctg agg gaa ttt aga gat atg gaa aag gag gac aga			1440
Glu Glu Arg Glu Leu Arg Glu Phe Arg Asp Met Glu Lys Glu Asp Arg			
465	470	475	480
gag ttc ccc gat gag atc gaa cta gag ccc agt gaa tct gcc atc gaa			1488
Glu Phe Pro Asp Glu Ile Glu Leu Glu Pro Ser Glu Ser Ala Ile Glu			
485	490	495	
cgt ttg aaa agg tat agc ggt ttg aaa aac tta tcc aac tgt gat tgg			1536
Arg Leu Lys Arg Tyr Arg Gly Leu Lys Asn Leu Tyr Asn Cys Asp Trp			
500	505	510	
caa gtt gat gaa aag gac cca tca tca nna gag gaa tgg aaa cgt cta			1584
Gln Val Asp Glu Lys Asp Pro Ser Ser Pro Ala Glu Trp Lys Arg Leu			
515	520	525	
tta agg att ggt aat tcc aaa aac act aaa aac aga ttc ata aag gaa			1632
Leu Arg Ile Gly Asn Tyr Lys Asn Thr Lys Asn Arg Ile Ala Tyr Glu			
530	535	540	
acc aag cct gaa gca cag gcc att gca ggt gat cgt att agg atg ttc			1680
Thr Lys Asn Glu Ala Gln Ala Ile Ala Gly Asp Arg Ile Arg Met Phe			
545	550	555	560
atc agg ttt cct aag ttt ctg ctt gaa aag att caa gat cct aaa caa			1728
Ile Arg Phe Pro Lys Phe Leu Leu Glu Lys Ile Gln Asp Pro Lys Glu			
565	570	575	
cta tta ttt gct gtc tac gga tta cta ctt cat gaa cac aaa aat gag			1776
Leu Leu Phe Ala Val Tyr Gly Leu Leu Leu His Glu His Lys Asn Ala			
580	585	590	

496/762

gta gtc aac ttc tct cta caa aga tgg gaa caa tat gac aaa cct gtg	1824
Val Val Asn Phe Ser Leu Glu Arg Trp Glu Gln Tyr Asp Lys Pro Val	
595 600 605	
cct tct cag gag cct ctc gta gta caa tac ggt gtt aga aga tac act	1872
Pro Ser Glu Glu Pro Ile Val Val Gln Tyr Gly Val Arg Arg Tyr Thr	
610 615 620	
att caa cct cta ttt tct caa ggc tct aac agt cct aat aat gtt caa	1920
Ile Gln Pro Leu Phe Ser Gln Gly Ser Asn Ser Pro Asn Asn Val His	
625 630 635 640	
aag tat gaa agg ttt ctg cat caa gat aca gta tca gtc gcc aca tgt	1968
Lys Tyr Glu Arg Phe Leu His Pro Asp Thr Val Ser Val Ala Thr Cys	
645 650 655	
att gat ccc gta gat ttc acc cag tca cct gaa att ttt ttc aag caa	2016
Ile Ala Pro Val Asp Phe Thr Gln Ser Pro Ala Ile Phe Phe Lys Pro	
660 665 670	
tca caa aca gat gcc aaa aat att gaa tgg att ggt caa ggt aca ttc	2064
Ser Pro Thr Asp Ala Lys Asn Ile Glu Ser Ile Gly His Gly Thr Phe	
675 680 685	
ctg aac gca gac cat tca aga ata tta gca aag aga gcc att ttg acc	2112
Leu Asn Ala Asp His Ser Arg Ile Leu Leu Lys Arg Ala Ile Leu Thr	
690 695 700	
ggg cat cca ttc aga ttc caa aaa act gtc gtt act gta cgt tac atg	2160
Gly His Pro Phe Arg Phe His Lys Thr Val Val Thr Val Arg Tyr Met	
705 710 715 720	
ttt ttc aga caa gaa gat gtc gaa tgg ttc aag tct atc cca ctg ttc	2208
Phe Phe Arg Pro Glu Asp Val Glu Trp Phe Lys Ser Ile Pro Leu Phe	
725 730 735	
acc aaa tca ggt agy tca ggt ttc att aaa gaa agt ttg ggt aag caa	2256
Thr Lys Ser Gly Arg Ser Gly Phe Ile Lys Glu Ser Leu Gly Thr His	
740 745 750	
ggg tat ttc aag gct aca ttt gat ggt aaa tta tct ggc cag gat gtt	2304
Gly Tyr Phe Lys Ala Thr Phe Asp Gly Lys Leu Ser Ala Gln Asp Val	

755

760

765

gtt gcr atg tcc ttg tac aaa cgt atg tgg ccc atg cct tag tta cct 2353

Val Ala Met Ser Leu Tyr Lys Arg Met Trp Pro Met Pro Ser Asn Pro

770

775

780

tgg aat ggt atg taa

2367

Trp Asn Gly Met

785

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<211> 788

<212> F2T

<213> *Saccharomyces cerevisiae*

<400> 214

Met Ala Gly His Ser His Arg Ser Ser Asn Lys Asn Gly His Lys Ser

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5

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15

Tyr Lys Ser Lys His Ala Ser Tyr Gly Ala Leu Lys Arg Leu Tyr Lys

20

25

30

Gly Lys Val Glu Lys Glu Pro Val Gly Thr Gly Lys Pro Asp Lys Gln

35

40

45

Val Ser Lys Leu Gln Arg Lys Asn Lys Ala Lys Gln Leu Arg Ala Gln

50

55

60

Arg Ile Leu Asp Ser Ile Glu Asn Arg Lys Leu Phe Gln Gly Lys Asn

65

70

75

80

Gly Ala Ala Lys Ile Ile Thr Ile Val Pro Leu Val Asn Asp Leu Asp

85

90

95

Pro Leu Asp Ile Leu Tyr Lys Leu Leu Lys Cys Ala Asp Asp Glu Gly
100 105 110

Ile Met Val Gln Glu Val Asp Ser Lys Arg Ile Phe Asn Val His Phe
115 120 125

Lys Lys Phe Lys Ser Asn Leu Lys Ile Ile Ile Pro Asp Met Thr Asn
130 135 140

Phe Leu Asn Ile Leu Asp Cys Ala Lys Val Ala Asp Phe Val Val Phe
145 150 155 160

Gly Leu Ser Gly Val Gln Glu Val Asp Glu Glu Phe Gly Glu Gln Ile
165 170 175

Ile Arg Ala Leu Glu Leu Gln Gly Ile Ala Ser Tyr Ile Gly Val Ile
180 185 190

Ser Asn Leu Ser Ala Val His Glu Lys Glu Lys Phe Gln Leu Asp Val
195 200 205

Lys Gln Ser Leu Glu Ser Tyr Phe Lys His Phe Phe Pro Ser Glu Glu
210 215 220

Arg Val Tyr Asn Leu Glu Lys Asn Ser Asp Ala Leu Asn Val Leu Arg
225 230 235 240

Thr Leu Cys Glu Arg Leu Pro Arg Ser Ile Asn Thr Arg Asp Asn Arg
245 250 255

Gly Tyr Val Val Ala Asp Phe Val Asp Phe Val Glu Thr Ser Pro Asp
260 265 270

Ser Gly Asp Leu Val Ile Glu Gly Thr Val Arg Gly Ile Gly Phe Asn
275 280 285

Ala Asn Arg Leu Val His Ile Pro Asp Phe Gly Asp Phe Gln Leu Asn
290 295 300

Lys Ile Glu Lys Ile Ser Glu Ser Ser Gln Lys Arg Lys Ile Ile Lys
305 310 315 320

Glu Lys Ala Thr Asp Ser Leu Ser Leu Glu Leu Asp Leu Gln Thr Val
325 330 335

Phe Glu Ser Asn Met Asn Arg Asp Thr Leu Asp Glu Tyr Ala Pro Cys
340 345 350

Gly Thr Glu Asp Trp Ser Asp Tyr Asp Glu Asp Phe Glu Tyr Asp Gly
355 360 365

Leu Thr Thr Ala Arg Tyr Asp Asp His Gly Phe Leu Pro Gly Arg Glu
370 375 380

Glu Thr Ser Lys Lys Ala Ala Val Pro Lys Gly Thr Ser Asp Tyr Gln
385 390 395 400

Ala Lys Trp Tyr Leu Asp Asp Val Ile Asp Ala Asn Glu Glu Glu Glu
405 410 415

Ala Glu Gln Thr Asn Gly Lys Asp Glu Thr Met Met Gln Ile Asp Asp
420 425 430

Glu Met Met Val Gln Gln Asp Asn Glu Glu Val Ala Gly Asp Glu Glu
435 440 445

Tyr Asp Ile Glu Asp Asn Glu Gly Phe Glu Glu Leu Ser Pro Glu Glu
450 455 460

Glu Glu Arg Glu Leu Arg Glu Phe Arg Asp Met Glu Lys Glu Asp Arg
465 470 475 480

Glu Phe Pro Asp Glu Ile Glu Leu Glu Pro Ser Glu Ser Ala Ile Glu
485 490 495

Arg Leu Lys Arg Tyr Arg Gly Leu Lys Asn Leu Tyr Asn Cys Asp Trp
500 505 510

Gln Val Asp Glu Lys Asp Pro Ser Ser Pro Ala Glu Trp Lys Arg Leu
515 520 525

Leu Arg Ile Gly Asn Tyr Lys Asn Tyr Lys Asn Arg Ile Ile Lys Glu
530 535 540

Thr Lys Asn Glu Ala Glu Ala Ile Ala Gly Asp Arg Ile Arg Met Phe
545 550 555 560

Ile Arg Phe Pro Lys Phe Leu Leu Glu Lys Ile Gln Asp Pro Lys Gln
565 570 575

Leu Leu Phe Ala Val Tyr Gly Leu Leu Leu His Glu His Lys Asn Ala
580 585 590

Val Val Asn Phe Ser Leu Gln Arg Trp Glu Gln Tyr Asp Lys Pro Val
595 600 605

Pro Ser Gln Gln Pro Ile Val Val Gln Tyr Gly Val Arg Arg Tyr Thr
 610 615 620

Ile Gln Pro Leu Phe Ser Gln Gly Ser Asn Ser Pro Asn Asn Val His
 625 630 635 640

Lys Tyr Glu Arg Phe Leu His Pro Asp Thr Val Ser Val Ala Thr Cys
 645 650 655

Ile Ala Pro Val Asp Phe Thr Gln Ser Pro Ala Ile Phe Phe Lys Pro
 660 665 670

Ser Pro Thr Asp Ala Lys Asn Ile Glu Leu Ile Gly His Gly Thr Phe
 675 680 685

Leu Asn Ala Asp His Ser Arg Ile Leu Ala Tyr Arg Ala Ile Leu Thr
 690 695 700

Gly His Pro Phe Arg Phe His Lys Thr Val Val Thr Val Arg Tyr Met
 705 710 715 720

Phe Thr Arg Pro Glu Asp Val Glu Trp Phe Lys Ser Ile Pro Leu Phe
 725 730 735

Thr Lys Ser Gly Arg Ser Gly Phe Ile Lys Glu Ser Leu Gly Thr His
 740 745 750

Gly Tyr Phe Lys Ala Thr Phe Asp Gly Lys Leu Ser Ala Gln Asp Val
 755 760 765

Val Ala Met Ser Leu Tyr Lys Arg Met Trp Phe Met Phe Ser Leu Pro
 770 775 780

Trp Asn Gly Met
 785

<210> 215
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 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1296)

<400> 215
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 Met Val Val Gln Asn Ser Pro Val Ser Ser Val His Thr Ala Asn Phe
 1 5 10 15
 tct gaa cgg ggg agc aat acc aga aca atg acg tat aaa aat aag att 96
 Ser Gln Arg Gly Ser Asn Thr Arg Thr Met Thr Tyr Lys Asn Lys Leu
 20 25 30
 aat gtt tgc ttc gat gac atc cta aaa gtt gga gca gaa atg atg atg 144
 Thr Val Cys His Asp Asp Ile Leu Tyr Val Gly Ala Gln Met Met Met
 35 40 45
 caa caa cag tta aaa aat gla caa cta gat tct tat ctc gtc aat ggt 192
 Gln Gln Gln Leu Lys Asn Val Gln Leu Asp Ser Tyr Leu Val Asn Gly
 50 55 60
 ttc agt caa tct cag caa aaa tta ttg aaa gag aag gtt aaa tta ttt 240
 Phe Ser Gln Ser Gln Gln Lys Leu Leu Tyr Glu Lys Val Lys Leu Phe
 65 70 75 80
 cat gga att tta gat gat tta gag act tct cta agc cag agt tct tca 288
 His Gly Ile Leu Asp Asp Leu Glu Thr Ser Leu Ser Gln Ser Ser Ser
 95 90 95

tat tta gaa act ctt act gca ctc gga aaa gaa aag gag aaa gaa aga	334
Tyr Leu Glu Thr Leu Thr Ala Leu Gly Lys Glu Lys Glu Lys Glu Arg	
100 105 110	
gag gaa gct gaa aaa aag agg gct gaa caa gan aat atg agg aag gtt	384
Glu Glu Ala Glu Lys Lys Arg Ala Gln Gln Gln Asn Met Arg Lys Val	
115 120 125	
aga gaa aan gaa gaa tta aaa aag aga caa gaa ctc gaa gaa gcc tcc	432
Arg Glu Gln Glu Glu Leu Lys Lys Arg Gln Glu Leu Glu Glu Ala Ser	
130 135 140	
aaa gag gag aca ctc cag caa aat tca aag gaa aaa aac ggc ctt ggt	480
Gln Gln Gln Gln Leu Gln Gln Asn Ser Lys Glu Lys Asn Gly Leu Gly	
145 150 155 160	
ttg aac ttc tcc aca aca gaa cct gcg aac aca acg gat gcc aac ggt	528
Leu Asn Phe Ser Thr Thr Ala Pro Ala Ser Thr Thr Asp Ala Asn Gly	
165 170 175	
tcc aaa gag aat tat caa gaa att gga tct ctt cac tca tca tgt aca	576
Ser Tyr Glu Asn Tyr Gln Glu Leu Gly Ser Leu Gln Ser Ser Ser Glu	
180 185 190	
acc caa cll gag aac gcu aat gct gct aat aac ggt gcc gaa ttt tct	624
Thr Gln Leu Glu Asn Ala Asn Ala Ala Asn Asn Gly Ala Ala Phe Ser	
195 200 205	
ccc tta acc act act cga atc caa agc cag cag gcc caa ccc tgg gat	672
Pro Leu Thr Thr Thr Arg Ile Gln Ser Gln Gln Ala Gln Pro Ser Asp	
210 215 220	
gta atg ttc aac gat tta aac tct atg gat att tgg atg ttt tca ggc	720
Val Met Phe Asn Asp Leu Asn Ser Met Asp Ile Ser Met Phe Ser Gly	
225 230 235 240	
cli gag agt act ggt ttt gac tcc aca gcc ttc aat gcc acg gtg gac	768
Leu Asp Ser Thr Gly Phe Asp Ser Thr Ala Phe Asn Ala Thr Val Asp	
245 250 255	
gaa acc aaa gcc ttt gac gat aat gac tca ggt aac aac tuc aat gac	816

Glu Thr Tyr Gly Phe Asp Asp Asn Asp Ser Gly Asn Asn Tyr Asn Asp			
260	255	270	
ala aal ali lct lct lct att gaa aac aac ata aat aat aat atc aat agc	864		
Ile Asn Ile Ser Ser Ile Glu Asn Arg Ile Asn Asn Asn Ile Asn Ser			
275	280	285	
acc aag aac ggc aag gat aac aac aac gaa agc aac nan aat aac aac	912		
Thr Lys Asn Gly Lys Asp Asn Asn Asn Glu Ser Asn Lys Asn Asn Asn			
290	295	300	
ggc gat gaa aag aat aag aac aac aac gag gac aac gag aac aac aac	960		
Gly Asp Glu Lys Asn Lys Asn Asn Asn Glu Asp Asn Glu Asn Asn Asn			
305	310	315	320
aac agc agt gag aag aac aac aal aat aat aat aat aac aat aac aac	1008		
Asn Ser Ser Glu Lys Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn			
325	330	335	
aat gac gat aac ggc aac aac aac aac aac aac agt ggc aac gac aat	1056		
Asn Asp Asp Asn Gly Asn Asn Asn Asn Asn Asn Ser Gly Asn Asp Asn			
340	345	350	
aac aat acc acc aac aac gac agc aat aac aag aac aat lal alu aul	1104		
Asn Asn Thr Thr Asn Asn Asp Ser Asn Asn Lys Asn Asn Ser Ile Thr			
355	360	365	
acc gga aat gat aat gaa aat ata gtt aat aat gat tta cca aac acc	1152		
Thr Gly Asn Asp Asn Glu Asn Ile Val Asn Asn Asp Leu Phe Thr Thr			
370	375	380	
gtt gtt toc aat cct gga gat aac cct cct cca gcc gat aac ggt gaa	1200		
Val Val Ser Asn Pro Gly Asp Asn Pro Pro Pro Ala Asp Asn Gly Glu			
385	390	395	400
gaa tac ttg aca tta aat gat lls aac gaa ctt aat att gac tgg tog	1248		
Glu Tyr Leu Thr Leu Asn Asp Phe Asn Asp Leu Asn Ile Asp Trp Ser			
405	410	415	
acc act gga gat aat ggc gaa tta gac ctc agc gcc ttc aat ata tag	1296		
Thr Thr Gly Asp Asn Gly Glu Leu Asp Leu Ser Gly Phe Asn Ile			
420	425	430	

<210> 216

<211> 431

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 216

Met	Val	Val	Gln	Asn	Ser	Pro	Val	Ser	Ser	Val	Phe	Thr	Ala	Asn	Phe
1				5						10				15	

Ser	Glu	Arg	Gly	Ser	Asn	Thr	Arg	Thr	Met	Thr	Tyr	Lys	Asn	Lys	Leu
			20					25					30		

Thr	Val	Cys	Phe	Asp	Asp	Ile	Leu	Lys	Val	Gly	Ala	Glu	Met	Met	Met
		35					40					45			

Gln	Gln	Gln	Leu	Lys	Asn	Val	Gln	Leu	Asp	Ser	Tyr	Leu	Val	Asn	Gly
		51					55				60				

Phe	Ser	Gln	Ser	Gln	Lys	Leu	Leu	Lys	Gln	Lys	Val	Lys	Leu	Phe	
65					70				75					80	

His	Gly	Ile	Leu	Asp	Asp	Leu	Glu	Thr	Ser	Leu	Ser	Glu	Ser	Ser	Ser
			85						90					95	

Tyr	Leu	Glu	Thr	Leu	Thr	Ala	Leu	Gly	Lys	Glu	Lys	Glu	Lys	Glu	Arg
			103					105						110	

Glu	Gln	Ala	Glu	Lys	Lys	Arg	Ala	Glu	Gln	Glu	Asn	Met	Arg	Lys	Val
		115						120						125	

Arg	Gln	Gln	Gln	Gln	Leu	Lys	Lys	Arg	Gln	Glu	Leu	Glu	Glu	Ala	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140	
Gln Gln Glu Glu Leu Gln Glu Asn Ser Lys Glu Lys Asn Gly Leu Gly			
145	150	155	160
Leu Asn Phe Ser Thr Thr Ala Pro Ala Asn Thr Thr Asp Ala Asn Gly			
	165	170	175
Ser Lys Glu Asn Tyr Gln Glu Leu Gly Ser Leu Gln Ser Ser Ser Gln			
	180	185	190
Thr Gln Leu Glu Asn Ala Asn Ala Ala Asn Asn Gly Ala Ala Phe Ser			
	195	200	205
Pro Leu Thr Thr Thr Arg Ile Gln Ser Glu Gln Ala Glu Pro Ser Asp			
	210	215	220
Val Met Phe Asn Asp Leu Asn Ser Met Asn Ile Ser Met Phe Ser Gly			
	225	230	235
Leu Asp Ser Thr Gly Phe Asp Ser Thr Ala Phe Asn Ala Thr Val Asp			
	245	250	255
Glu Thr Lys Gly Phe Asp Asp Asn Asp Ser Gly Asn Asn Tyr Asn Asp			
	260	265	270
Ile Asn Ile Ser Ser Ile Glu Asn Asn Ile Asn Asn Asn Ile Asn Ser			
	275	280	285
Thr Lys Asn Gly Lys Asp Asn Asn Asn Glu Ser Asn Lys Asn Asn Asn			
	290	295	300

Gly Asp Glu Lys Asn Lys Asn Asn Asn Glu Asp Asn Glu Asn Asn Asn
305 310 315 320

Asn Ser Ser Glu Lys Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
325 330 335

Asn Asp Asp Asn Gly Asn Asn Asn Asn Asn Asn Ser Gly Asn Asp Asn
340 345 350

Asn Asn Thr Thr Asn Asn Asp Ser Asn Asn Lys Asn Asn Ser Ile Thr
355 360 365

Thr Gly Asn Asp Asn Glu Asn Ile Val Asn Asn Asp Leu Pro Thr Thr
370 375 380

Val Val Ser Asn Pro Gly Asp Asn Pro Pro Pro Ala Asp Asn Gly Gly
385 390 395 400

Glu Tyr Leu Thr Leu Asn Asp Phe Asn Asp Leu Asn Ile Asp Thr Ser
405 410 415

Thr Thr Gly Asp Asn Gly Glu Leu Asp Leu Ser Gly Phe Asn Ile
420 425 430

<210> 217

<211> 1941

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1941)

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1 5 10 15
tct caa ttg aac att caa ttg tct caa gac gag cat tog cag gtc gaa 96
Ser Glu Leu Asn Ile Gln Leu Ser Gln Asp Glu His Ser Gln Val Glu
20 25 30
cag act tgc gtc aaa cta ttg gat tct gga tgt gag aat cca ggc gat 144
Gln Thr Cys Val Lys Leu Leu Asp Ser Gly Cys Glu Asn Pro Ala Asp
35 40 45
gta ttt aga cgt tgc tta gta gct gtt atc caa cag gac aag tat caa 192
Val Phe Arg Arg Cys Leu Val Ala Val Ile Gln Gln Asp Lys Tyr Glu
50 55 60
aag gct tta cat tat tta aaa aaa ttc aaa cat ata gct gac aag tac 240
Lys Ala Leu His Tyr Leu Lys Cys Phe Lys His Ile Asp Asp Tyr Tyr
65 70 75 80
ggc cgc aaa ttt ggc cta gaa aaa ttg tac att ttc tat aaa ttg aat 288
Gly Arg Lys Phe Ala Leu Glu Lys Leu Tyr Ile Phe Tyr Lys Leu Asn
85 90 95
atg cca gat gaa ttc aac aca ttg tac aca gaa att atc aca gat gat 336
Met Pro Asp Glu Phe Asn Thr Leu Tyr Thr Ala Ile Ile Thr Asp Asp
100 105 110
ctc gal cag gtc cta aaa aag gat atc gag taa ctt aga ggt atc cta 384
Leu Asp Thr Val Leu Lys Lys Asp Phe Glu Ser Leu Arg Gly Ile Leu
115 120 125
cgt gtc aga gct cca tat tgt tat aaa aat ggg ctg tac caa gaa gct 432
His Val Arg Ala Gln Tyr Cys Tyr Lys Asn Gly Leu Tyr Glu Gln Ala
130 135 140
ttt aaa ata tat caa cat tta gca agt cac aat gag aag gat cag gat 480
Phe Lys Ile Tyr Gln His Leu Ala Ser His Asn Glu Lys Asp Gln Asp
145 150 155 160

agc caa att gaa ctc tct tgt aac gaa agg gtt ccg cta tcc gtt gcg	528
Ser Gln Ile Glu Leu Ser Cys Asn Glu Arg Val Pro Leu Ser Val Ala	
165 170 175	
aca gag tta atg aac aga tta ccc tta gtc act cct atg gat gaa tct	576
Thr Glu Leu Met Asn Arg Ser Pro Leu Val Thr Pro Met Asp Glu Ser	
180 185 190	
tcc tac gat tta tta ttc aat gaa tca ttc atc atg gca tcc gta ggt	624
Ser Tyr Asp Leu Leu Phe Asn Glu Ser Phe Ile Met Ala Ser Val Gly	
195 200 205	
aaa tat gac aag gct atc gaa cta tta gaa aaa gcc ctt caa gga gcc	672
Lys Tyr Asp Lys Ala Ile Glu Leu Leu Glu Lys Ala Leu Gln Gly Ala	
210 215 220	
acg aat gaa ggc tat caa aac gat att aat act att aaa ttg caa tta	720
Thr Asn Glu Gly Tyr Gln Asn Asp Ile Asn Thr Ile Lys Leu Gln Leu	
225 230 235 240	
tta ttt gtt ttg caa atg ctg ggg aaa acc gct caa agt aaa gaa atc	768
Ser Phe Val Leu Gln Met Val Gly Lys Thr Ala Glu Ser Lys Glu Ile	
245 250 255	
tta asp gcc tta ttg ccg gaa ctg aaa gcc gct tct caa ttc ttt tta	816
Leu Lys Gly Leu Leu Glu Glu Leu Lys Ala Asp Ser Pro Phe Ser Leu	
260 265 270	
att tgt caa aat aac cta aat gcc ttt qtt cat ttc tct aac tac aat	864
Ile Cys Gln Asn Asn Leu Asn Ala Phe Val Asp Phe Ser Lys Tyr Asn	
275 280 285	
aca aac ttc aat tta ctg tta agg gaa tta aac gta gaa aaa cta aac	912
Thr Asn Phe Asn Leu Leu Leu Arg Glu Leu Asn Val Glu Lys Leu Asn	
290 295 300	
act ttt aat tta caa acc ttc acc cat gaa caa tgg tca aac att caa	960
Thr Phe Asn Leu Glu Thr Phe Thr His Glu Gln Trp Ser Asn Ile Gln	
305 310 315 320	
ccc aat gta ctt ttc ctg cgt ttg ttc aac aac gtc aaa att cac ttt	1008
Arg Asn Val Leu Phe Leu Arg Leu Phe Asn Asn Val Lys Ile His Ser	

323	330	335	
caa gag tcc ctt tta tca aga acg ttc gat aac tac tct aag tta gtt			1055
Gln Gln Ser Leu Leu Ser Arg Thr Phe Asp Lys Tyr Ser Lys Leu Val			
340	345	350	
gac aat gtt act ttg gaa agc tac aag acg cag gcc aag aaa ctt tac			1104
Asp Asn Val Thr Leu Glu Ser Tyr Lys Thr Gln Ala Lys Lys Leu Tyr			
355	360	365	
cac cac act aca aaa acc att tta agt gga aca gat gga agt aag att			1152
His His Thr Thr Lys Thr Ile Leu Ser Gly Thr Asp Gly Ser Thr Ile			
370	375	380	
gga ata ttn cta ctg acr atc caa ttg cta ata ata gag aag gaa tgg			1200
Gly Ile Leu Leu Leu Thr Ile Gln Leu Leu Ile Ile Glu Lys Glu Trp			
385	390	395	400
gaa aat got atc aga ate gga gaa tta ttt tta aat gaa agc tgg aaa			1248
Glu Asn Ala Ile Arg Ile Gly Glu Leu Phe Leu Asn Glu Ser Trp Lys			
405	410	415	
tug tcc ttt gaa aaa ttc aac gat tca daa gcc atc gtc tgt tac atc			1296
Ser Ser Phe Glu Lys Phe Asn Asp Ser Gln Ala Ile Val Cys Tyr Ile			
420	425	430	
tta ttt gaa tta tac aag att aag gga aga aac aac tcc aca agt gtc			1344
Leu Phe Glu Leu Tyr Lys Ile Lys Gly Arg Asn Asn Ser Lys Ser Val			
435	440	445	
ctg ctt aaa aaa tta ggc tcc gtg aga gtc caa ttg agc gga aaa atc			1392
Leu Leu Lys Lys Leu Gly Ser Val Arg Val Gln Leu Ser Gly Lys Ile			
450	455	460	
caa gaa aac ata cca ttt tgg aaa cac gtc ggg ttt gaa tra ttg tcc			1440
Gln Glu Asn Ile Pro Phe Trp Lys His Val Gly Phe Glu Leu Leu Ser			
465	470	475	480
atg ggt aat got aaa gaa tgg aag got tta ctc aga gag att tca aac			1488
Met Gly Asn Ala Lys Glu Ser Lys Ala Leu Leu Arg Glu Ile Ser Asn			
485	490	495	

ttt agt aaa ggt gat gca gat gtc ctt ghr gac aga gtt gtt tog tca 1536
 Phe Ser Lys Cly Asp Ala Asp val leu Val Asp Arg Val Val Ser Ser
 510 505 510

gat tct tly gat ata gca caa ggt ata gat cta gtg aga gat att gat 1584
 Asp Ser Leu Asp Ile Ala Gln Gly Ile Asp leu Val Arg Asp Ile Asp
 515 520 525

att gat aaa tta att caa ctt gyl gty aaa coo tta gaa tog tca gca 1632
 Ile Asp Lys Leu Ile Glu Leu Gly Val Lys Pro Leu Glu Ser Ser Ala
 530 535 540

aag aga agt aaa aac aac gca gll agy aaa gtt caa aag aga aza gtt 1680
 Lys Arg Ser Lys Asn Thr Ala Val Ser Tyr Val Gln Lys Arg Lys Val
 545 550 555 560

tta gag cta aag aag aca aga aag att aaa cgc ctc gaa aza ttt tta 1728
 Leu Glu Leu Lys Lys Lys Arg Lys Ile Lys Arg Leu Glu Lys Phe Leu
 565 570 575

caa ggt cgc gac acc tcc aca tta ctt gyl cct gaa agy tgg ctg cca 1776
 Gln Gly Arg Asp Thr Ser Lys Leu Pro Asp Pro Glu Arg Trp Leu Pro
 580 585 590

tta aga gac agy tct act tat agy cca aag aca aca caa ctt gca 1824
 Leu Arg Asp Arg Ser Thr Tyr Arg Pro Lys Lys Lys Gln Gln Cys Ala
 595 600 605

aaa caa act caa ggt ggt gct atg aac aaa aaa tca gaa cag gcc ctt 1872
 Lys Gln Thr Gln Gly Gly Ala Met Asn Lys Lys Ser Glu Gln Ala Leu
 610 615 620

gac ata tca aag aaa ggy aag ccc act gtt aat aaa aag cct aag aac 1920
 Asp Ile Ser Lys Lys Gly Lys Pro Thr Val Asn Lys Lys Pro Lys Asn
 625 630 635 640

aag aag aag ggc cgt aaa tag 1941
 Lys Lys Lys Gly Arg Lys
 645

<211> 646

<212> FET

<213> *Saccharomyces cerevisiae*

<400> 218

Met Lys Glu Ser Lys Lys Met Ala Lys Asp Asn Leu Thr Asn Leu Lys

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Ser Gln Leu Asn Ile Gln Leu Ser Gln Asp Glu His Ser Gln Val Glu

20 25 30

Gln Thr Cys Val Lys Leu Leu Asp Ser Gly Cys Glu Asn Pro Ala Asp

35 40 45

Val Phe Arg Arg Cys Leu Val Ala Val Ile Gln Gln Asp Lys Tyr Gln

50 55 60

Lys Ala Leu His Tyr Leu Lys Lys Phe Lys His Ile Asp Asp Lys Tyr

65 70 75 80

Gly Arg Lys Phe Ala Leu Glu Lys Leu Tyr Ile Phe Tyr Lys Leu Asn

85 90 95

Met Pro Asp Glu Phe Asn Thr Leu Tyr Thr Ala Ile Ile Thr Asp Asp

100 105 110

Leu Asp Thr Val Leu Lys Lys Asp Ile Glu Ser Leu Arg Gly Ile Leu

115 120 125

His Val Arg Ala Gln Tyr Cys Tyr Lys Asn Gly Leu Tyr Gln Glu Ala

130 135 140

Phe Lys Ile Tyr Gln His Leu Ala Ser His Asn Glu Lys Asp Gln Asp
 145 150 155 160

Ser Gln Ile Glu Leu Ser Cys Asn Gln Arg Val Pro Leu Ser Val Ala
 165 170 175

Thr Glu Leu Met Asn Arg Ser Pro Leu Val Thr Pro Met Asp Glu Ser
 180 185 190

Ser Tyr Asp Leu Leu Phe Asn Glu Ser Phe Ile Met Ala Ser Val Gly
 195 200 205

Lys Tyr Asp Lys Ala Ile Glu Leu Leu Glu Lys Ala Leu Gln Gly Ala
 210 215 220

Thr Asn Glu Gly Tyr Gln Asn Asp Ile Asn Thr Ile Lys Leu Gln Leu
 225 230 235 240

Ser Phe Val Leu Gln Met Val Gly Lys Thr Ala Gln Ser Lys Glu Ile
 245 250 255

Leu Lys Gly Leu Leu Gln Glu Leu Lys Ala Asp Ser Pro Phe Ser Leu
 260 265 270

Ile Cys Gln Asn Asn Leu Asn Ala Phe Val Asp Phe Ser Lys Tyr Asn
 275 280 285

Thr Asn Phe Asn Leu Leu Leu Arg Glu Leu Asn Val Glu Lys Leu Asn
 290 295 300

Thr Phe Asn Leu Gln Thr Phe Thr His Glu Gln Trp Ser Asn Ile Gln
 305 310 315 320

Arg Asn Val Leu Phe Leu Arg Leu Phe Asn Asn Val Lys Ile His Ser
325 330 335

Gln Glu Ser Leu Leu Ser Arg Thr Phe Asp Lys Tyr Ser Lys Leu Val
340 345 350

Asp Asn Val Thr Leu Glu Ser Tyr Lys Thr Gln Ala Lys Lys Leu Tyr
355 360 365

His His Thr Thr Lys Thr Ile Leu Ser Gly Thr Asp Gly Ser Thr Ile
370 375 380

Gly Ile Leu Leu Leu Thr Ile Gln Leu Leu Ile Ile Glu Lys Glu Trp
385 390 395 400

Glu Asn Ala Ile Arg Ile Gly Glu Leu Phe Leu Asn Glu Ser Trp Lys
405 410 415

Ser Ser Phe Glu Lys Phe Asn Asp Ser Gln Ala Ile Val Cys Tyr Ile
420 425 430

Leu Phe Glu Leu Tyr Lys Ile Lys Gly Arg Asn Asn Ser Lys Ser Val
435 440 445

Leu Leu Lys Lys Leu Gly Ser Val Arg Val Gln Leu Ser Gly Lys Ile
450 455 460

Gln Glu Asn Ile Pro Phe Trp Lys His Val Gly Phe Glu Leu Leu Ser
465 470 475 480

Met. Gly Asn Ala Lys Glu Ser Lys Ala Leu Leu Arg Glu Ile Ser Asn
 485 490 495

Phe Ser Lys Gly Asp Ala Asp Val Leu Val Asp Arg Val Val Ser Ser
 500 505 510

Asp Ser Leu Asp Ile Ala Gln Gly Ile Asp Leu Val Arg Asp Ile Asp
 515 520 525

Ile Asp Lys Leu Ile Gln Leu Gly Val Lys Pro Leu Glu Ser Ser Ala
 530 535 540

Lys Arg Ser Lys Asn Thr Ala Val Ser Lys Val Gln Lys Arg Lys Val
 545 550 555 560

Leu Glu Leu Lys Lys Lys Arg Lys Ile Lys Arg Leu Glu Lys Phe Leu
 565 570 575

Gln Gly Arg Asp Thr Ser Lys Leu Pro Asp Pro Glu Arg Trp Leu Pro
 580 585 590

Leu Arg Asp Arg Ser Thr Tyr Arg Pro Lys Lys Lys Gln Gln Gly Ala
 595 600 605

Lys Gln Thr Gln Gly Gly Ala Met Asn Lys Lys Ser Glu Gln Ala Leu
 610 615 620

Asp Ile Ser Lys Lys Gly Lys Pro Thr Val Asn Lys Lys Pro Lys Asn
 625 630 635 640

Lys Lys Lys Gly Arg Lys
 645

<210> 219
 <211> 543
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> {1}..(543)

<400> 219
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 Met Phe Ala Thr Arg Ser Phe Cys Leu Ser Ser Ser Leu Phe Arg Pro
 1 5 10 15
 gct gcc caa ctg ttg cgc cct gct ggc cgc tct act tta cga aat gtt 96
 Ala Ala Gln Leu Leu Arg Pro Ala Gly Arg Ser Thr Leu Arg Asn Val
 20 25 30
 tgg agt cgc tcc att gca acc gac cat ttg acc cag aag gag gct aat 144
 Trp Arg Arg Ser Ile Ala Thr Glu His Leu Thr Glu Thr Glu Ala Asn
 35 40 45
 tct cgt ctt gct tcc cag cgt gtt cgc cgt cca aat tct cct cat ttg 192
 Ser Arg Leu Ala Ser Gln Arg Val His Arg Pro Asn Ser Pro His Leu
 50 55 60
 act aia tat gaa cct caa ttg act tgg tat cta tcc agt tta cat cgt 240
 Thr Ile Tyr Gln Pro Gln Leu Thr Trp Tyr Leu Ser Ser Ser Leu His Arg
 65 70 75 80
 atc act ggt tgt gtt gtc gcc ggt act ctt tat gct tto got atg ggc 288
 Ile Thr Gly Cys Val Val Ala Gly Thr Leu Tyr Ala Phe Ala Met Gly
 85 90 95
 taa ttg gtg gct cct ctc gct gga tac tot ttg gat aca get acc all 336
 Tyr Leu Val Ala Pro Leu Ala Gly Tyr Ser Leu Asp Thr Ala Thr Ile
 100 105 110
 tct ggt ctt aat cag caa gtt ccc acc tgg atc aaa gtt cct gct aag 334

Ser Gly Leu Ile Gln Gln Val Pro Thr Trp Ile Lys Val Pro Ala Lys
 115 120 125

 ttt gtt att tot tat cct ttg act ttc cac att ttt aac ggt att cgt 432
 Phe Val Ile Ser Tyr Pro Leu Thr Phe His Ile Phe Asn Gly Ile Arg
 130 135 140

 cac ttg atc tgg gat acc acc aag gag tta agt cta aag ggt gtc tat 460
 His Leu Ile Trp Asp Thr Thr Lys Glu Leu Ser Leu Lys Gly Val Tyr
 145 150 155 160

 cgt acc ggt tat gct gtc ctt gcc ctt tcc gtt ttg acc tot gga tat 528
 Arg Thr Gly Tyr Ala Val Leu Ala Leu Ser Val Leu Thr Ser Gly Tyr
 165 170 175

 ttt gcg atg att tag 543
 Phe Ala Met Ile
 180

<210> 220
 <211> 180
 <212> PRT
 <213> *Caccharomyces cerevisiae*

 <400> 220

Met Phe Ala Thr Arg Ser Phe Cys Leu Ser Ser Ser Leu Phe Arg Pro
 1 5 10 15

Ala Ala Gln Leu Leu Arg Pro Ala Gly Arg Ser Thr Leu Arg Asn Val
 20 25 30

Trp Arg Arg Ser Ile Ala Thr Glu His Leu Thr Gln Thr Glu Ala Asn
 35 40 45

Ser Arg Leu Ala Ser Gln Arg Val His Arg Pro Asn Ser Pro His Leu
 50 55 60

Thr Ile Tyr Glu Pro Gln Leu Thr Trp Tyr Leu Ser Ser Leu Asn Arg
 65 70 75 80

Ile Thr Gly Cys Val Val Ala Gly Thr Leu Tyr Ala Asn Ala Met Gly
 85 90 95

Tyr Leu Val Ala Pro Leu Ala Gly Tyr Ser Leu Asp Thr Ala Thr Ile
 100 105 110

Ser Gly Leu Ile Gln Glu Val Pro Thr Trp Ala Tyr Val Pro Ala Tyr
 115 120 125

Phe Val Ile Ser Tyr Pro Leu Thr Phe His Ile Phe Asn Gly Ile Arg
 130 135 140

His Leu Ile Trp Asp Thr Thr Lys Glu Leu Ser Leu Lys Gly Val Tyr
 145 150 155 160

Arg Thr Gly Tyr Ala Val Leu Ala Leu Ser Val Leu Thr Ser Gly Tyr
 165 170 175

Phe Ala Met Ile
 180

<210> 221
 <211> 262
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> {1}..(262)

<400> 221
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 Met Val Thr Pro Arg Glu Pro Lys Lys Arg Thr Thr Arg Lys Lys Lys
 1 5 10 15

gac uca aat gcc cct aag agg gct ttg tcc gcc tac atg ttt ttc gct 80
 Asp Pro Asn Ala Pro Lys Arg Ala Leu Ser Ala Tyr Met Phe Phe Ala
 20 25 30

aac gaa aac aga gat att gtt cgt tct gaa aat uca gat atc aca ttt 120
 Asn Glu Asn Arg Asp Ile Val Arg Ser Glu Asn Pro Asp Ile Thr Phe
 35 40 45

gga caa gtc gcc aag aag ttt ggt gag aag tgg aag gct cta aag cca 160
 Gly Gln Val Gly Lys Lys Leu Gly Glu Lys Trp Tyr Ala Asn Thr Pro
 50 55 60

gag gaa aag cag cct tac gag gcc aag gcc cag gcc gat aag aag aga 200
 Glu Glu Lys Gln Pro Tyr Glu Ala Lys Ala Gln Ala Asp Lys Lys Arg
 65 70 75 80

tat gaa tcc gaa aag gag tta tat aac gcc act ttg gct tag 240
 Tyr Glu Ser Glu Lys Glu Leu Tyr Asn Ala Thr Leu Ala
 85 90

<210> 222
 <211> 93
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 222
 Met Val Thr Pro Arg Glu Pro Lys Lys Arg Thr Thr Arg Lys Lys Lys
 1 5 10 15

Asp Pro Asn Ala Pro Lys Arg Ala Leu Ser Ala Tyr Met Phe Phe Ala
 20 25 30

Asn Gln Asn Arg Asp Ile Val Arg Ser Glu Asn Pro Asp Ile Thr Phe
35 40 45

Gly Gln Val Gly Lys Lys Leu Gly Gln Lys Trp Lys Ala Leu Thr Pro
50 55 60

Glu Gln Lys Gln Pro Tyr Glu Ala Lys Ala Gln Ala Asp Lys Lys Arg
65 70 75 80

Tyr Glu Ser Gln Lys Glu Leu Tyr Asn Ala Thr Leu Ala
85 90

<210> 223

<211> 1110

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> [1]..(1110)

<400> 223

atg aat cag agc gat agc agc ttg atg gat tta cca atg gag ata cat 40
Met Asn Gln Ser Arg Ser Ser Leu Met Asp Leu Pro Leu Glu Ile His
1 5 10 15

tta tca tta cta gag tac gtg acc aat gac att cgt gct gtc aat aaa 80
Leu Ser Leu Leu Glu Tyr Val Pro Asn Gln Leu Arg Ala Val Asn Lys
20 25 30

tac ttc tac gtc ttg cat aac cac agc lal aag aag aag agt ttg cgc 144
Tyr Phe Tyr Val Leu His Asn His Ser Tyr Lys Glu Lys Ser Leu Ala
35 40 45

tgg ata gct gag gac aac tat ata tgg gcc gtc gtc aaa cat tca tta 192
Trp Ile Ala Glu Asp Asn Tyr Ile Trp Ala Val Val Lys His Ser Leu
50 55 60

tgt tta tat tat gtu aag agt ttg guc cuu ctt cga cag cat gcc aqa gaa	240
Cys Leu Tyr Val Lys Ser Leu Asp Pro Leu Arg Gln His Ala Arg Glu	
65 70 75 80	
atc att caa gaa acg aag gaa cca ggt ttt ant gtg cca ctg tgc atg	288
Ile Ile Gln Glu Thr Lys Glu Pro Gly Phe Asn Val Pro Leu Cys Met	
55 60 65	
act aaa tac aic gca gat tct tgg tat att gta tac aat gag ctg caa	336
Thr Lys Tyr Ile Ala Asp Ser Trp Tyr Ile Val Tyr Asn Ala Leu Gln	
100 105 110	
tat cct gga aag ata att aat atg gga tgg gan aaa tat acc aaa agt	264
Tyr Pro Gly Lys Ile Ile Asn Met Gly Trp Asp Lys Tyr Thr Lys Ser	
115 120 125	
caa gat toa aat ggt tct cat tct acc agt aac ttt aat agt cgg ccc	432
Glu Asp Ser Asn Gly Ser Asp Ser Thr Ser Asn Phe Asn Ser Arg Pro	
130 135 140	
aag gaa aag act ctt atg cag tgg tgg aca gct lla cct gtt aac ttt	480
Lys Glu Arg Thr Leu Met Gln Ser Leu Thr Ala Leu Pro Val Asn Phe	
145 150 155 160	
tgg tac agg aag aag gac gag cct aca cgg gta aac gtt tgg ttt tat	528
Trp Ser Arg Arg Lys Asp Glu Pro Thr Pro Val Asn Val Trp Phe Tyr	
165 170 175	
gta aaa aat gag cnc gtt gcc aga tac aca cag aaa att att acg gaa	576
Val Lys Asn Ala His Val Ala Arg Tyr Ile Pro Lys Ile Ile Thr Glu	
180 185 190	
ata ggc ata tgc aac tat ggg ccg aag cag atc gtg gca agt gca gga	624
Ile Gly Ile Cys Asn Tyr Gly Pro Lys Gln Ile Val Ala Ser Ala Gly	
195 200 205	
tat atc aac gaa ttg ata aca tct gaa gga ata tac tgt gll aac cta	672
Tyr Ile Asn Glu Leu Ile Thr Ser Glu Gly Ile Tyr Cys Val Asn Leu	
210 215 220	
ggc cag ctt ccc agg cta tac cat caa att ttt gaa ggc act gga	720

Gly His Leu Pro Arg Leu Tyr Asp Glu Gln Ile Phe Glu Gly Thr Gly	
225	230 235 240
acg acc cat ctt ccc ctg gaa ctg aaa gct atc gac agg uca gal lea	750
Thr Thr His Ileu Pro Leu Glu Leu Lys Ala Ile Asp Arg Thr Asp Ser	
245	250 255
gat gtt tgt atc aat ggt gat tta gtt cta ctc ggt tat gac ttt att	810
Asp Val Cys Ile Asn Gly Asp Leu Val leu Leu Gly Tyr Asp Phe Ile	
260	265 270
cca tat cag ata tgg aag cag tgg tta ctg ttt aga aca gaa uuc gta	861
Pro Tyr Gln Ile Ser Lys Pro Trp Leu Leu Phe Arg Ile Glu Pro Val	
275	280 285
aat agc att gaa gca atc ttc aac tat agt gaa tgt tct ttt tca tac	912
Asn Ser Ile Glu Ala Ile Phe Asn Tyr Ser Glu Cys Ser Phe Ser Tyr	
290	295 300
ccg ltt gaa tgg agt ctg ggc tgc tta caa tct gaa gag aaa att tca	960
Gln Phe Ala Trp Ser Leu Ala Cys Leu Glu Ser Glu Glu Lys Ile Ser	
305	310 315 320
ttt cct aga gac acg ata att ggg cac ggt tta cct tac aag cca tcc	1008
Val Pro Arg Asp Thr Ile Ile Gly His Gly Leu Pro Tyr Lys Pro Ser	
325	330 335
aaa ttg ata aga att ttc gtc luo aag cat ccg gaa caa aag caa gat	1056
Lys Leu Ile Arg Ile Phe Val Tyr Lys His Pro Glu Gln Lys Gln Asp	
340	345 350
ctt ggt caa gaa ata gca ttg ucu aac tgg aat acc cct tat ctt cga	1104
Leu Gly Gln Glu Ile Ala Leu Pro Asn Thr Pro Tyr Leu Arg	
355	360 365
aga tga	1110
Arg	

<210> 224

<211> 269

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 224

Met Don Glu Ser Asp Ser Ser Leu Met Asp Leu Pro Leu Glu Ile His
1 5 10 15

Leu Ser Leu Leu Glu Tyr Val Pro Asn Glu Leu Arg Ala Val Asn Lys
20 25 30

Tyr Phe Tyr Val Leu His Asn His Ser Tyr Lys Glu Lys Ser Leu Ala
35 40 45

Trp Ile Ala Glu Asp Asn Tyr Ile Trp Ala Val Val Lys His Ser Leu
50 55 60

Cys Leu Tyr Val Lys Ser Leu Asp Pro Leu Arg Glu His Ala Arg Glu
65 70 75 80

Ile Ile Gln Glu Thr Lys Glu Pro Gly Phe Asn Val Pro Leu Cys Met
85 90 95

Thr Lys Tyr Ile Ala Asp Ser Trp Tyr Ile Val Tyr Asn Ala Leu Gln
100 105 110

Tyr Pro Gly Lys Ile Ile Asn Met Gly Trp Asp Lys Tyr Thr Lys Ser
115 120 125

Gln Asp Ser Asn Gly Ser Asp Ser Thr Ser Asn Phe Asn Ser Arg Pro
130 135 140

Lys Glu Arg Thr Leu Met Gln Ser Leu Thr Ala Leu Pro Val Asn Phe

145 150 155 160

Trp Ser Arg Arg Lys Asp Glu Pro Thr Pro Val Asn Val Trp Phe Tyr
 165 170 175

Val Lys Asn Ala His Val Ala Arg Tyr Ile Pro Lys Ile Ile Thr Glu
 180 185 190

Ile Gly Ile Cys Asn Tyr Gly Pro Lys Gln Ile Val Ala Ser Ala Gly
 195 200 205

Tyr Ile Asn Glu Leu Ile Thr Ser Glu Gly Ile Tyr Cys Val Asn Leu
 210 215 220

Gly His Leu Pro Arg Leu Tyr Asp Glu Gln Ile Phe Glu Gly Thr Gly
225 230 235 240

Thr Thr His Leu Pro Leu Glu Leu Lys Ala Ile Asp Arg Thr Asp Ser
 245 250 255

Asp Val Cys Ile Asn Gly Asp Leu Val Leu Leu Gly Tyr Asp Phe Ile
 260 265 270

Pro Tyr Gln Ile Ser Lys Pro Trp Leu Leu Phe Arg Ile Glu Pro Val
 275 280 285

Asn Ser Ile Glu Ala Ile Phe Asn Tyr Ser Glu Cys Ser Phe Ser Tyr
 290 295 300

Gln Phe Ala Trp Ser Leu Ala Cys Leu Gln Ser Glu Glu Lys Ile Ser
305 310 315 320

Phe Pro Arg Asp Thr Ile Ile Gly His Gly Leu Pro Tyr Lys Pro Ser
 325 330 335

Lys Leu Ile Arg Ile Phe Val Tyr Lys His Pro Glu Gln Lys Gln Asp
 340 345 350

Leu Gly Gln Glu Ile Ala Leu Pro Asn Trp Asn Thr Pro Tyr Leu Arg
 355 360 365

Arg

<210> 225

<211> 333

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (333)

<400> 225

gag ttc tca aac ata att gat cgt cca aca cat gaa ctg tct aca gca 48
 Met Ser Ser Gln Phe Ile Asp Arg Pro Lys His Glu Leu Ser Arg Ala
 1 5 10 15

gaa tta gag gaa cta gaa gaa ttt gaa ttc aaa cat ggt cca atg tcc 96
 Gln Leu Glu Glu Leu Glu Glu Phe Glu Phe Lys His Gly Pro Met Ser
 20 25 30

ctg ata aat gat gct atg gtg aca aga aca cct ggg ata atc tca tta 144
 Leu Ile Asn Asp Ala Met Val Thr Arg Thr Pro Val Ile Ile Ser Leu
 35 40 45

aga aac aat cat aac ata ata ggg aga gtg aaa gct ttc gac agg cat 192
 Arg Asn Asn His Lys Ile Ile Ala Arg Val Lys Ala Phe Asp Arg His

50	55	60	
agt aat atg gtt tta gaa aat gtg aag gag att cgg aca gag aag aag			240
Cys Asn Met Val Leu Glu Asn Val Lys Glu Leu Trp Thr Glu Lys Tyr			
65	70	75	80
ggc aaa aat gta att aat cgg gaa aga ttc ata agt aaa cta ttc tta			288
Gly Lys Asn Val Ile Asn Arg Glu Arg Phe Ile Ser Lys Leu Phe Leu			
85	90	95	
aga ggt gat tca gtt atc gtt gtg tta aaa acc act gll gag taa			336
Arg Gly Asp Ser Val Ile Val Val Leu Lys Thr Pro Val Glu			
100	105	110	
 <210> 226			
<211> 110			
<212> PRT			
<213> Saccharomyces cerevisiae			
 <400> 226			
Met Ser Ser Gln Tle Ile Asp Arg Pro Lys His Glu Leu Ser Arg Ala			
1	5	10	15
 Glu Leu Glu Glu Leu Glu Glu Phe Glu Phe Lys His Gly Pro Met Ser			
20	35	36	
 Leu Ile Asn Asp Ala Met Val Thr Arg Thr Pro Val Ile Ile Ser Leu			
35	40	45	
 Arg Asn Asn His Lys Ile Ile Ala Arg Val Lys Ala Phe Asp Arg His			
50	55	60	
 Cys Asn Met Val Leu Glu Asn Val Lys Glu Trp Thr Thr Glu Lys Lys			
65	70	75	80

Gly Lys Asn Val Ile Asn Arg Glu Arg Phe Ile Ser Lys Leu Phe Leu
85 90 95

Arg Gly Asp Ser Val Ile Val Val Leu Lys Thr Pro Val Glu
100 105 110

<210> 227

<211> 2184

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2184)

<400> 127

atg aat gat tgg cat gag ttc aat gcc gcc ata aag tca att tat tgg 48
Met Asn Asp Trp His Glu Phe Asn Ala Ala Ile Lys Ser Ile Tyr Cys
1 5 10 15

aat gca gaa ggt gac tca agc agt ata att aat aga ttg gtt gcc ttg 96
Asn Ala Glu Gly Asp Ser Ser Ser Ile Ile Asn Arg Leu Val Gly Leu
20 25 30

gaa atg aaa agc gaa gat tcc act ttt att gag gcc gtt tta gtt ttg 144
Gln Met Lys Ser Glu Asp Ser Thr Phe Ile Glu Ala Val Leu Val Leu
35 40 45

aaa gaa aat gtg tgg aaa gla gat aaa gaa ttc aga ttt tta tgg ctt 192
Lys Glu Asn Val Ser Lys Val Asp Lys Gln Leu Arg Phe Leu Trp Leu
50 55 60

acc tca act att aat tca agg ttt tat ccc cct ata cct atc tca gaa 240
Thr Ser Thr Ile Asn Ser Arg Phe Tyr Pro Pro Ile Pro Ile Ser Glu
65 70 75 80

gcc tca cag gtt tct tgg aat aaa acc gaa tat tgc gaa cct ggt act 288
Ala Ser Pro Val Ser Trp Asn Lys Thr Glu Tyr Cys Ala Pro Gly Thr
85 90 95

gaa gaa cta caa agy cgt tat cca ggg aga gcc aag tta cag aat gaa Glu Glu Leu Glu Arg Arg Tyr Phe Gly Arg Ala Lys Leu Glu Asn Glu 101 105 110	336
gaa gac tat tca ggc gga ata gaa caa lyc cga gat gtc oca gat tgc Glu Asp Tyr Ser Gly Gly Ile Glu Glu Cys Arg Asp Val Pro Asp Cys 115 120 125	334
tta tta gtt gct tcl tca att aac ctt agg tct aag aac ttg aat ctc Ser Leu Val Ala Ser Leu Ile Asn Leu Arg Ser Lys Asn Leu Asn Leu 130 135 140	432
cct cta att aca caa ata tca tca act aaa lat cac gtc aat tta agt Pro Leu Ile Lys Glu Ile Ser Ser Thr Lys Tyr His Val Asn Leu Ser 145 150 155 160	480
ttt aac gga agc aac aaa ayy cta gtc aca gta gat aht tgg cag ala Phe Asn Gly Ser Asn Lys Arg Leu Val Thr Val Asp Ile Ser Glu Ile 165 170 175	528
cca acc taa gtc gat ggc aca cca att tct tta aag agt aac gat att Phe Thr Ser Val Asp Gly Lys Glu Asn Ser Leu Lys Ser Asn Asp Ile 180 185 190	576
tgg gac aac att ggc gag ctt gca tta ctg ttt gtt tot aca gga aca Ser Asp Lys Ile Gly Glu Leu Ala Leu Leu Leu Val Ser Lys Gly Thr 195 200 205	624
tat tcc aag gat ggc tca aat att agt ata gat aat tae cgc tta agt Tyr Ser Thr Asp Gly Ser Asn Ile Ser Ile Asp Thr Tyr Arg Leu Ser 210 215 220	672
ggc ttc tta cca gag ata aca caa gta aac ayy tat cct ttc gaa aca Gly Phe Asn Pro Glu Ile Thr Glu Val Asn Ser Tyr Pro Phe Glu Lys 225 230 235 240	720
tta tgg aag tct cac aaa tot aat tta hgt ctg atg ggc gct ggc acc Leu Trp Lys Phe His Lys Ser Asn Leu Cys Leu Met Gly Ala Gly Thr 245 250 255	768
ggc aat cgt tcc aat gac atg ata aag ccc cta gct gag aac cat gat	816

Gly Asn Arg Ser Asn Asp Met Ile Lys Pro Leu Val Glu Asn His Asp			
250	265	270	
tac tct ata att gat atc acg tat gat tct agy cta gta aaa ttg cga	864		
Tyr Ser His Ile Asp Val Thr Tyr Asp Ser Arg Leu Val Lys Leu Arg			
275	280	285	
gat ccg agy aac tgg gca cta aat gtt gaa atc agc tat gaa cag tat	912		
Asp Pro Arg Asn Ser Ala Leu Asn Val Glu Ile Ser Tyr Glu Gln Tyr			
290	295	300	
tta aaa aat ttc aaA caa att tat att aat tgg aac caa gaa aaa tta	960		
Leu Lys Asn Phe Lys Gln Leu Tyr Leu Asn Trp Asn Glu Glu Lys Leu			
305	310	315	320
tte aaa cgt tct cag gta att cat ttt cgg tac gal acg tca cgc tac	1008		
Phe Lys Arg Ser Glu Val Leu His Phe Arg Tyr Asp Thr Ser Arg Tyr			
325	330	335	
aat aaa ttt tct atc gtt gca gat aaa cct tta ttt cac ctg gta aac	1056		
Asn Lys Phe Ser Ile Val Ala Asp Lys Pro Leu Phe His Leu Val Asn			
340	345	350	
aat tct aaa gtc aca gag acg gta tgg tta ttg ata gaa tcc cat ttg	1104		
Asn Ser Lys Val Thr Glu Thr Val Trp Leu Leu Leu Glu Ser His Leu			
355	360	365	
caa gat gaa ggc agc caa gaa aat cgg tca gtt tcc ttt ttg aat gag	1152		
Gln Asp Glu Gly Ser Gln Glu Asn Arg Ser Val Ser Phe Leu Asn Glu			
370	375	380	
gct ccc gaa tgc ata att tgt cca att gan cct ccc gta gan tgc ggt	1200		
Ala Pro Glu Cys Ile Ile Cys Pro Ile Glu Pro Pro Val Glu Cys Gly			
385	390	395	400
ggc aat cac att gga att cag ctg gta aag ttg aga tta gal gct gag	1248		
Gly Asn His Ile Gly Leu Gln Leu Val Lys Leu Arg Leu Asp Ala Glu			
405	410	415	
act gag agy tta ctg tat tgt tat tca cca cca aac aac aat ttc agt	1296		
Thr Glu Arg Leu Leu Tyr Cys Tyr Ser Thr Thr Asn Asn Asn Phe Ser			
420	425	430	

att caa tat ttc tca gtt gtg aag gaa ata tgt ttt caa aga ttg aaa	1344
ile his ser phe ser val val lys glu ile cys phe gln arg leu lys	
435 440 445	
gat aca aaa agt att ttt gcc aaa gtc att ttc tct ttt cat tat gaa	1392
asp thr lys ser leu phe ala lys val leu phe ser phe pro tyr glu	
450 455 460	
ata gag gga aaa gcc taa ttt gat act tgt aat ttt ttt caa aat cgg	1440
ile glu gly lys ala ser phe asp thr cys asp phe phe gln asp pro	
465 470 475 480	
act ttt gag ttg gaa gtc aac tct gaa caa gat tat caa gta att atg	1488
thr phe glu leu glu val his ser glu gln asp tyr gln val leu met	
485 490 495	
gac gcc gca tgt atc tca act agc tca cat gat tta att aac atc caa	1536
asp ala ala cys ile ser thr ser ser his asp leu ile asp ile gln	
500 505 510	
gta tat taa lll aal gaa tal gaa ttg ata aag cca ata atg ttt gat	1584
val tyr tyr phe asp asp tyr glu leu ile lys pro ile met phe asp	
515 520 525	
aac caa tat cag ccc ggg cag ggc att aaa caa gac gtg ccc atc tta	1632
asn his tyr gln pro gly gln gly leu lys gln asp val pro ile leu	
530 535 540	
act aat gtc aaa tat atg att gta tgc tca act tac gcc cat cca gcc	1680
thr asn val lys tyr met ile val cys ser thr tyr gly pro phe ala	
545 550 555 560	
tca acg gaa ttt gaa tta att gcc tgg ata egg tta tcc tct tca tgg	1728
ser thr glu phe glu leu leu ala ser ile arg leu ser ser ser tip	
565 570 575	
agg tta ata tct gga ata aat lla cgg ayl gtt aac ttg ata tac ggc	1776
arg leu ile ser gly ile thr leu arg ser val asp leu ile tyr gly	
580 585 590	
act tat cca tat cat tgt cgc aac agg ttc cat tgg aag gaa act tca	1824

Thr Tyr Pro Tyr His Cys Arg Asn Arg Phe His Trp Lys Glu Thr Ser	
595 600 605	
gac aaa ctt aaa att cag atg act ttg cca acc aaa aag tat tct acg	1873
Asp Lys Leu Lys Ile Glu Met Thr Leu Pro Thr Lys Lys Tyr Ser Thr	
610 615 620	
aac aaa ctt ttt ata cgt gta gta ccc gcg guu tca tca gca dga tta	1920
Asn Lys Leu Phe Ile Arg Val Val Pro Val Glu Ser Ser Ala Arg Leu	
625 630 635 640	
agg atg cga tgt aat att ttc gag cct gaa tca gct ctc tgt gtt tat	1969
Arg Met Arg Cys Asn Ile Phe Glu Pro Glu Ser Ala Leu Cys Val Tyr	
645 650 655	
gaa tgt cta gag tat agg aca tgt cca tct ggg ggc acg gtt ata cct	2016
Glu Cys Glu Glu Tyr Arg Thr Cys Pro Ser Gly Gly Ile Val Ile Pro	
660 665 670	
gat cgg gaa gtc tct cgt acg aac att gtt gta ttg atg ata gaa aga	2064
Asp Leu Glu Val Ser Arg Thr Asn Ile Val Val Leu Met Ile Glu Arg	
675 680 685	
agt gta cct att tcc agt tgt tta cct acg gaa gga caa ttg gat gaa	2112
Ser Val Pro Ile Ser Ser Cys Leu Pro Thr Glu Gly Glu Leu Asp Glu	
690 695 700	
ttg gag ttg ttt gtt ggg tcc agt caa aaa atc aga att gaa aaa tac	2160
Leu Glu Leu Phe Val Gly Ser Ser Glu Lys Ile Arg Ile Glu Lys Tyr	
705 710 715 720	
tcc gat gat ggg ata cca aaa taa	2208
Ser Asp Asp Val Ile Pro Lys	
725	
<210> 228	
<211> 727	
<212> ERT	
<213> Saccharomyces cerevisiae	
<400> 228	

Met Asn Asp Thr His Glu Phe Asn Ala Ala Ile Lys Ser Ile Tyr Cys
 1 5 10 15

Asn Ala Glu Gly Asp Ser Ser Ser Ile Ile Asn Arg Leu Val Gly Leu
 20 25 30

Ala Met Lys Ser Glu Asp Ser Thr Phe Ile Glu Ala Val Leu Val Leu
 35 40 45

Lys Glu Asn Val Ser Lys Val Asp Lys Glu Leu Arg Phe Leu Trp Leu
 50 55 60

Thr Ser Thr Ile Asn Ser Arg Phe Tyr Pro Pro Ile Pro Ile Ser Glu
 65 70 75 80

Ala Ser Pro Val Ser Trp Asn Lys Thr Glu Tyr Cys Ala Pro Gly Thr
 85 90 95

Glu Glu Leu Gln Arg Arg Tyr Pro Gly Arg Ala Lys Leu Gln Asn Glu
 100 105 110

Glu Asp Tyr Ser Gly Gly Ile Glu Gln Cys Arg Asp Val Pro Asp Cys
 115 120 125

Ser Leu Val Ala Ser Leu Ile Asn Leu Arg Ser Lys Asn Leu Asn Leu
 130 135 140

Pro Leu Ile Lys Gln Ile Ser Ser Thr Lys Tyr His Val Asn Leu Ser
 145 150 155 160

Phe Asn Gly Ser Asn Lys Arg Leu Val Thr Val Asp Ile Ser Gln Ile

168

170

175

Pro Thr Ser Val Asp Gly Lys Gln Leu Ser Leu Lys Ser Asn Asp Ile
 180 185 190

Ser Asp Lys Ile Gly Glu Ser Ala Leu Leu Leu Val Ser Lys Gly Thr
 195 200 205

Tyr Ser Thr Asp Gly Ser Asn Ile Ser Ile Asp Thr Tyr Arg Leu Ser
 210 215 220

Gly Phe Leu Pro Glu Ile Thr Gln Val Asn Ser Tyr Pro Phe Glu Lys
 225 230 235 240

Leu Tyr Lys Phe His Lys Ser Asn Leu Cys Leu Met Gly Ala Gly Thr
 245 250 255

Gly Asn Arg Ser Asn Asp Met Ile Lys Pro Leu Val Glu Asn His Asp
 260 265 270

Tyr Ser Ile Ile Asp Ile Thr Tyr Asp Ser Arg Leu Val Lys Leu Arg
 275 280 285

Asp Pro Arg Asn Ser Ala Leu Asn Val Glu Ile Ser Tyr Glu Gln Tyr
 290 295 300

Leu Lys Asn Phe Lys Gln Leu Tyr Leu Asn Tyr Asn Glu Glu Lys Leu
 305 310 315 320

Phe Lys Arg Ser Gln Val Leu His Phe Arg Tyr Asp Thr Ser Arg Tyr
 325 330 335

Asn Lys Phe Ser Ile Val Ala Asp Lys Pro Leu Phe His Leu Val Asn
 340 345 350

Asn Ser Lys Val Thr Glu Thr Val Trp Leu Leu Leu Glu Ser His Leu
 355 360 365

Glu Asp Glu Gly Ser Gln Glu Asn Arg Ser Val Ser Phe Leu Asn Glu
 370 375 380

Ala Pro Glu Cys Ile Ile Cys Pro Ile Glu Pro Pro Val Glu Cys Gly
 385 390 395 400

Gly Asn His Ile Gly Leu Gln Leu Val Lys Leu Arg Leu Asp Ala Glu
 405 410 415

Thr Glu Arg Leu Leu Tyr Cys Tyr Ser Thr Thr Asn Asn Asn Phe Ser
 420 425 430

Ile His Ser Phe Ser Val Val Lys Glu Ile Cys Phe Gln Arg Leu Lys
 435 440 445

Asp Thr Lys Ser Leu Phe Ala Lys Val Leu Phe Ser Phe Pro Tyr Glu
 450 455 460

Ile Gln Gly Lys Ala Ser Phe Asp Thr Cys Asn Phe Phe Gln Asn Pro
 465 470 475 480

Thr Phe Glu Leu Glu Val His Ser Glu Gln Asp Tyr Glu Val Leu Met
 485 490 495

Asp Ala Ala Cys Ile Ser Thr Ser Ser His Asp Leu Ile Asn Ile Gln

500

505

510

Val Tyr Tyr Phe Asn Asp Tyr Glu Leu Ile Lys Pro Ile Met Phe Asp
515 520 525

Asn His Tyr Gln Pro Gly Gln Gly Leu Lys Gln Asp Val Pro Ile Leu
530 535 540

Thr Asn Val Lys Tyr Met Ile Val Cys Ser Thr Tyr Gly Pro Pro Ala
545 550 555 560

Ser Thr Glu Phe Glu Leu Leu Ala Ser Ile Arg Leu Ser Ser Ser Trp
565 570 575

Arg Leu Ile Ser Gly Ile Thr Leu Arg Ser Val Asn Leu Ile Tyr Gly
580 585 590

Thr Tyr Pro Tyr His Cys Arg Asn Arg Phe His Trp Lys Glu Thr Ser
595 600 605

Asp Lys Leu Lys Ile Gln Met Thr Leu Pro Thr Lys Lys Tyr Ser Thr
610 615 620

Asn Lys Leu Phe Ile Arg Val Val Pro Val Glu Ser Ser Ala Arg Leu
625 630 635 640

Arg Met Arg Cys Asn Ile Phe Glu Pro Glu Ser Ala Leu Cys Val Tyr
645 650 655

Glu Cys Gln Glu Tyr Arg Thr Cys Pro Ser Gly Gly Ile Val Ile Pro
660 665 670

Asp Leu Glu Val Ser Arg Thr Asn Ile Val Val Leu Met Ile Glu Arg
 675 680 685

Ser Val Pro Ile Ser Ser Cys Leu Pro Thr Glu Gly Glu Leu Asp Glu
 690 695 700

Leu Glu Leu Phe Val Gly Ser Ser Gln Lys Ile Arg Ile Glu Lys Tyr
 705 710 715 720

Ser Asp Asp Val Ile Pro Lys
 725

<210> 229

<211> 2223

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2223)

<400> 229

atg gat aqa ggc aag tgg tgt ttc ctc gtg tcc gta tca aac aqa ata 48
 Met Asp Arg Gly Arg Trp Cys Phe Leu Val Ser Val Ser Ser Arg Ile
 1 5 10 15

atg aat ctg caa gaa cta tta gcg aag gta ccg ctg ttg tta tgg tat 96
 Met Asn Leu Gln Glu Leu Leu Ala Lys Val Pro Leu Leu Leu Ser Tyr
 20 25 30

ccg aac att att cta tcc agt aat aag atc gta cct tcc cat aat gat 144
 Pro Thr Ile Ile Leu Ser Ser Asn Leu Ile Val Pro Ser His Asn Asp
 35 40 45

ctc ata tca oga gca gcc tct aca tca gca gca gag tat gct gac gaa 192
 Leu Ile Ser Arg Ala Ala Ser Thr Ser Ala Ala Glu Tyr Ala Asp Glu

50	55	60	
aaq cta ata ttt ttc agt aca gat cac gcc acc aga ctg att ttt ctg			240
Lys Leu Ile Phe Phe Ser Thr Asp His Ala Ile Arg Leu Ile Phe Leu			
65	70	75	80
aca acc ttc gta gct tet tcc ttt aac cta ttt gcg cac tat ttt aac			288
Pro Thr Phe Val Ala Ser Ser Phe Asn Leu Phe Ala His Tyr Phe Asn			
85	90	95	
llu ulc aut tac tet agc cga agg aag tat tat gtt tta ttt act gca			336
Phe Ile Asn Tyr Ser Ser Arg Arg Lys Tyr Tyr Val Leu Phe Thr Ala			
100	105	110	
att tat ttc cta tcc ata ttg act gcg att tts cat cca att cag tca			384
Ile Tyr Phe Leu Ser Ile Leu Thr Ala Ile Phe His Pro Ile Gln Ser			
115	120	125	
aca tgc atc aot cta ttg att atc sag ctc ctg act acc gct gat gag			432
Thr Cys Ile Thr Leu Leu Ile Ile Lys Leu Leu Thr Thr Ala Asp Glu			
130	135	140	
tet tog cca aaa att gcu ctc wat ttc aag acc att ttg aaa aca ttt			480
Ser Ser Pro Lys Ile Ala Leu Asn Phe Lys Thr Ile Leu Lys Thr Phe			
145	150	155	160
gtt ccc ttt att act tta aca tta gtt ata ttg cgt tgg gat cct tet			528
Val Pro Phe Ile Thr Leu Thr Leu Val Ile Leu Arg Trp Asp Pro Ser			
165	170	175	
ttt gat gcc agc tca gga gat gtg aac aaa att tet acg tet ttg gcc			576
Phe Asp Ala Ser Ser Gly Asp Val Asn Lys Ile Ser Thr Ser Leu Ala			
180	185	190	
gca tat gct ctc tta ata tta acg cta aga tat gca tca cag ctg ata			624
Ala Tyr Ala Leu Leu Ile Leu Thr Leu Arg Tyr Ala Ser Pro Leu Ile			
195	200	205	
tta tog acy tta tca agt agc ata ggt gtt gtt tcc aaa gac acc ego			672
Leu Ser Thr Leu Ser Ser Ser Ile Gly Val Val Ser Lys Asp Thr Ser			
210	215	220	

538/762

gtc gca gag cat tog ata agt aga aat cag aga ttt cgg cta att etc	720			
Val Ala Gln His Ser Ile Ser Arg Asn Lys Arg Phe Pro Leu Ile Leu				
225	230	235	240	
gtg tta cgg att ttt tcc ttt gtt ctt ttg tat cta atg act ara gtt	763			
Val Leu Pro Ile Phe Ser Phe Val Leu Leu Tyr Leu Met Thr Ile Val				
	245	250	255	
aac aag act tac aat atc cag tta tta atg gta ttt gta ttt ttt gga	810			
Asn Lys Thr Tyr Asn Ile Gln Leu Leu Met Val Phe Val Phe Phe Gly				
	260	265	270	
tgt ctg tcc att ttc ttt tta tog tta aaa gat ttg ttc acc gag gat	864			
Cys Leu Ser Ile Phe Phe Leu Ser Leu Lys Asp Leu Phe Thr Glu Asp				
	275	280	285	
gga aat aac aag aag gga ggc cag gag gat gaa tat tgt cgt atg ttt	912			
Gly Asn Gln Phe Lys Gly Gly Gln Glu Asp Glu Tyr Cys Arg Met Phe				
	290	295	300	
gac ata aag tac atg att tcc tat tta tgg ctg aca agg ttc acc att	960			
Asp Ile Lys Tyr Met Ile Ser Tyr Leu Trp Leu Thr Arg Phe Thr Ile				
	305	310	315	320
tta ttg aca ggc ata atg gct att gta gta cat ttt tta tog ttt aat	1005			
Leu Leu Thr Gly Ile Met Ala Ile Val Val His Phe Leu Ser Phe Asn				
	325	330	335	
gaa att act tct tcc atc aaa act gat ttg tta agt tta ctt ttc gtc	1053			
Glu Ile Thr Ser Ser Ile Lys Thr Asp Leu Leu Ser Leu Leu Phe Val				
	340	345	350	
gta gtg gca ga3 tat gtt tcc agt ttc tct aac aac aac cct gat tgg	1104			
Val Val Ala Glu Tyr Val Ser Ser Phe Ser Asn Lys Gln Pro Asp Ser				
	355	360	365	
gac tuc cat aat cat gca cat cac cat tcc cat cta acc gat tca ttg	1152			
His Ser His Asn His Ala His His His Ser His Leu Thr Asp Ser Leu				
	370	375	380	
cct ctc gaa aat gaa agt atg ttc aaa caa atg gca ttg aat aag gac	1200			
Pro Leu Glu Asn Glu Ser Met Phe Lys Gln Met Ala Leu Asn Lys Asp				

539/762

385	390	395	400	
acc agg tcc att ttt tgg ttt tta ttg ttg aat acc gct ttc atg ttt				1240
Thr Arg Ser Ile Phe Ser Phe Leu Leu Leu Asn Thr Ala Phe Met Phe				
	405	410	415	
gta caa ctt tta tat tcc ttt ogt tcc aaa tra ttg ggc tta tta tct				1296
Val Glu Leu Leu Tyr Ser Phe Arg Ser Lys Ser Leu Gly Leu Leu Ser				
	420	425	430	
gat tgg ttg cat atg gcc tta gat tgc aca tct ttg ctc tta ggt cta				1344
Asp Ser Leu His Met Ala Leu Asp Cys Thr Ser Leu Leu Leu Gly Leu				
	435	440	445	
att gct ggt gta ttg acc aag aaa cca gca agt gal aac ttc cct ttc				1392
Ile Ala Gly Val Leu Thr Lys Lys Pro Ala Ser Asp Lys Phe Pro Phe				
	450	455	460	
ggt cta aat tat ctt ggt acc ttg gca ggt ttc acc aat ggt gtt cly				1440
Gly Leu Asn Tyr Ser Gly Thr Leu Ala Gly Phe Thr Asn Gly Val Leu				
	465	470	475	480
tta ctc ggc ata gtg tgc ggt atc ttt gtg gag gca att gag aga act				1488
Leu Leu Gly Ile Val Cys Gly Ile Phe val Glu Ala Ile Glu Arg Ile				
	485	490	495	
ttc aac cdc att cat ctt cat gca aca aat gag ttg ttg gtt gtt gct				1536
Phe Asn Pro Ile His Leu His Ala Thr Asn Glu Leu Leu Val Val Ala				
	500	505	510	
acc tta ggc tta tta gtg aac ctt gta ggt ttg tll gaa ttc gaa cat				1584
Thr Leu Gly Leu Leu Val Asn Leu Val Gly Leu Phe Ala Phe Asp His				
	515	520	525	
ggt gca cat gat cat ggt ggt act gat aat gaa aac atg aag ggg att				1632
Gly Ala His Asp His Gly Gly Thr Asp Asn Glu Asn Met Lys Gly Ile				
	530	535	540	
ttt tta cat ata ttg gca gat aca tta ggt tct gtt ggc gtt gtt att				1680
Phe Leu His Ile Leu Ala Asp Thr Leu Gly Ser Val Gly Val Val Ile				
	545	550	555	560

540/762

tcg acg tta tta alc aag tta aga gag tgg coa att ttt gat cag atc	1728
Ser Thr Leu Leu Ile Lys Leu Thr His Trp Pro Ile Phe Asp Pro Ile	
568 590 595	
ccc tct tta tta att ggt tcc ttg alc tta ctt agc gat ctg ccc ctg	1776
Ala Ser Leu Leu Ile Gly Ser Leu Ile Leu Leu Ser Ala Leu Pro Leu	
580 585 590	
cta aca tct act tcc gca aat att tta cta aga ctg gat gac aag aag	1824
Leu Tyr Ser Thr Ser Ala Asn Ile Leu Leu Arg Leu Asp Asp Lys Tyr	
595 600 605	
cat aat cta gta aag agt gcg cta aac cag att tca aag aag cca gga	1872
His Asn Leu Val Lys Ser Ala Leu Asn Gln Ile Ser Thr Thr Pro Gly	
610 615 620	
atc aca ggt tat aca act cct aga ttt tgg cag aca gag tca ggc agt	1920
Ile Thr Gly Tyr Thr Thr Pro Arg Phe Trp Pro Thr Glu Ser Gly Ser	
625 630 635 640	
tcc ggg cat tca cat gca cac acg cat tct cat gca gag aat cat agc	1968
Ser Gly His Ser His Ala His Thr His Ser His Ile Glu Asn Ile Ser	
645 650 655	
cat gag cat cat cat gat cag cca aac ggt tca cca gaa cac cag agc	2016
His Glu His His His Asp Gln Lys Asn Gly Ser Gln Glu His Pro Ser	
660 665 670	
ttg gcg ggc tat att cat gta cag tat gta gac ggc gag aat tgg aca	2064
Leu Val Gly Tyr Ile His Val Gln Tyr Val Asp Gly Glu Asn Ser Thr	
675 680 685	
att atc aag aaa aga gtt gaa aca ata ttc gaa aat gtc tgg att aaa	2112
Ile Ile Lys Lys Arg Val Glu Lys Ile Phe Glu Asn Val Ser Ile Lys	
690 695 700	
gca tgg gta caa gtt gag cct caa aat tcc act tgt tgg tgc cgg gct	2160
Ala Trp Val Gln Val Glu Pro Gln Asn Ser Thr Cys Trp Cys Arg Ala	
705 710 715 720	
act tct atg aac aca att tca gct aac cag aat tct tta cag cta cag	2208
Thr Ser Met Asn Thr Ile Ser Ala Asn Pro Asn Ser Leu Pro Leu Gln	

725

730

735

CCT ATA GCA AAT TGA

2223

Pro Ile Ala Asn

740

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<211> 740

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 230

Met Asp Arg Gly Arg Trp Cys Phe Leu Val Ser Val Ser Ser Arg Ile

1

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15

Met Asn Leu Gln Glu Leu Leu Ala Lys Val Pro Leu Leu Leu Ser Tyr

20

25

30

Pro Thr Ile Ile Leu Ser Ser Asn Leu Ile Val Pro Ser His Asn Asp

35

40

45

Leu Ile Ser Arg Ala Ala Ser Thr Ser Ala Ala Glu Tyr Ala Asp Glu

50

55

60

Lys Leu Ile Phe Phe Ser Thr Asp His Ala Ile Arg Leu Ile Phe Leu

65

70

75

80

Pro Thr Phe Val Ala Ser Ser Phe Asn Leu Phe Ala His Tyr Phe Asn

85

90

95

Phe Ile Asn Tyr Ser Ser Arg Arg Lys Tyr Tyr Val Leu Phe Thr Ala

100

105

110

Ile Tyr Phe Leu Ser Ile Leu Thr Ala Ile Phe His Pro Val Gln Ser
115 120 125

Thr Cys Ile Thr Leu Leu Ile Ile Lys Leu Leu Thr Thr Ala Asp Gln
130 135 140

Ser Ser Pro Lys Ile Ala Leu Asn Phe Lys Thr Ile Leu Lys Thr Phe
145 150 155 160

Val Pro Phe Ile Thr Leu Thr Leu Val Ile Leu Arg Trp Asp Pro Ser
165 170 175

Phe Asp Ala Ser Ser Gly Asp Val Asn Lys Ile Ser Thr Ser Leu Ala
180 185 190

Ala Tyr Ala Leu Leu Ile Leu Thr Leu Arg Tyr Ala Ser Pro Leu Ile
195 200 205

Leu Ser Thr Leu Ser Ser Ser Ile Gly Val Val Ser Lys Asp Thr Ser
210 215 220

Val Ala Gln His Ser Ile Ser Arg Asn Lys Arg Phe Pro Leu Ile Leu
225 230 235 240

Val Leu Pro Ile Phe Ser Phe Val Leu Leu Tyr Leu Met Thr Ile Val
245 250 255

Asn Lys Thr Tyr Asn Ile Gln Leu Leu Met Val Phe Val Phe Phe Gly
260 265 270

Cys Leu Ser Ile Phe Phe Leu Ser Leu Lys Asp Leu Phe Thr Glu Asp
275 280 285

Gly Asn Gln Lys Lys Gly Gly Gln Glu Asp Glu Tyr Cys Arg Met Phe
 290 295 300

asp Ile Lys Tyr Met Ile Ser Tyr Leu Tyr Leu Thr Arg Phe Thr Ile
 305 310 315 320

Leu Leu Thr Gly Ile Met Ala Ile Val Val His Phe Leu Ser Phe Asn
 325 330 335

Glu Ile Thr Ser Ser Ile Lys Thr Asp Leu Leu Ser Leu Leu Phe Val
 340 345 350

Val Val Ala Glu Tyr Val Ser Ser Phe Ser Asn Lys Gln Pro Asp Ser
 355 360 365

His Ser His Asn His Ala His His His Ser His Leu Thr Asp Ser Leu
 370 375 380

Pro Leu Glu Asn Glu Ser Met Phe Lys Gln Met Ala Leu Asn Lys Asp
 385 390 395 400

Thr Arg Ser Ile Phe Ser Phe Leu Leu Leu Asn Thr Ala Phe Met Phe
 405 410 415

Val Gln Leu Leu Tyr Ser Phe Arg Ser Lys Ser Leu Gly Leu Leu Ser
 420 425 430

Asp Ser Leu His Met Ala Leu Asp Cys Thr Ser Leu Leu Leu Gly Leu
 435 440 445

Thr Ala Gly Val Leu Thr Lys Lys Pro Ala Ser Asp Lys Phe Pro Phe
 450 465 480

Gly Leu Ser Tyr Leu Gly Thr Leu Ala Gly Phe Thr Asn Gly Val Leu
 465 470 475 480

Leu Leu Gly Ile Val Cys Gly Ile Phe Val Glu Ala Thr Glu Arg Ile
 485 490 495

Phe Asn Pro Ile His Leu His Ala Thr Asn Glu Leu Leu Val Val Ala
 500 505 510

Thr Leu Gly Leu Leu Val Asn Leu Val Gly Leu Phe Ala Phe Asp His
 515 520 525

Gly Ala His Asp His Gly Gly Thr Asp Asn Glu Asn Met Lys Gly Thr
 530 535 540

Phe Leu His Ile Leu Ala Asp Thr Leu Gly Ser Val Gly Val Val Thr
 545 550 555 560

Ser Thr Leu Leu Ile Lys Leu Thr His Trp Pro Ile Phe Asp Pro Ile
 565 570 575

Ala Ser Leu Leu Ile Gly Ser Leu Ile Leu Met Ser Ala Leu Pro Leu
 580 585 590

Leu Lys Ser Thr Ser Ala Asn Ile Leu Leu Arg Leu Asp Asp Lys Lys
 595 600 605

His Asn Leu Val Lys Ser Ala Leu Asn Glu Ile Ser Thr Thr Pro Gly
 610 615 620

Ile Thr Gly Tyr Thr Thr Pro Arg Phe Trp Pro Thr Glu Ser Gly Ser
 525 533 535 540

Ser Gly His Ser His Ala His Thr His Ser His Ala Glu Asn His Ser
 545 550 555

His Glu His His His Asp Gln Lys Asn Gly Ser Gln Glu His Pro Ser
 560 565 570

Leu Val Gly Tyr Ile His Val Gln Tyr Val Asp Gly Glu Asn Ser Thr
 575 580 585

Ile Ile Lys Lys Arg Val Gln Lys Ala Phe Glu Asn Val Ser Ile Lys
 590 595 600

Ala Trp Val Gln Val Glu Pro Gln Asn Ser Thr Cys Trp Cys Arg Ala
 705 710 715 720

Thr Ser Met Asn Thr Ile Ser Ala Asn Pro Asn Ser Leu Pro Leu Gln
 725 730 735

Pro Ile Ala Asn
 740

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 <211> 591
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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<222> (1) .. (591)

<400> 211

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Met	Lys	Gln	Ile	Val	Lys	Arg	Ser	His	Ala	Ile	Arg	Ile	Val	Ala	Ala	
1				5					10				15			

tta	gga	atc	ata	ggc	ctg	tgg	atg	ttc	ttc	tcg	tct	aat	gaa	ctt	tcg	96
Leu	Gly	Ile	Ile	Gly	Leu	Trp	Met	Phe	Phe	Ser	Ser	Asn	Glu	Leu	Ser	
				20				25					30			

atc	gct	acg	cag	ggc	cta	atc	aag	ggg	aag	tct	ggt	ata	gat	gaa	gtg	144
Ile	Ala	Thr	Pro	Gly	Leu	Ile	Lys	Ala	Lys	Ser	Gly	Ile	Asp	Glu	Val	
	35					40					45					

caa	ggg	ggg	gct	gct	gag	aag	aac	gac	gct	cgg	ttg	aaa	gag	atc	gag	192
Gln	Gly	Ala	Ala	Ala	Glu	Lys	Asn	Asp	Ala	Arg	Leu	Lys	Glu	Ile	Glu	
	50					55				60						

aag	gaa	adc	ttt	ttg	cca	ttg	atg	ggc	gat	gat	aag	ggg	aag	aag	gaa	240
Lys	Gln	Thr	Ile	Met	Pro	Leu	Met	Gly	Asp	Asp	Lys	Val	Lys	Lys	Glu	
65				70					75				80			

gtg	ggc	agg	ggc	tcg	tgg	aag	tac	ttc	cat	acc	ctg	ctg	ggc	cgt	ttt	288
Val	Gly	Arg	Ala	Ser	Irp	Lys	Tyr	Phe	Ala	Thr	Leu	Leu	Ala	Arg	Phe	
				85				90					95			

cag	gac	gag	cct	act	cct	gaa	gaa	aga	gag	aaa	ctg	caa	acg	ttt	att	336
Pro	Asp	Glu	Pro	Thr	Pro	Glu	Glu	Arg	Glu	Lys	Leu	His	Thr	Phe	Ala	
			100					105					110			

ggg	ttg	tat	gca	gaa	ctc	tat	cca	tgc	ggg	gaa	tgt	tca	tat	cac	ttt	384
Gly	Leu	Tyr	Ala	Glu	Leu	Tyr	Pro	Cys	Gly	Glu	Cys	Ser	Tyr	His	Phe	
	115							120				125				

gta	aag	ttg	att	gag	aag	tat	cca	gta	cag	aca	tct	agg	agg	acg	gct	432
Val	Lys	Leu	Ile	Glu	Lys	Tyr	Pro	Val	Gln	Thr	Ser	Ser	Arg	Thr	Ala	
	130							135				140				

ggc	gca	atg	tgg	gga	tgc	cac	att	cac	aac	acg	gtg	aac	gaa	tac	cta	480
Ala	Ala	Met	Trp	Gly	Cys	His	Ile	His	Asn	Lys	Val	Asn	Glu	Tyr	Leu	
145					150					155			160			

aag aaa gac ata tat qac tgt gct acc atc cta gag gac tac cat tgt 528
 Lys Lys Asp Ile Tyr Asp Cys Ala Thr Ile Leu Glu Asp Tyr Asp Cys
 165 170 175

gga tgt agt gac agc gac ggt aaa cgc gtg tot ctc gag aag gag gct 576
 Gly Cys Ser Asp Ser Asp Gly Lys Arg Val Ser Leu Glu Lys Glu Ala
 180 195 190

aaa gag cac ggt tga 591
 Lys Glu His Gly
 195

<210> 232

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<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 232

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 20 25 30

Ile Ala Thr Pro Gly Leu Ile Lys Ala Lys Ser Gly Ile Asp Glu Val
 35 40 45

Gln Gly Ala Ala Ala Glu Lys Asn Asp Ala Arg Leu Lys Glu Ile Glu
 50 55 60

Lys Glu Thr Ile Met Pro Leu Met Gly Asp Asp Lys Val Lys Lys Glu
 65 70 75 80

Val Gly Arg Ala Ser Trp Lys Tyr Phe His Thr Leu Leu Ala Arg Phe

85

90

95

Phe Asp Glu Pro Thr Pro Glu Glu Arg Glu Lys Leu His Thr Phe Ile
103 105 110

Gly Leu Tyr Ala Glu Leu Tyr Pro Cys Gly Glu Cys Ser Tyr His Phe
115 120 125

Val Lys Leu Ile Glu Lys Tyr Pro Val Gln, Thr Ser Ser Arg Thr Ala
130 135 140

Ala Ala Met Trp Gly Cys His Ile His Asn Lys Val Asn Gln Tyr Leu
145 150 155 160

Lys Lys Asp Ile Tyr Asp Cys Ala Thr Ile Leu Glu Asp Tyr Asp Cys
165 170 175

Gly Cys Ser Asp Ser Asp Gly Lys Arg Val Ser Leu Glu Lys Glu Ala
180 185 190

Lys Gln His Gly
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<210> 233
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<213> *Saccharomyces cerevisiae*

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<222> (1) .. (1986)

<400> 233

549/762

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1 5 10 15	
gat gaa aac nat aaa ggg ggt tct gtt cat aac aag cga gag agt aga	96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg	
20 25 30	
aac caa all cat cat caa cag gga tta ggc cat aag aga aga agg ggt	144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Gly Gly	
35 40 45	
atc agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac aag	192
Ile Ser Gly Ser Ala Tyr Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg	
50 55 60	
aaa aga gac ggg aac ggt aga aaa cgt tgg cga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt cca ttc tta ggt gta ctt ttg cag ttt ago ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc ggt tat cat gtt cat aat apc gat agc gac ttg ttt gac aac lit	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gta aul ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa cat gtc	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc caa caa ggt ata agt tog ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	

165	170	175	
atg gtt cct ggt glc att tct acg gga att gaa agc tgg gga gtt att			576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Gln Ser Trp Gly Val Ile			
180	185	190	
gga gac gal gag lgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg			624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
195	200	205	
gga agt ttt tac atg ctg aga aca atg gtt atg gal aaa gtt tgt tgg			672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
210	215	220	
ttg aaa cat gta atg tta gat cct gaa aca ggt cgg gac aua cag aac			720
Leu Lys His Val Met Leu Asp Pro Gln Thr Gly Leu Asp Pro Pro Asn			
225	230	235	240
ttt acg ctc cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc			768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
245	250	255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att			816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
260	265	270	
ggc tac gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt			864
Gly Tyr Gln Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
275	280	285	
gca tai tta gat cta gaa aga cgc gal agg tac tti aag aag cta aag			912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
290	295	300	
gaa caa atc gaa ctg ttt cat caa ttg agl ggt gaa aca gtt tgt tta			960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
305	310	315	320
atg gga cat tct arg ggt cct cag att atc ttt tac ttt atg aaa tgg			1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			
325	330	335	

gtc gag gat gaa ggc ccc ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	
340 345 350	
aac gaa cac ata gat tcc ttc att aah gaa gaa ggg aag ctt ctg ggc	1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	
355 360 365	
gct cca aag gca gtt cca got cta att agt ggt gan atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	
370 375 380	
all caa lla aal aag tta gcc atg tat ggt ttg gaa aag ttc ttc tca	1200
Ile Glu Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	
385 390 395 400	
aga att gag aga gta aaa atg lla caa aag tgg ggt ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys Met Leu Glu Thr Trp Gly Gly Ile Pro Ser	
405 410 415	
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg cag tca tct	1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	
420 425 430	
tca gag gat gcc ttg aat aac aac acc gag aca tcc ggc aal lta att	1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	
435 440 445	
cga lli gaa agg aat aag agc gat gct ttc aac aaa aat ttg aca atg	1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	
450 455 460	
aaa gac gcc att aac atg aca tta tog ata tca cct gaa tgg ctg caa	1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Glu	
465 470 475 480	
aga aga gta cat gag cag tac tog ttc ggc tat tcc aag aat gaa gaa	1488
Arg Arg Val His Glu Glu Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	
485 490 495	
gaq tca aga aaa aat gag cta cac cac aag cac tgg tgg aat cca atg	1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	

500	505	510	
gaa gta cca ctt cca gaa gct acc cac atg aaa atc tat tgt ata tac			1584
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr			
514	520	525	
ggg gty aac aac cca act gaa agg gca tat gta tat aag gaa gag gat			1632
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp			
530	535	540	
gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag cca cct			1680
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro			
545	550	555	560
gta ttc ctc acc gag ggg gac gga acc gtt cgg ctg gtg gcg cat taa			1728
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser			
565	570	575	
atg tgt cac aac tgg gcc cca ggt gct tca ccg tac aac cct gcc gga			1776
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly			
580	585	590	
att aac gtt acc att gtg gaa atg aaa cac cag cca gat cga ttt gat			1824
Ile Asn Val Thr Ile Val Glu Met Cys His Gln Pro Asp Arg Phe Asp			
595	600	605	
ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc			1872
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser			
610	615	620	
ggg gag ttg aac gat tac atc ttg aac att gca agc ggt aat ggg gat			1920
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp			
625	630	635	640
ctc ggc ggg cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cgg			1968
Leu Val Glu Pro Arg Glu Leu Ser Asn Leu Ser Gln Trp Val Ser Glu			
645	650	655	
atg acc ttc cca atg taa			1986
Met Pro Phe Pro Met			
660			

<210> 334
 <211> 661
 <212> FRT
 <213> Saccharomyces cerevisiae

<400> 234

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Asn Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

Lys Glu Leu Leu Arg Asp Cys Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

Gly Ser Thr Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240

Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255

Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Glu Asn Leu Gly Val Ile
 260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Gln Trp Leu Gln
465 470 475 480

Arg	Arg	Val	His	Glu	Glu	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu
				485					490					495	

Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Tyr	Ser	Asn	Pro	Met
			500					505					510		

Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr
			515					520					525		

Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp
			530				535					540			

Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro
545					550					555					560

Val	Thr	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser
				565					570					575	

Met	Cys	His	Lys	Tyr	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly
				580				585					590		

Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Glu	Pro	Asp	Arg	Phe	Asp
			595				600					605			

Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser
		610				615					620				

Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp
625						630				635				640	

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 545 650 655

Met Pro Phe Pro Met
 660

<210> 235
 <211> 1164
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1164)

<400> 235
 atg gaa cag aac agy ttc aag aua gaa acg aaa act tgt agc gct agc 48
 Met Glu Gln Asn Arg Phe Lys Lys Gln Thr Lys Thr Cys Ser Ala Ser
 1 5 10 15
 tgg ccy cgc gca ccy cag tgg acg ctg tgt gcg aca gat cgc ctc gac 96
 Trp Pro Arg Ala Pro Gln Ser Thr Leu Cys Ala Thr Asp Arg Leu Glu
 20 25 30
 atc aca tac gat gtg tac act agc gca gag cgg aaa cgc cgc tct cgc 144
 Leu Thr Tyr Asp Val Tyr Thr Ser Ala Glu Arg Gln Arg Arg Ser Arg
 35 40 45
 act gcc act aag ctt aac ctt gtg ttt ttg cac ggc agc ggc atg agc 192
 Thr Ala Thr Arg Leu Asn Leu Val Phe Leu His Gly Ser Gly Met Ser
 50 55 60
 aag gtg gta tgg gag tac tat ttg cag cgt ctg gta gcc gcc gat gcg 240
 Lys Val Val Trp Glu Tyr Tyr Leu Pro Arg Leu Val Ala Ala Asp Ala
 65 70 75 80
 gag ggc aat tat gcc atc gac aag gtc ttg ttg atc gac cag gtt aac 288
 Glu Gly Asn Tyr Ala Ile Asp Lys Val Leu Leu Ile Asp Gln Val Asn
 85 90 95

cac ggt gat tct gag gta cgc aac cgc ggc aga ctc gcc acc aat ttc	336
His Gly Asp Ser Ala Val Arg Asp Arg Gly Arg Leu Gly Thr Asn Phe	
100 195 110	
auc tgg atc gac ggg gcc cgc gac gtg ctc aag att gcc asa tgc gag	384
Asn Trp Ile Asp Gly Ala Arg Asp Val Leu Lys Ile Ala Thr Cys Glu	
115 120 125	
tfg ggc agt att gac tgu cgc cug gca cta aac gta gtc atc ggc cac	432
Leu Gly Ser Ile Asp Ser His Pro Ala Leu Asn Val Val Ile Gly His	
130 135 140	
tcg atg gcc ggg ttc cag gct ctt ggc tgt gac gtc atg cag acc aat	480
Ser Met Gly Gly Phe Gln Ala Leu Ala Cys Asp Val Leu Gln Pro Asn	
145 150 155 160	
ctg ttt cat tgg ctc atc tta atc gag cct gta gta ctc aca cgg aaa	528
Leu Phe His Leu Leu Ile Leu Ile Glu Pro Val Val Ile Thr Arg Lys	
165 170 175	
gcc atc gcc gcc ggg agg cca ggg ctt cag aac gct tct cgc cag atc	576
Ala Ile Gly Ala Gly Arg Pro Gly Leu Pro Pro Arg Ser Pro Gln Ile	
180 185 190	
cca gaa aat ctt tat aac tcc cta cgt tta aag acg tgc gac ctt ttc	624
Pro Glu Asn Leu Tyr Asn Ser Leu Arg Leu Lys Thr Cys Asp His Phe	
195 200 205	
gct aac gag tcc gaa tat gta aac tat atg agg aac cgt tcc ttt ttt	672
Ala Asn Glu Ser Glu Tyr Val Lys Tyr Met Arg Asn Gly Ser Phe Phe	
210 215 220	
acc aat gcc cag agc caa atc atg caa aac atc atc gat ttt gag agg	720
Thr Asn Ala His Ser Gln Ile Leu Glu Asn Ile Ile Asp Phe Glu Arg	
225 230 235 240	
aca aaa gcc tct gga gcc gat gaa gat ggt gga ccc gtt cgc ucy aag	768
Thr Lys Ala Ser Gly Asp Asp Glu Asp Gly Gly Pro Val Arg Thr Lys	
245 250 255	
atg gag cag gct caa aat ctc ctc tgc tac atg aac atg cag act ttt	816

Met Glu Gln Ala Gln Asn Leu Leu Cys Tyr Met Asn Met Gln Thr Phe
260 265 270

ggc cct ttc cly aid agc aat gty aag ttt gty agy aag cgg acg ucu 564
Ala Pro Phe Leu Ile Ser Asn Val Lys Phe Val Arg Lys Arg Tyr Trp
275 280 285

cac att gty ggc gcy cgc tcc aac tgg tgt cct ccg caa aat cag ctg 912
His Ile Val Gly Ala Arg Ser Asn Trp Cys Pro Pro Gln Asn Gln Leu
290 295 300

ttt ttg cag aaa acg cta cag aac tac cal cto gat gtc att ccc ggc 960
Phe Leu Gln Lys Thr Leu Gln Asn Tyr His Leu Asp Val Ile Pro Gly
305 310 315 320

ggc tcc ccc ttg gtc aac gtt gag gct ccg gac ctg gty atc gag agg 1008
Gly Ser His Leu Val Asn Val Glu Ala Pro Asp Leu Val Ile Gln Arg
325 330 335

att aat ccc ccc atc ccc gag ttt gtc ctt acc tcc ccg ctg cag tcc 1056
Ile Asn His His Ile His Glu Phe Val Leu Thr Ser Pro Leu Gln Ser
340 345 350

tca ccc att ccg caa ttg acc ctt gaa gaa aga ggc gtg atg ttt gac 1104
Ser His Ile Pro Gln Leu Thr Leu Glu Glu Arg Ala Val Met Phe Asp
355 360 365

ogy gct ttc gac tgg ttc aag aat gaa got ttg gtc aaa ccg cct aac 1152
Arg Ala Phe Asp Ser Phe Lys Asn Glu Ala Leu Val Lys Thr Thr Lys
370 375 380

cac aaa ctg taa 1164
Gln Lys Leu
385

<210> 236
<211> 387
<212> PRT
<213> Saccharomyces cerevisiae

<400> 236

Met Glu Gln Asn Arg Phe Lys Lys Glu Thr Lys Thr Cys Ser Ala Ser
 1 5 10 15

Trp Pro Arg Ala Pro Gln Ser Thr Leu Cys Ala Thr Asp Arg Leu Glu
 20 25 30

Leu Thr Tyr Asp Val Tyr Thr Ser Ala Glu Arg Gln Arg Arg Ser Arg
 35 40 45

Thr Ala Thr Arg Leu Asn Leu Val Phe Leu His Gly Ser Gly Met Ser
 50 55 60

Lys Val Val Trp Glu Tyr Tyr Leu Pro Arg Leu Val Ala Ala Asp Ala
 65 70 75 80

Glu Gly Asn Tyr Ala Ile Asp Lys Val Leu Leu Ile Asp Gln Val Asn
 85 90 95

His Gly Asp Ser Ala Val Arg Asn Arg Gly Arg Leu Gly Thr Asn Phe
 100 105 110

Asn Trp Ile Asp Gly Ala Arg Asp Val Leu Lys Ile Ala Thr Cys Glu
 115 120 125

Leu Gly Ser Ile Asp Ser His Pro Ala Leu Asn Val Val Ile Gly His
 130 135 140

Ser Met Gly Gly Phe Gln Ala Leu Ala Cys Asp Val Leu Gln Pro Asn
 145 150 155 160

Leu Phe His Leu Leu Ile Leu Ile Glu Pro Val Val Ile Thr Arg Lys

163

170

175

Ala Ile Gly Ala Gly Arg Pro Gly Leu Pro Pro Asp Ser Pro Gln Ile
180 185 190

Pro Glu Asn Leu Tyr Asn Ser Leu Arg Leu Lys Thr Cys Asp His Phe
195 200 205

Ala Asn Glu Ser Glu Tyr Val Lys Tyr Met Arg Asn Gly Ser Phe Phe
210 215 220

Thr Asp Ala His Ser Gln Ile Leu Gln Asn Ile Ile Asp Phe Glu Arg
225 230 235 240

Thr Lys Ala Ser Gly Asp Asp Glu Asp Gly Gly Pro Val Arg Thr Lys
245 250 255

Met Glu Glu Ala Glu Asn Leu Leu Cys Tyr Met Asn Met Glu Thr Phe
260 265 270

Ala Pro Phe Leu Ile Ser Asn Val Lys Phe Val Arg Lys Arg Thr Ile
275 280 285

His Ile Val Gly Ala Arg Ser Asn Trp Cys Pro Pro Gln Asn Gln Leu
290 295 300

Phe Leu Gln Lys Thr Leu Gln Asn Tyr His Leu Asp Val Ile Pro Gly
305 310 315 320

Gly Ser His Leu Val Asn Val Glu Ala Pro Asp Leu Val Ile Glu Arg
325 330 335

Ile Asn His His Ile His Glu Phe Val Leu Thr Ser Pro Leu Gln Ser
340 345 350

Ser His Ile Pro Gln Leu Thr Leu Gln Glu Arg Ala Val Met Phe Asp
355 360 365

Arg Ala Phe Asp Ser Phe Lys Asn Glu Ala Leu Val Lys Thr Thr Lys
370 375 380

Gln Lys Leu
385

<210> 237
<211> L929
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1939)

<400> 237
atg tca tct cag ttt ttu ctg aaa acc tct cag gat ata gag ctg ttc 48
Met Ser Ser Gln Phe Phe Leu Lys Thr Ser Gln Asp Ile Glu Leu Phe
1 5 10 15
caa agc tac cca act ttt gag caa tcc aac aca aac tcc aag gat ttc 96
Glu Ser Tyr Pro Thr Phe Glu Gln Ser Asn Thr Asn Ser Lys Asp Phe
20 25 30
cot gtc att tcc tct gtt tta tct cca tgt ggc aga ttt ttg got tta 144
Pro Val Ile Ser Ser Val Leu Ser Pro Cys Gly Arg Phe Leu Ala Leu
35 40 45
tct acg aag gaa aac ctg aaa gtt ttt sca ggt cca tgt ttg gat aac 192
Ser Thr Lys Glu Asn Val Lys Val Phe Thr Gly Pro Cys Leu Asp Asn

50	55	60	
glt cta tta acc atg aag ttg tcc gac gtc tat gac cta cac ttc lct			240
Val Tau Leu Thr Met Lys Leu Ser Asp Val Tyr Asp Leu His Phe Ser			
65	70	75	80
cca gca ggt aac tac tta agc act tgg gag aga gcg tct ata aca gag			280
Pro Ala Gly Asn Tyr Leu Ser Thr Trp Glu Arg Ala Ser Ile Gln Asp			
85	90	95	
cca aat cac aag aau gll aua gtt tgg tat ttg aat aaa cca ttt aag			320
Pro Asn His Tyr Asn Val Lys Val Trp Tyr Leu Asn Lys Pro Phe Lys			
100	105	110	
aaa gal tgc gtt tog gag gat cta gtc cct gct tac gaa tat caa guc			360
Lys Asp Cys Val Ser Glu Asp Ile Val Pro Ala Tyr Glu Tyr Gln Asn			
115	120	125	
aaa tcc caa agc ggt tgg ctt tta cca ttc tcc aca tta gac aat tat			400
Lys Ser Gln Ser Gly Trp Phe Leu Gln Phe Ser Lys Leu Asp Asn Tyr			
130	135	140	
aaa cta aga ctt ttt aaa caa gac ttg aag atc gtc aac tta agc tcc			440
Gly Leu Arg Leu Phe Lys His Asp Leu Lys Ile Val Lys Leu Ser Ser			
145	150	155	160
gct aat guc gnc aat ttc gac ttc caa tct cgg tll gct gtc ttg tot			520
Ala Asn Ala Asp Asn Phe Asp Phe Glu Ser Pro Phe Ala Val Leu Ser			
165	170	175	
gac gat gaa aag tcc caa cat ttc acc acc tac cta atc lcl aua gul			576
Asp Asp Glu Thr Ser Gln His Phe Thr Thr Tyr Leu Ile Ser Pro Ala			
180	185	190	
gaa cat cca acc att tgt act ttc acc cca gaa aag ggt ggt aau cgg			624
Glu His Pro Thr Ile Cys Thr Phe Thr Pro Glu Lys Gly Gly Lys Pro			
195	200	205	
gct caa tta atc ata tgg gac ctc tot gaa ggt aaa atc acc aag aaa			672
Ala Gln Leu Ile Ile Trp Ala Leu Ser Glu Gly Lys Ile Thr Lys Lys			
210	215	220	

aat cca tta ggt aat got att tta tgt tta get att got gat ttt gat 769
asn pro leu gly asn ala ile leu cys leu ala ile thr asp phe asp
245 250 255

ttc caa ggt gtc aac ggg act ttg ggt ggt aac tct gta ggt gtt tct 864
Phe Glu Gly Val Asn Gly Thr Leu Gly Gly Asn Ser Val Arg Val Ser
275 280 285

Sta acc act ggn cat gtc cac gat ttc act Lgg bog con act tca agg 91.2
Leu Thr Thr Gly Pro Val His Asp Phe Thr Trp Ser Pro Thr Ser Arg
290 295 300

dea tta qgt gtc atc gct ggt laa atg cca gca acc att tcc ttc ttt 963
 Gln Phe Gly Val Ile Ala Gly Tyr Met Pro Ala Thr Ile Ser Phe Phe
 305 310 315 320

gac tta aga ggt aat gtt ggc cat tca tta cct caa cae ggc aaa aat 1008
Asp Leu Arg Gly Asn Val Val His Ser Leu Pro Glu Glu Ala Lys Asn
325 330 335

AGC ATG CTT TTT TCT GCG TAT GGT CAT TAC ATT CTT ATC GGC GGG TTT 1056
 Thr Met Leu Phe Ser Pro Ser Gly His Tyr Ile Leu Ile Ala Gly Phe
 340 345 350

99L aa: tta cag ggc tcc gtc gaa atc cta gat cgt ctc gac aca ttc 1104
 Gly Asn Leu Glu Gly Ser Val Glu Ile Leu Asp Arg Leu Asp Lys Phe
 355 360 365

aag tgc gtg agt aaa ttt gac gct acc aac act tot gtc tgc aaa tgg 1152
 Lys Cys Val Ser Lys Phe Asp Ala Thr Asn Thr Ser Val Cys Lys Trp
 370 375 380

taa cag qgt qga gaa ttt atc atg aca gct acc act tca cca aga ttg 1200
Ser Pro Gly Gly Glu Phe Ile Met Thr Ala Thr Thr Ser Pro Pro Leu

385	390	395	400	
aga gtc gat aac ggc gtt aaa ata tgg cat gta tca ggc tct tta gta				1218
Arg Val Asp Asn Gly Val Lys Ile Trp His Val Ser Gly Ser Leu Val				
405	410	415		
ttt gtc aac gag ttc aag gag ctt ttg aag gta gac tgg agg tca cca				1296
Phe Val Lys Glu Phe Lys Glu Leu Leu Lys Val Asp Trp Arg Ser Pro				
420	425	430		
tgt aat tac aaa act ttg gaa aac aaa gac gaa gca ttt ttc gag aac				1344
Cys Asn Tyr Lys Thr Leu Glu Asn Lys Asp Glu Ala Phe Phe Glu Asn				
435	440	445		
aat atc att aat aac tgg gaa ccg cta cct gat tgg acc aca tct tca				1392
His Ile Ile Asn Asn Trp Glu Pro Leu Pro Asp Ser Thr Thr Ser Ser				
450	455	460		
ctt gat cct aac ata tcc aat aac tca gaa ttg cca ata cat tct agc				1440
Leu Asp Asn Lys Ile Ser Asn Lys Ser Glu Leu Glu Ile His Ser Ser				
465	470	475	480	
glt cca gag tac ata agt cca cca cca agc aga gaa gca agc ttc aat				1488
Val Glu Glu Tyr Ile Ser Glu His Pro Ser Arg Glu Ala Ser Ser Asn				
485	490	495		
gga aac gga tct aag gcc aaa gct gga ggc gct tat aac cca cct ccc				1536
Gly Asn Gly Ser Lys Ala Lys Ala Gly Gly Ala Tyr Tyr Pro Pro His				
500	505	510		
gca aga aga aca ggc ggt gga cgt att gtc ccc gga gtt cct cct ggt				1584
Ala Arg Arg Thr Gly Gly Gly Arg Ile Val Pro Gly Val Pro Pro Gly				
515	520	525		
gca gca aag aag aac atc cca ggc cta gtt ccg gcc atg agt gcc aac				1632
Ala Ala Lys Lys Thr Ile Pro Gly Leu Val Pro Gly Met Ser Ala Asn				
530	535	540		
aag gac gcc aac acc aag acc agg aga aga aga gcc aat aac aag tca				1680
Lys Asp Ala Asn Thr Lys Asn Arg Arg Arg Arg Ala Asn Lys Lys Ser				
545	550	555	560	

agc gaa aag tca cct gat tct act ccc gcc cca tct gct cct gcc tcc 1728
 Ser Glu Thr Ser Ser Pro Asp Ser Thr Pro Ala Pro Ser Ala Pro Ala Ser
 565 570 575

aca aat gcc ccc aca aac aat aaa gaa act tct cca gag gag aag aaa 1776
 Thr Asn Ala Pro Thr Asn Asn Lys Glu Thr Ser Pro Glu Glu Lys Lys
 580 585 590

ala aua tct tta cta aag aaa tta agc gct att gaa acc ttg aag gaa 1824
 Ile Arg Ser Leu Leu Lys Lys Leu Arg Ala Ile Glu Thr Leu Lys Glu
 595 600 605

aga cag ggc glc ggc gac aaa cta gaa gat acg caa gtt cta aaa att 1872
 Arg Glu Ala Val Gly Asp Lys Leu Glu Arg Thr Gln Val Leu Lys Ile
 610 615 620

caa act gaa gaa aaa gtc ttg aaa gat ttg gaa aag ttg ggc tgg aag 1920
 Gln Thr Glu Glu Lys Val Leu Lys Asp Leu Glu Lys Leu Gly Trp Lys
 625 630 635 640

gat caa caa 1929
 Asp Glu

<210> 238
 <211> 642
 <212> ERT
 <213> *Saccharomyces cerevisiae*
 <400> 238

Met Ser Ser Gln Phe Phe Leu Lys Thr Ser Gln Asp Ile Glu Leu Phe
 1 3 10 15

Gln Ser Tyr Pro Thr Phe Gln Gln Ser Asn Thr Asn Ser Lys Asp Phe
 20 25 30

Pro Val Ile Ser Ser Val Leu Ser Pro Cys Gly Arg Phe Leu Ala Leu
 35 40 45

Ser Thr Lys Glu Asn Val Lys Val Phe Thr Gly Pro Cys Leu Asp Asn
50 55 60

Val Leu Leu Thr Met Lys Leu Ser Asp Val Tyr Asp Leu His Phe Ser
65 70 75 80

Pro Ala Gly Asn Tyr Leu Ser Thr Trp Glu Arg Ala Ser Ile Gln Asp
85 90 95

Pro Asn His Lys Asn Val Lys Val Trp Tyr Leu Asn Lys Pro Phe Lys
100 105 110

Lys Asp Cys Val Ser Glu Asp Ile Val Pro Ala Tyr Glu Tyr Gln Ala
115 120 125

Lys Ser Glu Ser Gly Trp Phe Leu Gln Phe Ser Lys Leu Asp Asn Tyr
130 135 140

Gly Leu Arg Leu Phe Lys His Asp Leu Lys Ile Val Lys Leu Ser Ser
145 150 155 160

Ala Asn Ala Asp Asn Phe Asp Phe Gln Ser Pro Phe Ala Val Leu Ser
165 170 175

Asp Asp Glu Thr Ser Gln His Phe Thr Thr Tyr Leu Ile Ser Pro Ala
180 185 190

Glu His Pro Thr Ile Cys Thr Phe Thr Pro Gln Lys Gly Gly Lys Pro
195 200 205

Ala Gln Leu Ile Ile Trp Ala Leu Ser Glu Gly Lys Ile Thr Lys Lys-
 210 215 220

Ile Ala Ser Lys Thr Phe Phe Lys Ala Asp Ser Cys Gln Leu Lys Trp
 225 230 235 240

Asn Pro Leu Gly Asn Ala Ile Leu Cys Leu Ala Ile Thr Asp Phe Asp
 245 250 255

Ser Ser Asn Lys Ser Tyr Tyr Gly Glu Asn Thr Leu Tyr Leu Leu Ser
 260 265 270

Phe Gln Gly Val Asn Gly Thr Leu Gly Gly Asn Ser Val Arg Val Ser
 275 280 285

Leu Thr Thr Gly Pro Val His Asp Phe Thr Trp Ser Pro Thr Ser Arg
 290 295 300

Gln Phe Gly Val Ile Ala Gly Tyr Met Pro Ala Thr Ile Ser Phe Phe
 305 310 315 320

Asp Leu Arg Gly Asn Val Val His Ser Leu Pro Gln Gln Ala Lys Asn
 325 330 335

Thr Met Leu Phe Ser Pro Ser Gly His Tyr Ile Leu Ile Ala Gly Phe
 340 345 350

Gly Asn Leu Gln Gly Ser Val Glu Ile Leu Asp Arg Leu Asp Lys Phe
 355 360 365

Lys Cys Val Ser Gln Phe Asp Ala Thr Asn Thr Ser Val Cys Lys Trp
 370 375 380

FIG. 10. Amino acid sequence of the protein.

Ser Pro Gly Gly Glu Phe Ile Met Thr Ala Thr Thr Ser Pro Arg Leu
385 390 395 400

Arg Val Asp Asn Gly Val Lys Ile Trp His Val Ser Gly Ser Leu Val
405 410 415

Phe Val Lys Glu Phe Lys Glu Leu Leu Lys Val Asp Trp Arg Ser Pro
420 425 430

Cys Asn Tyr Lys Thr Leu Glu Asn Lys Asp Glu Ala Phe Phe Glu Asn
435 440 445

His Ile Ile Asn Asn Trp Glu Pro Ser Pro Asp Ser Thr Thr Ser Ser
450 455 460

Leu Asp Pro Lys Ile Ser Asn Tyr Ser Gly Leu Gln Ile His Ser Ser
465 470 475 480

Val Ala Glu Tyr Ile Ser Gln His Pro Ser Arg Glu Ala Ser Ser Asn
485 490 495

Gly Asn Gly Ser Lys Ala Lys Ala Gly Gly Ala Tyr Lys Pro Pro His
500 505 510

Ala Arg Arg Thr Gly Gly Gly Arg Ile Val Pro Gly Val Pro Pro Gly
515 520 525

Ala Ala Lys Lys Thr Ile Pro Gly Leu Val Pro Gly Met Ser Ala Asn
530 535 540

1. The amino acid sequence of the protein is:

Lys Asp Ala Asn Thr Lys Asn Arg Arg Arg Ala Asn Lys Lys Ser
545 550 555 560

Ser Glu Thr Ser Pro Asp Ser Thr Pro Ala Pro Ser Ala Pro Ala Ser
565 570 575

Thr Asn Ala Pro Thr Asn Asn Lys Glu Thr Ser Pro Glu Glu Lys Lys
580 585 590

Ile Asn Ser Ser Ser Lys Lys Leu Arg Ala Ile Glu Thr Leu Lys Glu
595 600 605

Arg Glu Ala Val Gly Asp Lys Leu Glu Asp Thr Glu Val Leu Lys Ile
610 615 620

Glu Thr Glu Glu Lys Val Leu Lys Asp Leu Glu Lys Leu Gly Trp Lys
625 630 635 640

Asp Glu

<210> 239

<211> 450

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(450)

<400> 239

atg tca gcc acc aga gcc aat aaa gat att ttc aca cta ttc gac aag 48
Met Ser Ala Thr Arg Ala Asn Lys Asp Ile Phe Thr Leu Phe Asp Lys
1 5 10 15

aag ggt cca ggc gcc att gcc aag gat tcc ttg gga gat tac ctg agg 96
 Lys Gly Glu Gly Ala Ile Ala Lys Asp Ser Leu Gly Arg Tyr Leu Arg
 20 25 30

gca att ggc tcc aac ccc acc aac cag ctg gta cag gac atc ala aac 144
 Ala Ile Gly Tyr Asn Pro Thr Asn Glu Leu Val Glu Asp Ile Ile Asn
 35 40 45

gag gat tgg agc ttg cga gac gcc tcc agc ttg acg ctg gac cag att 192
 Ala Asp Ser Ser Leu Arg Asp Ala Ser Ser Leu Thr Leu Asp Glu Ile
 50 55 60

aca ggc cta att gaa gtc aac gaa aag gaa ttg gat gca act acc aag 240
 Thr Gly Leu Ile Glu Val Asn Gln Lys Glu Leu Asp Ala Thr Thr Lys
 65 70 75 80

gca aag aca gaa gac ttc gtc aag gca ttc cag gtc ttc gac aag gaa 288
 Ala Lys Thr Glu Asp Phe Val Lys Ala Thr Glu Val Phe Asp Lys Glu
 85 90 95

agt acc ggc aag gtc tcc gtt ggt gac tta cgg tcc arg ctg act ggc 336
 Ser Thr Gly Lys Val Ser Val Gly Asp Leu Arg Tyr Met Leu Gly
 100 105 110

ttg ggt gaa aag tta acc gac gct gaa gta gac gag ctg ttg aag ggt 384
 Leu Gly Glu Lys Leu Thr Asp Ala Glu Val Arg Glu Leu Leu Lys Gly
 115 120 125

gth gaa gtg gac agc aac gga gaa att gac tac aag aag ttc atc gaa 432
 Val Glu Val Asp Ser Asn Gly Glu Ile Arg Tyr Lys Lys Phe Ile Glu
 130 135 140

gat gtt ttg aga caa tga 480
 Asp Val Leu Arg Glu
 145

<210> 240

<211> 149

<212> PRT

<213> Saccharomyces cerevisiae

<400> 240

Met Ser Ala Thr Arg Ala Asn Lys Asp Ile Phe Thr Leu His Asp Lys
 1 5 10 15

Lys Gly Gln Gly Ala Ile Ala Lys Asp Ser Leu Gly Asp Tyr Leu Arg
 20 25 30

Ala Ile Gly Tyr Asn Pro Thr Asn Glu Leu Val Gln Asp Ile Ile Asn
 35 40 45

Ala Asp Ser Ser Leu Arg Asp Ala Ser Ser Leu Thr Leu Asp Gln Ile
 50 55 60

Thr Gly Leu Ile Glu Val Asn Glu Lys Glu Leu Asp Ala Thr Thr Lys
 65 70 75 80

Ala Lys Thr Glu Asp Phe Val Lys Ala Phe Gln Val Phe Asp Lys Glu
 85 90 95

Ser Thr Gly Lys Val Ser Val Gly Asp Asn Arg Tyr Met Asn Thr Gly
 100 105 110

Leu Gly Glu Lys Leu Thr Asp Ala Glu Val Asp Glu Leu Leu Lys Gly
 115 120 125

Val Glu Val Asp Ser Asn Gly Glu Ile Asp Tyr Lys Lys Phe Ile Glu
 130 135 140

Asp Val Leu Arg Gln
 145

1. The following sequence is a sequence of the DNA sequence of the

<210> 241
 <211> 1762
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1762)

<400> 241
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 Met Tyr Ser Ile Val Lys Glu Ile Ile Val Asp Pro Tyr Lys Arg Leu
 1 5 10 15
 aaa tgg ggt ttt att cca gta aag cgg cgg gtg gaa gac ctg cca gat 96
 Lys Trp Gly Phe Ile Pro Val Tyr Arg Gln Val Glu Asp Leu Pro Asp
 20 25 30
 gac tta aat tca aca gaa att gtc acc atc tcc aac agt atc cag agt 144
 Asp Leu Asn Ser Thr Glu Ile Val Thr Ile Ser Asn Ser Ile Val Asn
 35 40 45
 cat gaa ace gct gaa aat ttc atc atg aat aca agt gaa aaa gat aaa 192
 His Glu Thr Ala Glu Asn Phe Ile Thr Thr Thr Ser Glu Lys Asp Gln
 50 55 60
 cta cat ttt gag act agt ago tat agt gaa cat aaa cgc aat gtg aac 240
 Leu His Phe Glu Thr Ser Ser Tyr Ser Glu His Lys Asp Asn Val Asn
 65 70 75 80
 gtt act aga agt tat gaa tat aga gat gaa gcc gat agg cca tgg tgg 288
 Val Thr Arg Ser Tyr Glu Tyr Arg Asp Glu Ala Asp Arg Pro Trp Trp
 85 90 95
 aga ttt ttc gat gaa caa gag tat cgg atc aat gaa aag gaa aga tot 336
 Arg Phe Phe Asp Glu Glu Tyr Arg Ile Asn Glu Lys Glu Arg Ser
 100 105 110
 cac aat aaa tgg tat agt tgg ttc aaa cag ggt acc tot ttc aaa gaa 384
 His Asn Lys Trp Tyr Ser Trp Phe Lys Gln Gly Thr Ser Phe Lys Glu

115	120	125	
aaa aaa tta tta att aaa ttg gat gtc ctt tta gcc ttt tat tct tgt			432
Lys Lys Leu Leu Ile Lys Leu Asp Val Leu Leu Ala Phe Tyr Ser Cys			
130	135	140	
att gct tat tgg gtg aaa tat ctg gat acg gtt aat ata aac aac gct			480
Ile Ala Tyr Trp Val Lys Tyr Leu Asp Thr Val Asn Ile Asn Asn Ala			
145	150	155	160
lac gtt tgg ggu atg aag gaa gat tta ggc ttt caa ggt aat gat tgg			528
Tyr Val Ser Gly Met Lys Glu Asp Leu Gly Phe Gln Gly Asn Asp Leu			
165	170	175	
gtg cct act caa gta atg tac aca ggt ggt aat att ata ttt caa ttg			576
Val His Thr Gln Val Met Tyr Thr Val Gly Asn Ile Ile Phe Gln Leu			
180	185	190	
cca ttt ttg att tac ctg aac aag ctg cca tta aac tat gtr tta cca			624
Pro Phe Leu Ile Tyr Leu Asn Lys Leu Pro Asn Asp Tyr Val Leu Pro			
195	200	205	
agc ctg gac tta tgt tgg tgg ctt tta acg gtt ggt gct gaa tat gtc			672
Ser Leu Asp Leu Cys Trp Ser Leu Leu Thr Val Gly Ala Ala Tyr Val			
210	215	220	
aat tct gta cca cac ttg aaa gca att agg ttt ttc att ggg gct ttt			720
Asn Ser Val Pro His Leu Lys Ala Ile Arg Phe Phe Ile Gly Ala Phe			
225	230	235	240
gaa gcg cca agt tat ttg gca tac caa tat ttg ttt ggt tcc ttt taa			768
Glu Ala Pro Ser Tyr Leu Ala Tyr Gln Tyr Leu Phe Gly Ser Phe Tyr			
245	250	255	
aca cat gat gaa atg gtg cgt cgt tct gct ttt taa tat ttg ggc cag			816
Lys His Asn Glu Met Val Arg Arg Ser Ala Phe Tyr Tyr Leu Gly Gln			
260	265	270	
tat atc ggt att cta tcc gct ggt ggg atc cag taa gcc gta tat tta			864
Tyr Ile Gly Ile Leu Ser Ala Gly Gly Ile Cln Ser Ala Val Tyr Ser			
275	280	285	

ttg tta aat ggt gta aat ggt tta gag gga tgg aga tgg aac ttt att	912
Ser Leu Asn Gly Val Asn Gly Leu Glu Gly Trp Arg Trp Asn Phe Ile	
290 295 300	
att gac gct att gtg tct gtc gta gtg ggc ctt att gga ttt tac tcc	960
Ile Asp Ala Ile Val Ser Val Val Val Gly Leu Ile Gly Phe Tyr Ser	
305 310 315 320	
ctg cca ggt gac cca tac aac tgt tac tct att ttc tta act gat gat	1008
Leu Pro Gly Asp Pro Tyr Asn Cys Tyr Ser Ile Phe Leu Thr Asp Asn	
325 330 335	
gaa att agg ttg gog agg aaa aga tta aaa gaa aac caa aca ggt aaa	1056
Gln Tle Arg Leu Ala Arg Lys Arg Leu Lys Glu Asn Gln Thr Gly Lys	
340 345 350	
agt gat ttt gaa aca aaa gta ttc gai att aaa ctg tgg aaa aca att	1104
Ser Asp Phe Glu Thr Lys Val Phe Asp Ile Lys Leu Trp Lys Thr Ile	
355 360 365	
ttc agt gai tgg aaa ata tac att tta act tta tgg aat att ttc tgt	1152
Phe Ser Asp Trp Lys Ile Tyr Ile Leu Thr Leu Trp Asn Ile Phe Cys	
370 375 380	
ttg aat gac tgt aat gtt tca tct ggg gca tac cta cta tgg ttg aaa	1200
Trp Asn Asp Ser Asn Val Ser Ser Gly Ala Tyr Leu Leu Trp Leu Lys	
385 390 395 400	
tct ttg aaa aga tac tct att cct aag ctc aat cag tta tcc atg att	1248
Ser Leu Lys Arg Tyr Ser Ile Pro Lys Leu Asn Gln Leu Ser Met Ile	
405 410 415	
act ccg ggt tta ggt atg gtt tat ttg atg ctt act ggt att att gca	1296
Thr Pro Gly Leu Gly Met Val Tyr Leu Met Leu Thr Gly Ile Ile Ala	
420 425 430	
gat aaa tta cac tct cgt tgg ttt gog att att ttc act cag gtt ttc	1344
Asp Lys Leu His Ser Arg Trp Phe Ala Ile Ile Phe Thr Gln Val Phe	
435 440 445	
aat atc att ggt aac tcc ata tta gcc gct tgg gac gtc gca gaa gga	1392
Asn Ile Ile Gly Asn Ser Ile Leu Ala Ala Trp Asp Val Ala Glu Gly	

450
 455
 460

gcc aaa tgg ttt gca ttt atg ctg caa tgt ttt ggt tgg gct atg gct 1440
 Ala Lys Trp Phe Ala Phe Met Leu Gln Cys Phe Gly Trp Ala Met Ala
 465 470 475 480

cct gtt tta tac tct tgg caa aac gat att tgt cgc cga gat gct caa 1488
 Pro Val Leu Tyr Ser Trp Gln Asn Asp Ile Cys Arg Arg Asp Ala Gln
 485 490 495

act aga gct att act tta gtt aca atg aat att atg gct caa tca tct 1536
 Thr Arg Ala Ile Thr Leu Val Thr Met Asn Ile Met Ala Gln Ser Ser
 500 505 510

aca gca tgg ata agt gtt ttg gtt tgg aca aca gaa gaa gct ccc agg 1584
 Thr Ala Trp Ile Ser Val Leu Val Trp Lys Thr Glu Glu Ala Pro Arg
 515 520 525

tat ata aag ggg ttt act ttc act gca tgt tct gct ttt tgt ctc tcc 1632
 Tyr Leu Lys Gly Phe Thr Phe Thr Ala Cys Ser Ala Phe Cys Leu Ser
 530 535 540

act tgg act ttt gtt gta ctg tan ttc tat aaa cgt gat gaa agg aac 1680
 Ile Trp Thr Phe Val Val Leu Tyr Phe Tyr Lys Arg Asp Glu Arg Asn
 545 550 555 560

aat gac aag aag aac ggt att gtg ctt tat aac tct aaa cat ggt gta 1728
 Asn Ala Lys Lys Asn Gly Ile Val Leu Tyr Asn Ser Lys His Gly Val
 565 570 575

gaa aag cca atg tca aaa gac gtt gaa acc tta tca gta tct gat gaa 1776
 Glu Lys Pro Thr Ser Lys Asp Val Glu Thr Leu Ser Val Ser Asp Glu
 580 585 590

aaa taa 1702
 Lys

<210> 342

<211> 593

<212> PRT

Fig. 1. Amino acid sequence of the protein.

577/762

<213> Saccharomyces cerevisiae

<400> 242

Met Tyr Ser Ile Val Lys Glu Ile Ile Val Asp Pro Tyr Lys Arg Leu

1 5 10 15

Lys Trp Gly Cys Ile Pro Val Lys Arg Gln Val Glu Asp Leu Pro Asp

20 25 30

Asp Leu Asn Ser Thr Glu Ile Val Thr Ile Ser Asn Ser Ile Glu Ser

35 40 45

His Glu Thr Ala Glu Asn Phe Ile Thr Thr Thr Ser Glu Lys Asp Glu

50 55 60

Leu His Phe Glu Thr Ser Ser Tyr Ser Glu His Lys Asp Asn Val Asn

65 70 75 80

Val Thr Arg Ser Tyr Glu Tyr Arg Asp Glu Ala Asp Arg Pro Trp Trp

85 90 95

Arg Phe Phe Asp Glu Gln Glu Tyr Arg Ile Asn Glu Lys Glu Arg Ser

100 105 110

His Asn Lys Trp Tyr Ser Trp Phe Lys Gln Gly Thr Ser Phe Lys Glu

115 120 125

Lys Lys Leu Leu Ile Lys Leu Asp Val Leu Leu Ala Phe Tyr Ser Cys

130 135 140

Ile Ala Tyr Trp Val Lys Tyr Leu Asp Thr Val Asn Ile Asn Asn Ala

145 150 155 160

Tyr Val Ser Gly Met Lys Glu Asp Leu Gly Phe Gln Gly Asn Asp Leu
 165 170 175

Val His Thr Gln Val Met Tyr Thr Val Gly Asn Ile Ile Phe Gln Leu
 180 185 190

Pro Phe Leu Ile Tyr Leu Asn Lys Leu Pro Leu Asn Tyr Val Leu Pro
 195 200 205

Ser Leu Asp Leu Cys Trp Ser Leu Leu Thr Val Gly Ala Ala Tyr Val
 210 215 220

Asn Ser Val Pro His Leu Lys Ala Ile Arg Phe Phe Ile Gly Ala Phe
 225 230 235 240

Glu Ala Pro Ser Tyr Leu Ala Tyr Gln Tyr Leu Phe Gly Ser Phe Tyr
 245 250 255

Lys His Asp Glu Met Val Arg Arg Ser Ala Phe Tyr Tyr Leu Gly Gln
 260 265 270

Tyr Ile Gly Ile Leu Ser Ala Gly Gly Ile Gln Ser Ala Val Tyr Ser
 275 280 285

Ser Leu Asn Gly Val Asn Gly Leu Glu Gly Trp Arg Trp Asn Phe Ile
 290 295 300

Ile Asp Ala Ile Val Ser Val Val Val Gly Leu Ile Gly Phe Tyr Ser
 305 310 315 320

Leu Pro Gly Asp Pro Tyr Asn Cys Tyr Ser Ile Phe Leu Thr Asp Asp
 325 330 335

Glu Ile Arg Leu Ala Arg Lys Arg Leu Lys Glu Asn Gln Thr Gly Tyr
 340 345 350

Ser Asp Phe Glu Thr Lys Val Phe Asp Ile Lys Leu Trp Lys Thr Ile
 355 360 365

Phe Ser Asp Trp Lys Ile Tyr Ile Leu Thr Leu Trp Asn Ile Phe Cys
 370 375 380

Trp Asn Asp Ser Asn Val Ser Ser Gly Ala Tyr Leu Leu Trp Leu Lys
 385 390 395 400

Ser Leu Lys Arg Tyr Ser Ile Pro Tyr Leu Asn Gln Leu Ser Met Ile
 405 410 415

Thr Pro Gly Leu Gly Met Val Tyr Leu Met Leu Thr Gly Ile Ile Ala
 420 425 430

Asp Lys Leu His Ser Arg Trp Phe Ala Ile Ile Phe Thr Gln Val Phe
 435 440 445

Asn Ile Ile Gly Asn Ser Ile Leu Ala Ala Trp Asp Val Ala Glu Gly
 450 455 460

Ala Lys Trp Phe Ala Phe Met Leu Gln Cys Phe Gly Trp Ala Met Ala
 465 470 475 480

Pro Val Leu Tyr Ser Trp Glu Asn Asp Ile Cys Arg Arg Asp Ala Gln
 485 490 495

Thr Arg Ala Ile Thr Leu Val Thr Met Asn Thr Met Ala Gly Ser Ser
 500 505 510

Thr Ala Trp Ile Ser Val Leu Val Trp Lys Thr Glu Glu Ala Pro Arg
 515 520 525

Tyr Leu Lys Gly Phe Thr Phe Thr Ala Cys Ser Ala Phe Cys Leu Ser
 530 535 540

Ile Trp Thr Phe Val Val Leu Tyr Phe Tyr Lys Arg Asp Glu Arg Asn
 545 550 555 560

Asn Ala Lys Lys Asn Gly Ile Val Leu Tyr Asn Ser Lys His Gly Val
 565 570 575

Glu Lys Pro Thr Ser Lys Asp Val Glu Thr Leu Ser Val Ser Asp Glu
 580 585 590

Lys

<210> 243
 <211> 1041
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1041)

<400> 243
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Met Lys Ala Ser His Ile Cys Ser Tyr Leu Leu Ser Ile Ala Pro Leu	
1 5 10 15	
gtg gtg tcc cat gga gta cac cat aat cga gat cat cgc cac gag gca	96
Val Val Ser His Gly Val His His Asn Arg Asp His Gly His Glu Ala	
20 25 30	
aac cat gag tcc aag caa agt ttc ttg att ttg aag caa gaa tcc att	144
Asn His Glu Ser Lys Gln Ser Phe Leu Ile Leu Lys Gln Gln Ser Ile	
35 40 45	
ttt tac tct cta gtt tgc ttt ctg cag aac caa ctg ttt gtc ctg gga	192
Phe Tyr Ser Leu Val Cys Phe Leu Glu Asn His Leu Phe Val Leu Gly	
50 55 60	
cac cgt tac aat gag att gtg gct atc cta atc ata caa ctt atg cag	240
Pro Arg Tyr Asn Ala Ile Val Ala Ile Leu Ile Ile Glu Leu Met Pro	
65 70 75 80	
tgt ctt ttc gta ctg ttt gtt cat gaa ctg cgc aag aac gat cgt gcc	288
Cys Leu Phe Val Leu Phe Val Pro Gly Asn Arg Lys Asn Asp Arg Ala	
85 90 95	
agc tgg aca ctg tcc ttu cta gtt tcc ttt tct cta gga aca ctg ctg	336
Ser Leu Thr Leu Ser Leu Leu Val Ser Phe Ser Leu Gly Thr Leu Leu	
100 105 110	
ggc gat att tta tta cac gtg ata cat gaa agt ctg agc ggc gta act	384
Gly Asp Ile Leu Leu His Val Ile Pro Glu Ser Leu Ser Gly Val Thr	
115 120 125	
gat gtc aca arg gtt gga gga gcc ata ttt ctg ggg ttc ata agc ttc	432
Asp Val Thr Met Val Gly Gly Ala Ile Phe Leu Gly Phe Ile Ser Phe	
130 135 140	
ttg act ctg gat aaa aag atg cgt att ctg tca ggg aag tcc aac gat	480
Leu Thr Leu Asp Lys Thr Met Arg Ile Leu Ser Gly Thr Ser Asn Asp	
145 150 155 160	
cac ggc agc ata caa tct cat tcc cat agt cat act cca caa caa act	528
Asp Gly Ser Ile His Ser His Ser His Ser His Thr Pro Gln Gln Thr	
165 170 175	

gaa gag aag auu gag ggc ttt aac atg tct gcg tat ctg aat gtc ata 576
 Ala Glu Lys Tyr Ala Gly Phe Asn Met Ser Ala Tyr Leu Asn Val Ile
 100 185 190

tcc gcc att gct cat cac atc acg gat ggc ata gcg ctg gct acg tca 624
 Ser Gly Ile Ala His His Ile Thr Asp Gly Ile Ala Leu Ala Thr Ser
 195 200 205

ttc tat agt tcc aca caa gtt ggc ata atg acc agc ata gct gtc act 672
 Phe Tyr Ser Ser Thr Gln Val Gly Ile Met Thr Ser Ile Ala Val Thr
 210 215 220

ttc cat gag atc cct cat gag cta ggt gac ttc gcc att ctg ctt tcc 720
 Phe His Glu Ile Pro His Glu Leu Gly Asp Phe Ala Ile Leu Leu Ser
 225 230 235 240

agt ggg ile acg ctc cca caa gcg ata aga gcc caa gcg gtg cca gcc 768
 Ser Gly Phe Thr Thr Pro Gln Ala Ile Arg Ala Gln Ala Val Thr Ala
 245 250 255

ttc gcc gcc gtc gtt gga aag tcc atc ggc tgc tgg atg aac gaa atc 816
 Phe Gly Ala Val Val Gly Thr Ser Ile Gly Cys Trp Met Asn Glu Ile
 260 265 270

ggc aac acc agc cat aac gcc acg tct tca tcc gcg aac gca tct gaa 864
 Gly Asn Asn Ser His Lys Ala Thr Ser Ser Ser Ala Asn Ala Ser Glu
 275 280 285

ctt atg ctg ccg ttc acg gcg ggc ggc ctc ata tac ata gcc act aat 912
 Leu Met Leu Pro Phe Thr Ala Gly Gly Leu Ile Tyr Ile Ala Thr Thr
 290 295 300

agc gtt gla ccg cag atc tta cat agc tcc gca ccc gat agc aag ctt 960
 Ser Val Val Pro Gln Ile Leu His Ser Ser Ala Pro Asp Ser Lys Leu
 305 310 315 320

cga gag ttt aag aag tgg gcc ttg cag cta gtc ttc att ttt gta gga 1008
 Arg Glu Phe Lys Lys Trp Ala Leu Gln Leu Val Phe Ile Phe Val Gly
 325 330 335

ttt gcc gtt atg gcg ctc atg gat gag cat tga 1044

Seq. ID No. 1

Phe Ala Val Met Ala Leu Met Asp Glu His

340

345

<210> 244

<311> 346

<212> ERT

<213> Saccharomyces cerevisiae

<400> 244

Met Lys Ala Ser His Ile Cys Ser Tyr Leu Leu Ser Ile Ala Pro Leu

1

5

10

15

Val Val Ser His Gly Val His His Asn Arg Asp His Gly His Glu Ala

20

25

30

Asn His Glu Ser Lys His Ser Phe Leu Ile Leu Lys Gln Glu Ser Ile

35

40

45

Phe Tyr Ser Leu Val Cys Phe Leu Gln Asn His Leu Phe Val Leu Gly

50

55

60

Pro Arg Tyr Asn Ala Ile Val Ala Ile Leu Ile Ile Gln Leu Met Pro

65

70

75

80

Cys Leu Phe Val Leu Phe Val Pro Gly Leu Arg Lys Asn Asp Arg Ala

85

90

95

Ser Leu Thr Leu Ser Leu Leu Val Ser Phe Ser Leu Gly Thr Leu Leu

100

105

110

Gly Asp Ile Leu Leu His Val Ile Pro Glu Ser Leu Ser Gly Val Thr

115

120

125

Fig. 1. Amino acid sequence of the protein.

Asp Val Thr Met Val Gly Gly Ala Ile Phe Leu Gly Phe Ile Ser Phe
120 135 140

Leu Thr Leu Asp Lys Thr Met Arg Ile Leu Ser Gly Thr Ser Asn Asp
145 150 155 160

Asp Gly Ser Ile His Ser His Ser His Ser His Thr Pro Gln Gln Thr
165 170 175

Ala Glu Lys Lys Ala Gly Phe Asn Met Ser Ala Tyr Leu Asn Val Ile
180 185 190

Ser Gly Ile Ala His His Ile Thr Asp Gly Ile Ala Leu Ala Thr Ser
195 200 205

Phe Tyr Ser Ser Thr Gln Val Gly Ile Met Thr Ser Ile Ala Val Thr
210 215 220

Phe His Glu Ile Pro His Glu Leu Gly Asp Phe Ala Ile Leu Leu Ser
225 230 235 240

Ser Gly Phe Thr Phe Pro Gln Ala Ile Arg Ala Gln Ala Val Thr Ala
245 250 255

Phe Gly Ala Val Val Gly Thr Ser Ile Gly Cys Trp Met Asn Glu Ile
255 260 265 270

Gly Asn Asn Ser His Lys Ala Thr Ser Ser Ser Ala Asn Ala Ser Glu
275 280 285

Leu Met Leu Pro Phe Thr Ala Gly Gly Leu Ile Tyr Ile Ala Thr Thr

230

295

300

Ser Val Val Pro Gln Ile Leu His Ser Ser Ala Pro Asp Ser Lys Leu
 305 310 315 320

Arg Gln Phe Lys Lys Trp Ala Leu Gln Leu Val Phe Ile Phe Val Gly
 325 330 335

Phe Ala Val Met Ala Leu Met Asp Gln His
 340 345

<210> 245

<211> 429

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(459)

<400> 245

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 1 5 10 15

gag ctc gta ggc att att gga aaa gbg ttc ttt ctc tta ata gaa gag 55
 Glu Leu Val Gly Ile Ile Gly Lys Val Phe Phe Leu Leu Ile Glu Glu
 20 25 30

att aag tac cag ata atc aca ccc aaa att att gtg gat gcc cag ata 144
 Ile Lys Tyr Pro Ile Ile Thr Pro Lys Ile Ile Val Asp Ala Gln Ile
 35 40 45

tct tct tgg tca tly ttt ttt ttc gct tca atc tgt aat ctc tct gca 192
 Ser Ser Trp Ser Leu Phe Phe Phe Ala Ser Ile Cys Asn Leu Ser Ala
 50 55 60

Ser Ser Trp Ser Leu Phe Phe Phe Ala Ser Ile Cys Arg Leu Ser Ala
50 55 60

FIG. 10. Amino acid sequence of the protein.

Lys Phe Arg Glu Pro Ile Val Thr Thr Ser Ser Ile Ile Ser Leu Met
65 70 75 80

Glu Ser Glu Lys Asp Leu Lys Asn Val Asn Glu Tyr Phe Gln Ile Met
85 90 95

Ala Lys Met Leu Phe Ile Leu Glu Asn Lys Ile Val Val Ser Leu Phe
100 105 110

Val Val Phe Asn Ile Ser Val Leu Ile Ile Val Lys Ser Glu Pro Tyr
115 120 125

Ser Tyr Gly Lys Val Leu Phe Lys Pro Ser Ser Ser Ile Phe
130 135 140

<210> 247
<211> 1167
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> {1}..(1167)

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Val Lys His Leu His Arg Phe Phe Ser Ser Asp Ala Ser Gly Gly Ile
1 5 10 15
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Ile Leu Ile Ile Ala Ala Ile Leu Ala Met Ile Met Ala Asn Ser Gly
20 25 30
gca acc agt gga tgg tat cac gac ttt ctg gag acg cag gtt cag ctg 144

Protein Data Bank

Ala Thr Ser Gly Trp Tyr His Asp Phe Leu Glu Thr Pro Val Gln Leu	
35 40 45	
ccg gtt ggc tca ctc gaa atc aac aaa uac atg ctg tta. Egg ata aat	192
Arg Val Gly Ser Leu Glu Ile Asn Lys Asn Met Leu Leu Trp Ile Asn	
50 55 60	
gac gag ctg atg gag gta ttt ttc ctg tta gtc ggt ctg gaa gtl aaa	240
Asp Ala Leu Met Ala Val Phe Phe Leu Leu Val Gly Leu Glu Val Lys	
65 70 75 80	
cgt gaa ctg atg caa gga tgg cta gcc agc tta cgc aag gcc gca ttt	288
Arg Glu Leu Met Gln Gly Ser Leu Ala Ser Leu Arg Glu Ala Ala Phe	
85 90 95	
cca gtt atc gnn gct aat ggt ggg atg att gtg ccg gca tta ctc tat	336
Pro Val Ile Ala Ala Phe Gly Gly Met Ile Val Pro Ala Leu Leu Tyr	
100 105 110	
ctg gcl ttt aac tat gcc gat ccg att acc cgc gaa ggg tgg gcc utc	384
Phe Ala Phe Asn Tyr Ala Asp Pro Phe Thr Arg Glu Gly Trp Ala Phe	
115 120 125	
ccg ggg gct aul gac att gct ttt gca ctt ggt gta ctg gag ctg ttg	432
Pro Ala Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Leu Ala Leu Leu	
130 135 140	
gga agt cgt gtt ccg tta gag ctg aag atc ttt ttg atg gcl ctg gct	480
Gly Ser Arg Val Pro Leu Ala Leu Lys Ile Phe Leu Met Ala Leu Ala	
145 150 155 160	
att aho gac gat ctt ggg gcc atc att atc atc gca ttt tta tac act	528
Ile Ile Asp Asp Leu Gly Ala Ile Ile Ile Ile Ala Leu Phe Tyr Thr	
165 170 175	
aat gac tta tgg atg gcc ttt ctt ggc gtc gag gct gta gca ala gag	576
Asn Asp Leu Ser Met Ala Ser Leu Gly Val Ala Ala Val Ala Ile Ala	
180 185 190	
gla ctc gag gta ttg aat ctg tgt ggc gca cgc cgc aag ggc gtc ttc	624
Val Leu Ala Val Leu Asn Leu Cys Gly Ala Arg Arg Thr Gly Val Tyr	
195 200 205	

FIG. 10. Amino acid sequence of the protein.

att ctt gtt ggc gtg gta ttg tgg act ggc gtg ttg aaa tgg ggg gtt	672
Ile Leu Val Gly Val Val Leu Trp Thr Ala Val Leu Lys Ser Gly Val	
210 215 220	
aac gca act ctg ggc ggg gta att gta ggc ttc ttt att cct ttg aaa	720
His Ala Thr Leu Ala Gly Val Ile Val Gly Phe Phe Ile Pro Leu Lys	
225 230 235 240	
gag aag cat ggg gat tct cca ggc aag cga ctg gag cat gtg ttg cac	768
Glu Lys His Gly Arg Ser Pro Ala Lys Arg Leu Glu His Val Leu His	
245 250 255	
acg tgg gtg gcy taa ctg att ttg ccg cng ttt gca ttt gct aat gct	816
Pro Trp Val Ala Tyr Leu Ile Leu Pro Leu Phe Ala Phe Ala Asn Ala	
260 265 270	
ggc gtt taa ctg cca ggc gtc acg ctg gat ggc ttg aac tcc att ctg	864
Gly Val Ser Leu Glu Gly Val Thr Leu Asp Gly Leu Thr Ser Ile Leu	
275 280 285	
caa ttg aag atc atc gct ggc ttg ctg att ggc aac ccg ctg ggg att	912
Pro Leu Gly Ile Ile Ala Gly Leu Leu Ile Gly Lys Pro Leu Gly Ile	
290 295 300	
agt ctg ttc tgc tgg ttg ggc ctg cgt ttg aac ctg ggc cat ctg cct	960
Ser Leu Phe Cys Trp Leu Ala Leu Arg Leu Lys Leu Ala His Leu Pro	
305 310 315 320	
gag gga aag act tat cag cca att atg gtg gta ggg atc ctg tgc ggt	1008
Glu Gly Thr Thr Tyr Glu Glu Ile Met Val Val Gly Ile Leu Cys Gly	
325 330 335	
atc ggt ttt act atg tct atc ttt atc gcc agc ctg gcc ttt ggt agc	1056
Ile Gly Phe Thr Met Ser Ile Phe Ile Ala Ser Leu Ala Phe Gly Ser	
340 345 350	
gta gat cca gaa ctg att aac tgg ggc aaa ctg ggt atc ctg gtc ggt	1104
Val Asp Pro Glu Leu Ile Ser Trp Ala Lys Leu Gly Ile Leu Val Gly	
355 360 365	
tct atc tct tgg ggc gta att gga taa agc tgg tta cys gtl cgt ttg	1152

Seq. ID: 1 (1-116) (1-116) (1-116)

Ser Ile Ser Ser Ala Val Ile Gly Tyr Ser Trp Leu Arg Val Arg Leu
 370 375 380

cgt cca tca gtt tga 1157
 Arg Pro Ser Val
 385

<210> 248
 <211> 386
 <212> PRT
 <213> Escherichia coli

<430> 248

Val Lys His Leu His Arg Phe Phe Ser Ser Asp Ala Ser Gly Gly Ile
 1 3 10 15

Ile Leu Ile Ile Ala Ala Ile Leu Ala Met Ile Met Ala Asn Ser Gly
 20 25 30

Ala Thr Ser Gly Trp Tyr His Asp Phe Leu Glu Thr Pro Val Gln Leu
 35 40 45

Arg Val Gly Ser Leu Glu Ile Asn Lys Asn Met Leu Leu Trp Ile Asp
 50 55 60

Asp Ala Leu Met Ala Val Phe Phe Leu Leu Val Gly Leu Glu Val Lys
 65 70 75 80

Arg Glu Leu Met Gln Gly Ser Leu Ala Ser Leu Arg Gln Ala Ala Phe
 85 90 95

Pro Val Ile Ala Ala Ile Gly Gly Met Ile Val Pro Ala Leu Leu Tyr
 100 105 110

Leu Ala Phe Asn Tyr Ala Asp Pro Ile Thr Arg Glu Gly Trp Ala Ile
115 120 125

Pro Ala Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Leu Ala Leu Leu
130 135 140

Gly Ser Arg Val Pro Leu Ala Leu Lys Ile Phe Leu Met Ala Leu Ala
145 150 155 160

Ile Ile Asp Asp Leu Gly Ala Ile Ile Ile Ile Ala Leu Phe Tyr Thr
165 170 175

Asn Asn Leu Ser Met Ala Ser Leu Gly Val Ala Ala Val Ala Ile Ala
180 185 190

Val Leu Ala Val Leu Asn Leu Cys Gly Ala Arg Arg Thr Gly Val Tyr
195 200 205

Ile Leu Val Gly Val Val Leu Trp Thr Ala Val Leu Lys Ser Gly Val
210 215 220

His Ala Thr Leu Ala Gly Val Ile Val Gly Phe Phe Ile Pro Leu Tyr
225 230 235 240

Glu Lys His Gly Arg Ser Pro Ala Lys Arg Leu Glu His Val Leu His
245 250 255

Pro Thr Val Ala Tyr Leu Ile Leu Pro Leu Phe Ala Phe Ala Asn Ala
260 265 270

Gly Val Ser Leu Gln Gly Val Thr Leu Asp Gly Leu Thr Ser Ile Leu

275

280

285

Pro Leu Gly Ile Ile Ala Gly Leu Leu Ala Gly Lys Pro Leu Gly Ile
 290 295 300

Ser Leu Phe Cys Trp Leu Ala Leu Arg Leu Lys Leu Ala His Leu Pro
 305 310 315 320

Glu Gly Thr Thr Tyr Gln Gln Ile Met Val Val Gly Ile Leu Cys Gly
 325 330 335

Ile Gly Phe Thr Met Ser Val Phe Ile Ala Ser Leu Ala Phe Gly Ser
 340 345 350

Val Asp Pro Glu Leu Ile Asn Trp Ala Tyr Leu Gly Ile Leu Val Gly
 355 360 365

Ser Ile Ser Ser Ala Val Ile Gly Tyr Ser Trp Leu Arg Val Arg Met
 370 375 380

Arg Pro Ser Val
 385

<210> 249
 <211> 1011
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> {1}..(1011)

<400> 249

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Met Ser Ala Leu Asn Lys Lys Ser Phe Leu Thr Tyr Leu Lys Glu Gly
1 5 10 15

ggc att tac gtc gtt ctt tta gtt ttg ctg gcg att att att ttc cag 56
Gly Ile Tyr Val val leu leu val leu leu ala ile ile ile phe ctn
20 25 30

gac cca aca ttt tta agt ctg ttg aac tta agt aat att ctc acc cag 144
asp pro thr phe leu ser leu leu asn leu ser leu ile leu thr ctn
35 40 45

tca tgg gtg cgt att att atc gcg ctc ggt gtg gca ggg tta att gtc 192
ser ser val arg ile ile ile ala leu gly val ala gly leu ile val
50 55 60

acc cag ggg acc gat ctt tct gct ggt cgt cag gta ggg ctg gcg gaa 240
thr ctn gly thr asp leu ser ala gly arg ctn val gly leu ala ala
65 70 75 80

gtg gtg gct gcg aca tta ttg cag tcc atg gat aac gcc aac aas gtc 288
val val ala ala thr leu leu ctn ser met asp asn ala asn lys val
85 90 95

ttc cgg gac ctg gcg ccg atg ccg att gcg ctg gtt att ctg att gtc 336
phe pro ctn met ala thr met pro ile ala leu val ile leu ile val
100 105 110

tgt gcc att ggt gcg gtg atc ggt ttg atc aac ggt ctg att ata gct 384
cys ala ile gly ala val ile gly leu ile asn gly leu ile ile ala
115 120 125

tat ctc aac gtg acg ccg ttc att acc acg ctc ggc aag atg ata atc 432
tyr leu asn val thr pro phe ile thr thr leu gly thr met ile ile
130 135 140

gtc tac gcc atc aac tgg ctc tat tac gac ttt gtc ggg gcg tgg cca 480
val tyr gly ile asn ser leu tyr tyr asp phe val gly ala ser pro
145 150 155 160

att tct ggt ttt gcc agt ggc ttc tct acc ttt gct cag gcc ttt gtc 528
ile ser gly phe asp ser gly phe ser thr phe ala ctn gly phe val

165	170	175	
gag ctg ggg agt ttc cgt ctc tct tan ctc acc ttc tac gag ttg att			576
Ala Leu Gly Ser Phe Arg Leu Ser Tyr Ile Thr Phe Tyr Ala Leu Ile			
180	185	190	
gag gly ggg ttc gtc tgg gtg ttg tgg acc aaa acc cgc ttc ggt aag			634
Ala Val Ala Phe Val Trp Val Leu Trp Asn Lys Thr Arg Phe Gly Lys			
195	200	205	
aac att ttt gcc att ggc ggt aac cag gaa gag gca aaa gta tct ggt			672
Asn Ile Phe Ala Ile Gly Gly Asn Pro Glu Ala Ala Lys Val Ser Gly			
210	215	220	
gtc aac gtc ggc ctg aac ucy ucy atg atc tac gag ttg tct gcc gtg			720
Val Asn Val Gly Leu Asn Leu Leu Met Ile Tyr Ala Leu Ser Gly Val			
225	230	235	240
tcc tac gcc ttt ggc ggg atg tta gaa gcc gga cgt atc ggc tct gcc			768
Phe Tyr Ala Phe Gly Gly Met Leu Glu Ala Gly Arg Thr Gly Ser Ala			
245	250	255	
acc aac aac ctc ggc ttt atg tat gag ctg gat gct atc gag gag tgc			816
Thr Asn Asn Leu Gly Phe Met Tyr Glu Leu Asp Ala Ile Ala Ala Cys			
260	265	270	
gag gta ggc ggt gta tgg ttc agc ggc ggt gta aag acg atg att ggc			864
Val Val Gly Val Ser Phe Ser Gly Gly Val Gly Thr Val Ile Gly			
275	280	285	
gtg gtg acc ggg gta att att ttt acc gtc atc aac tat ggc ctg acc			912
Val Val Thr Gly Val Ile Ile Phe Thr Val Ile Asn Tyr Gly Leu Thr			
290	295	300	
tat aic ggc gta aac cca tac tgg cag tac atc atc aaa ggg gag att			960
Tyr Ile Gly Val Asn Pro Tyr Trp Gln Tyr Ile Ile Lys Gly Ala Ile			
305	310	315	320
att atc ttc gcc gta gag ctg gat tca ctg aaa tac gag cgt aag aaa			1008
Ile Ile Phe Ala Val Ala Leu Asp Ser Leu Lys Tyr Ala Arg Lys Lys			
325	330	335	

tga

1911

<210> 253

<211> 336

<212> FRT

<213> Escherichia coli

<400> 250

Met Ser Ala Leu Asn Lys Lys Ser Phe Leu Thr Tyr Leu Lys Glu Gly

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Gly Ile Tyr Val Val Leu Leu Val Leu Leu Ala Ile Ile Ile Phe Glu

20 25 30

Asp Pro Thr Phe Leu Ser Leu Leu Asn Leu Ser Asn Ile Leu Thr Gln

35 40 45

Ser Ser Val Arg Ile Ile Ile Ala Leu Gly Val Ala Gly Leu Ile Val

50 55 60

Thr Gln Gly Thr Asp Leu Ser Ala Gly Arg Gln Val Gly Leu Ala Ala

65 70 75 80

Val Val Ala Ala Thr Leu Leu Gln Ser Met Asp Asn Ala Asn Lys Val

85 90 95

Phe Pro Glu Met Ala Thr Met Pro Ile Ala Leu Val Ile Leu Ile Val

100 105 110

Cys Ala Ile Gly Ala Val Ile Gly Leu Ile Asn Gly Leu Ile Ile Ala

115 120 125

Tyr Leu Asn Val Thr Pro Phe Ile Thr Thr Leu Gly Thr Met Ile Ile
130 135 140

Val Tyr Gly Ile Asn Ser Leu Tyr Tyr Asp Phe Val Gly Ala Ser Pro
145 150 155 160

Ile Ser Gly Phe Asp Ser Gly Phe Ser Thr Phe Ala Glu Gly Phe Val
165 170 175

Ala Leu Gly Ser Phe Arg Leu Ser Tyr Ile Thr Phe Tyr Ala Leu Ile
180 185 190

Ala Val Ala Phe Val Trp Val Leu Trp Asn Lys Thr Arg Phe Cys Lys
195 200 205

Asn Ile Phe Ala Ile Gly Gly Asn Pro Glu Ala Ala Tyr Val Ser Gly
210 215 220

Val Asn Val Gly Leu Asn Leu Leu Met Ile Tyr Ala Leu Ser Gly Val
225 230 235 240

Phe Tyr Ala Phe Gly Gly Met Leu Glu Ala Cys Arg Ile Gly Ser Ala
245 250 255

Thr Asn Asn Leu Gly Phe Met Tyr Glu Leu Asp Ala Ile Ala Ala Cys
260 265 270

Val Val Gly Gly Val Ser Phe Ser Gly Gly Val Gly Thr Val Ile Gly
275 280 285

Val Val Thr Gly Val Ile Ile Phe Thr Val Ile Asn Tyr Gly Asn Thr
290 295 300

Tyr Ile Gly Val Asn Pro Tyr Trp Gln Tyr Ile Ile Lys Gly Ala Ile
 305 310 315 320

Ile Ile Phe Ala Val Ala Met Arg Ser Leu Lys Tyr Ala Arg Lys Lys
 325 330 335

<210> 251
 <211> 1290
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1290)

<400> 251
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 Met Glu Thr Thr Gln Thr Ser Thr Ile Ala Ser Lys Asp Ser Arg Ser
 1 5 10 15
 gcc tgg cgc aag aca gac acc atg tgg atg ctg gcc ctt tac ggc acg 96
 Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
 20 25 30
 gca atc gcc gcg gcc ctg ctg ttc ctg cca atc aac gcc ggt gtt ggc 144
 Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 35 40 45
 ggt atg atc cag ctg atc atc atg gct atc ctt gcg ttc cag atg acg 192
 Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
 50 55 60
 ttt ttt gct cag gcc gcc ctg act cgc ttc gta ctg tct ggt aaa aac 240
 Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Ile Asn
 65 70 75 80
 cag gcc gaa gac atc acc gag gtt gta gaa gaa cac ttt ggt att gcc 288

Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly	
85 90 95	
gca ggt aaa ctg att acc ctg ctc tac ttc ttc gct atc tac cag atc	336
Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile	
100 105 110	
ctg ctg gtt tat acc gtg gca atc acc aat acc gtt gaa agc ttc atg	384
Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met	
115 120 125	
tat cac cag ctg ggt arg acg cca ccc ccc cgt gcg att ctg tgg ctg	432
Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu	
130 135 140	
atc ctg atc gtg ggt atg atg acc atc gtt cgc ttc ggt gag cag atg	480
Ile Leu Ile Val Gly Met Met Thr Ile Val Arg Phe Gly Glu Glu Met	
145 150 155 160	
leu gtt aac gag atg agt att ctg gta ttc ccc ttt gtt ggc gta ctg	528
Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu	
165 170 175	
atg ctg ctg gct ctg tac ctg atc ccc cag tgg aac ggc gct gca ctg	576
Met Leu Leu Ala Leu Tyr Leu Ile Pro Cln Trp Asn Gly Ala Ala Leu	
180 185 190	
gaa acg ctg tcc ctg gac act gca tct gca acc gga aac ggt ctg tgg	624
Glu Thr Leu Ser Leu Asp Thr Ala Ser Ala Thr Gly Asn Gly Leu Trp	
195 200 205	
atg acc ctg tgg ctg gca att ccc gta atg gtg ttc tgg ttc aac ccc	672
Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His	
210 215 220	
tct ccc atc atc tct tct tct gcc gtt gcg aag cgt gaa gag tac gcc	720
Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly	
225 230 235 240	
gat atg gca gaa cag aaa tgc tgg aag atc ctg gca ttc gca cac atc	768
Asp Met Ala Glu Gln Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile	
245 250 255	

atg atg gtg ctg acc gta atg ttc ttc gtc tta agc tgt gta ctg agc	866
Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser	
260 265 270	
ctg act cgg gca gaa ctg gct gcg gct aaa gag cag aac atc tgg att	864
Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile	
275 280 285	
atg tct tac ctg gct aac cac ttt aag gca cgg gtt atc gcg tgg atg	912
Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Cys Met	
290 295 300	
ggt cgg att atc ggc att atc gct atc acc aaa tcc ttc ctc ggt ccc	960
Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His	
305 310 315 320	
tac ctg ggc gca agt gaa ggc ttc aac ggt atg gtg att aaa tct ctg	1008
Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu	
325 330 335	
cyl ggt aaa ggt aag tct atc gcc atc aac aag ctg aac cgt atc act	1056
Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr	
340 345 350	
gcg ctg ttc atg ctg gta ccg acc tgg att gtt gcc acc ctg aac cgg	1104
Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro	
355 360 365	
agc atc ctg ggt atg att gaa acc ctg ggc ggt cca atc atc gcg arg	1152
Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met	
370 375 380	
atc ctg ttc ctg atg ccg atg tac gca att cag aaa gta cgg gca atg	1200
Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met	
385 390 395 400	
ggt aag tac agc ggt cac atc agc aac gta ttc gtt gtc gtg atg ggt	1248
Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Val Met Gly	
405 410 415	
ctg att gca atc tcc gca atc ttc tac tct ctg ttc agc taa	1296

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
420 425

<210> 252

<211> 439

<212> PRT

<213> *Escherichia coli*

<400> 252

Met Glu Thr Thr Glu Thr Ser Thr Ile Ala Ser Lys Asp Ser Arg Ser
1 5 10 15

Ala Tyr Arg Lys Thr Asp Tyr Met Trp Met Leu Gly Leu Tyr Gly Thr
20 25 30

Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
35 40 45

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
65 70 75 80

Pro Gly Glu Asp Glu Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
100 105 110

Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met
115 120 125

Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu
 130 135 140

Ile Leu Ile Val Gly Met Met Thr Ile Val Arg Phe Gly Glu Gln Met
 145 150 155 160

Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu
 165 170 175

Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
 180 185 190

Glu Thr Leu Ser Leu Asp Thr Ala Ser Ala Thr Gly Asn Gly Leu Trp
 195 200 205

Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
 210 215 220

Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly
 225 230 235 240

Asp Met Ala Glu Gln Lys Cys Ser Tyr Ile Leu Ala Phe Ala His Ile
 245 250 255

Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
 260 265 270

Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile
 275 280 285

Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Trp Met

290

295

300

Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His
 305 310 315 320

Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
 325 330 335

Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr
 340 345 350

Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
 355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
 370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
 385 390 395 400

Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Val Met Gly
 405 410 415

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
 420 425

<210> 253

<211> 219

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(219)

<400> 253

atg tll uul lgt cot tta tgc cag cat gcc gca cat gcg cgt aca agc 48
 Met Phe His Cys Pro Leu Cys Gln His Ala Ala His Ala Arg Thr Ser
 1 5 10 15

cgc tat atc act gac acg acc aac gag cgt tat cac cag tgt cag aac 96
 Arg Tyr Ile Thr Asp Thr Thr Lys Glu Arg Tyr His Gln Cys Gln Asn
 20 25 30

gtg aat tgc agc gcc acg ttc atc act tat gag tgg gla cag cga tac 144
 Val Asn Cys Ser Ala Thr Phe Ile Thr Tyr Glu Ser Val Gln Arg Tyr
 35 40 45

att atg aag cag gga gaa gtc caa gtc gta agc cag cac cag tly cag 192
 Ile Val Lys Pro Gly Glu Val His Val Val Arg Pro His Pro Leu Pro
 50 55 60

tta ggg cag caa att atg tgg atg taa 219
 Ser Gly Gln Gln Ile Met Trp Met
 65 70

<110> 254

<211> 73

<212> PRT

<213> Escherichia coli

<400> 254

Met Phe His Cys Pro Leu Cys Gln His Ala Ala His Ala Arg Thr Ser
 1 5 10 15

Arg Tyr Ile Thr Asp Thr Thr Lys Glu Arg Tyr His Gln Cys Gln Asn
 20 25 30

Val Asn Cys Ser Ala Thr Phe Ile Thr Tyr Glu Ser Val Gln Arg Tyr
 35 40 45

Ile Val Lys Pro Gly Glu Val His Val Val Arg Pro His Pro Leu Pro
 50 55 60

Ser Gly Gln Gln Ile Met Trp Met
 65 70

<210> 255
 <211> 2391
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> {1}..(2391)

<400> 255
 atg gca att aac aat acc ggc tgc cga cga tta ctc gtc acg cta acc 48
 Met Ala Ile Asn Asn Thr Gly Ser Arg Arg Leu Leu Val Thr Leu Thr
 1 5 10 15

gac ctt ttt gca gag ctt tgc ggg ctg tat cta ctc att ggc gga ggc 96
 Ala Leu Phe Ala Ala Leu Cys Gly Leu Tyr Leu Leu Ile Gly Gly Gly
 20 25 30

tgg ctg gtc gag att ggc ggc tcc tgg tac tac cct atc gct ggc ctt 144
 Trp Leu Val Ala Ile Gly Gly Ser Trp Tyr Tyr Pro Ile Ala Gly Leu
 35 40 45

gtg atg ctc ggc gtc gcc tgg atg ctg tgg cgc agt aac cgc gcc ggc 192
 Val Met Leu Gly Val Ala Trp Met Leu Trp Arg Ser Lys Arg Ala Ala
 50 55 60

ctt tgg cca tac gca gcc ctg ctg ctc ggc acc atg att tgg ggc gcc 240
 Leu Trp Leu Tyr Ala Ala Leu Leu Leu Gly Thr Met Ile Trp Gly Val
 65 70 75 80

tgg gaa gtt ggt ttc gac ttc tgg gag ctg act cag cgc agc gac att 288

Trp Glu Val Gly Phe Asp Phe Trp Ala Leu Thr Pro Arg Ser Asp Ile	85	90	95	
ctg gtc ttc ttc ggc atc tgg ctg acc ctg cag ttt gtc tca cgt cgc			336	
Leu Val Phe Phe Gly Ile Trp Leu Ile Leu Pro Phe Val Trp Arg Arg	100	105	110	
ctg gtc att cct gcc agc ggc gca gtt gcc gca ctg ggc gtc gca ctg			384	
Leu Val Ile Pro Ala Ser Gly Ala Val Ala Ala Leu Val Val Ala Tyr	115	120	125	
ctg att agc ggt ggt atc ctg acc tgg gcc gga ttt aac gat ccg cag			432	
Leu Ile Ser Gly Gly Ile Leu Thr Trp Ala Gly Phe Asn Asp Pro Glu	130	135	140	
gag atc aac ggc acc tta agc gcc gat gcc aca cct gat gaa gct atc			480	
Glu Ile Asn Gly Thr Leu Ser Ala Asp Ala Thr Pro Ala Glu Ala Ile	145	150	155	160
tcc ccc gta gcc gat cag gac tgg cct gcc tat ggt cgt aac cag gac			528	
Ser Pro Val Ala Asp Glu Asp Trp Pro Ala Tyr Gly Arg Asn Glu Glu	165	170	175	
ggt caa cgc ttt tca cag ctg aaa uaa att aac gcc gat aac gta cct			576	
Gly Glu Arg Phe Ser Phe Leu Lys Glu Ile Asn Ala Asp Asn Val His	180	185	190	
aat ctg aaa gaa gcc tgg gta ttc cgt aat ggc gat gta aag cag ccg			624	
Asn Leu Lys Glu Ala Trp Val Phe Arg Thr Gly Asp Val Lys Glu Pro	195	200	205	
aac gat ccg ggt gaa atc acc aat gaa gta acc ccg cgt att aca gta gcc			672	
Asn Asp Pro Gly Glu Ile Thr Asn Glu Val Thr Pro Ile Lys Val Gly	210	215	220	
gac acc ctt tac ctg tgt acc gat cac cag cgc ctg ttt gag att gat			720	
Asp Thr Leu Tyr Leu Cys Thr Ala His Glu Arg Leu Phe Ala Leu Asp	225	230	235	240
gcc gcc agc gcc aaa gag aaa tgg cat taa gat cct gag ctg aaa acc			768	
Ala Ala Ser Gly Lys Glu Lys Trp His Tyr Asp Pro Glu Leu Tyr Thr	245	250	255	

auc gag tct ttc cag cac qta acc tgc cgt ggt gtc tct tat act gaa	816
Asp Glu Ser Phe Gln His Val Thr Cys Arg Gly Val Ser Tyr His Glu	
260 265 270	
gcc aaa gaa gan acc gct tgg cgg gaa gtg atg ggg gat tgc cgg cgt	864
Ala Lys Ala Glu Thr Ala Ser Pro Glu Val Met Ala Asp Cys Pro Arg	
275 280 285	
cgt atc att ttt cgg gtc aat gat ggt cga atg att ggg att aac gcc	912
Arg Ile Ile Leu Pro Val Asn Asp Gly Arg Leu Ile Ala Ile Asn Ala	
290 295 300	
gaa aac ggc aaa atg tgc gaa acc ttc gcc aat aaa ggc gtg ctg aat	960
Glu Asn Gly Lys Leu Cys Glu Thr Phe Ala Asn Lys Gly Val Leu Asn	
305 310 315 320	
ctg caa agc aat atg cca gac acc aaa cgg ggt atg tat gaa cgg aat	1008
Leu Gln Ser Asn Met Pro Asp Thr Lys Pro Gly Leu Tyr Glu Pro Thr	
325 330 335	
tgg cca cgg att atc acc gat aac acc atc gtg atg gcc ggt tca att	1056
Ser Pro Pro Ile Ile Thr Asp Lys Thr Ile Val Met Ala Gly Ser Val	
340 345 350	
acc gat aac ttc tca acc cgc gaa acc tct ggc gtg atc cgt ggt ttt	1104
Thr Asp Asn Phe Ser Thr Arg Glu Thr Ser Gly Val Ile Arg Gly Phe	
355 360 365	
gat gtc aac acc ggg gag atg ctg tgg gct ttt gat acc ggc ggg aca	1152
Asp Val Asn Thr Gly Glu Leu Leu Tip Ala Phe Asp Pro Gly Ala Lys	
370 375 380	
gat cgg aac gaa atc cgg tct gac gaa cac acc ttt acc ttt aac tgg	1200
Asp Pro Asn Ala Ile Pro Ser Asp Glu His Thr Phe Thr Phe Asn Ser	
385 390 395 400	
cca aac tcc tgg gca cca cgg gcc tat gac ggg aag ctg gat ctg gtc	1248
Pro Asn Ser Trp Ala Pro Ala Ala Tyr Asp Ala Lys Leu Asp Leu Val	
405 410 415	
tat ctg cgg atg ggc gtg acc acg cgg gat atc tgg ggc ggt aac cgc	1296

607/762

Tyr	Asn	Pro	Met	Gly	Val	Thr	Pro	Asp	Ile	Trp	Gly	Gly	Asn	Arg	
			420					425					430		
aga	ccg	gaa	cag	gaa	cgl	tat	gaa	aga	tug	att	ctg	gag	ctg	aat	gac
Thr	Pro	Glu	Gln	Arg	Tyr	Ala	Ser	Ser	Tle	Leu	Ala	Leu	Asn	Ala	
			435				440					445			
act	acc	ggg	aaa	ctg	gag	tgg	agc	tac	cag	acc	gtt	caa	cac	gac	ctg
Thr	Thr	Gly	Lys	Leu	Ala	Trp	Ser	Tyr	Gln	Thr	Val	Phe	His	Asp	Leu
	450					455					460				
tgg	gac	atg	gat	ctt	ccg	gaa	cag	ccg	acg	ctg	gag	gac	atc	acc	gtt
Trp	Asp	Met	Asp	Leu	Pro	Ala	Gln	Pro	Thr	Leu	Ala	Asp	Ile	Thr	Val
	465					470				475			480		
aat	ggt	cag	aaa	gtg	cca	gtt	att	tac	gct	ccg	gag	aaa	acc	ggc	aac
Asn	Gly	Gln	Lys	Val	Pro	Val	Ile	Tyr	Ala	Pro	Ala	Lys	Thr	Gly	Asn
			485						490				495		
att	ttt	gtg	ctc	gat	cgt	ggt	aat	ggc	gaa	ctg	gtg	gtt	ccg	aca	ccg
Ile	Phe	Val	Leu	Asp	Arg	Arg	Asn	Gly	Glu	Leu	Val	Val	Pro	Ala	Pro
			500						505				510		
gaa	aaa	ccg	gtt	ccc	caa	ggt	aca	gag	aaa	ggc	gat	tac	gta	acc	cca
Glu	Lys	Pro	Val	Pro	Gln	Gly	Ala	Ala	Lys	Gly	Asp	Tyr	Val	Thr	Pro
			515					520					525		
act	caa	ccg	ttt	tct	gaa	ctg	agc	tta	ogt	ccg	acg	aca	gat	tta	agc
Thr	Gln	Pro	Phe	Ser	Glu	Leu	Ser	Phe	Arg	Pro	Thr	Lys	Asp	Leu	Ser
			530				535					540			
ggt	gag	gat	atg	tgg	gga	gac	acc	atg	ttt	gac	caa	ctg	gtg	tgc	agc
Gly	Ala	Asp	Met	Trp	Gly	Ala	Thr	Met	Phe	Asp	Gln	Leu	Val	Cys	Arg
	545					550				555				560	
gtg	atg	ttc	cac	cag	atg	cgc	tat	gaa	ggc	att	ttc	acc	ccg	cca	tat
Val	Met	Phe	His	Gln	Met	Arg	Tyr	Glu	Gly	Ile	Phe	Thr	Pro	Pro	Ser
			565						570				575		
gaa	cag	ggt	acg	ctg	gtc	ttc	ccg	ggt	aac	ctg	ggg	atg	tta	gaa	tgg
Glu	Gln	Gly	Thr	Leu	Val	Phe	Pro	Gly	Asn	Leu	Gly	Met	Phe	Glu	Trp
			580					585					590		

ggc ggg att tcc gcc gat cca aat cgt gaa gtg gog att gcc aac cca Gly Gly Ile Ser Val Asp Pro Asn Arg Glu Val Ala Ile Ala Asn Pro 595 600 605	1824
atg gca ctg ceg ttt gtt tgg aaa cly atc cag cgt ggt cct ggc aac Met Ala Leu Pro Phe Val Ser Lys Leu Ile Pro Arg Gly Pro Gly Asn 610 615 620	1872
cag atg gag cag cag aaa gat gcc aaa ggc acg ggt acg gaa tcc ggc Pro Met Glu Gln Pro Lys Asp Ala Lys Gly Thr Gly Thr Glu Ser Gly 625 630 635 640	1920
att cag cca cag tcc ggt gta cag tat ggt gtc acg ctc aac cug ttc Ile Glu Pro Glu Tyr Gly Val Pro Tyr Gly Val Thr Leu Asn Pro Phe 645 650 655	1968
ctc tca cca ttt ggt ctg cca tgt aaa cag cca gca tgg ggt tat atc Leu Ser Pro Phe Gly Leu Pro Cys Lys Gln Pro Ala Trp Gly Tyr Cys 660 665 670	2016
tgg ggg ctg gat ctg aaa act aat gaa gtg atg tgg aag aaa cgt att Ser Ala Leu Asp Leu Lys Thr Asn Glu Val Val Trp Lys Lys Arg Ile 675 680 685	2064
ggt tgg cgg cag gac agt atg cgg ttc cag atg cgg gtt cgg gly cgg Gly Thr Pro Glu Asp Ser Met Pro Phe Pro Met Pro Val Pro Val Pro 690 695 700	2112
ttc aat atg gag atg cgg atg ctg ggc ggg cca atc tcc acg ggg ggt Phe Asn Met Gly Met Pro Met Leu Gly Gly Pro Ile Ser Thr Ala Gly 705 710 715 720	2160
aac ctg ctg ttt atc gcc ggt acg gca gat aac tcc ctg cgg ggt tcc Asn Val Leu Phe Ile Ala Ala Thr Ala Asp Asn Tyr Leu Arg Ala Tyr 725 730 735	2208
aac atg agc aac ggt gaa aaa ctg tgg cag ggt cgt tta cca gcg ggt Asn Met Ser Asn Gly Glu Lys Leu Trp Glu Gly Arg Leu Pro Ala Gly 740 745 750	2256
ggt cag gct cag cca atg acc tat gaa gtg aat ggt aag cag tat gtg	2304

Gly Gln Ala Thr Pro Met Thr Tyr Glu Val Asn Gly Lys Gln Tyr Val
 755 760 765

gtg atc tcc gca ggc ggt cac ggt Leu ttt ggt acg aag atg ggc gac 2352
 Val Ile Ser Ala Gly Gly His Gly Ser Phe Gly Thr Lys Met Gly Asp
 770 775 780

tat att gtg gct tat gcg ctg ccg gat gat gtg aag taa 2391
 Tyr Ile Val Ala Tyr Ala Leu Pro Asp Asp Val Lys
 785 790 795

<210> 256

<211> 796

<212> FRT

<213> Escherichia coli

<400> 256

Met Ala Ile Asn Asn Thr Gly Ser Arg Arg Leu Leu Val Thr Leu Thr
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Ala Leu Phe Ala Ala Leu Cys Gly Leu Tyr Leu Leu Ile Gly Gly Gly
 20 25 30

Trp Leu Val Ala Ile Gly Gly Ser Trp Tyr Tyr Pro Ile Ala Gly Leu
 35 40 45

Val Met Leu Gly Val Ala Trp Met Leu Trp Arg Ser Lys Arg Ala Ala
 50 55 60

Leu Trp Leu Tyr Ala Ala Leu Leu Leu Gly Thr Met Lys Trp Gly Val
 65 70 75 80

Trp Glu Val Gly Phe Asp Ile Trp Ala Leu Thr Pro Arg Ser Asp Ile
 85 90 95

Leu Val Phe Phe Gly Ile Trp Leu Ile Leu Pro Phe Val Trp Arg Arg
100 105 110

Leu Val Ile Pro Ala Ser Gly Ala Val Ala Ala Leu Val Val Ala Ser
115 120 125

Leu Ile Ser Gly Gly Ile Leu Thr Trp Ala Gly Phe Asn Asp Pro Gln
130 135 140

Glu Ile Asn Gly Thr Leu Ser Ala Asp Ala Thr Pro Ala Glu Ala Ile
145 150 155 160

Ser Pro Val Ala Asp Glu Asp Trp Pro Ala Tyr Gly Arg Asn Glu Glu
165 170 175

Gly Glu Arg Phe Ser Pro Leu Lys Glu Ile Asn Ala Asp Asn Val His
180 185 190

Asn Leu Lys Glu Ala Trp Val Phe Arg Thr Gly Asp Val Lys Glu Pro
195 200 205

Asn Arg Pro Gly Glu Ile Thr Asn Glu Val Thr Pro Ile Lys Val Gly
210 215 220

Asp Thr Leu Tyr Leu Cys Thr Ala His Glu Arg Leu Phe Ala Leu Asp
225 230 235 240

Ala Ala Ser Gly Lys Glu Lys Trp His Tyr Asp Pro Glu Leu Lys Thr
245 250 255

Asn Glu Ser Phe Glu His Val Thr Cys Arg Gly Val Ser Tyr His Glu

260

265

270

Ala Lys Ala Glu Thr Ala Ser Pro Glu Val Met Ala Asp Cys Pro Arg
 275 380 285

Arg Ile Ile Leu Pro Val Asn Asp Gly Arg Leu Ile Ala Ile Asn Ala
 290 295 300

Glu Asn Gly Lys Leu Cys Glu Thr Phe Ala Asn Lys Gly Val Ile Asn
 305 310 315 320

Leu Gln Ser Asn Met Pro Asp Thr Lys Pro Gly Leu Tyr Glu Pro Thr
 325 330 335

Ser Pro Pro Phe Ile Thr Asp Lys Thr Ile Val Met Ala Gly Ser Val
 340 345 350

Thr Asp Asn Phe Ser Thr Arg Glu Thr Ser Gly Val Ile Arg Gly Phe
 355 360 365

Asp Val Asn Thr Gly Glu Leu Leu Trp Ala Phe Asp Pro Gly Ala Lys
 370 375 380

Asp Pro Asn Ala Ile Pro Ser Asp Glu His Thr Phe Thr Phe Asn Ser
 385 390 395 400

Pro Asn Ser Trp Ala Pro Ala Ala Tyr Asp Ala Lys Leu Asp Leu Val
 405 410 415

Tyr Leu Pro Met Gly Val Thr Thr Pro Asp Ile Trp Gly Gly Asn Arg
 420 425 430

Thr Pro Glu Glu Glu Arg Tyr Ala Ser Ser Ile Leu Ala Leu Asn Ala
435 440 445

Thr Thr Gly Lys Leu Ala Trp Ser Tyr Gln Thr Val His His Asp Leu
450 455 460

Trp Asp Met Asp Leu Pro Ala Gln Pro Thr Leu Ala Asp Ile Thr Val
465 470 475 480

Asn Gly Gln Lys Val Pro Val Ile Tyr Ala Pro Ala Lys Thr Gly Asn
485 490 495

Ile Phe Val Leu Asp Arg Arg Asn Gly Glu Leu Val Val Pro Ala Pro
500 505 510

Glu Lys Pro Val Pro Glu Gly Ala Ala Lys Gly Asp Tyr Val Thr Pro
515 520 525

Thr Gln Pro Phe Ser Glu Leu Ser Phe Arg Pro Thr Lys Asp Leu Ser
530 535 540

Gly Ala Asp Met Trp Gly Ala Thr Met Phe Asp Cln Leu Val Cys Arg
545 550 555 560

Val Met Phe His Gln Met Arg Tyr Glu Gly Ile Phe Thr Pro Pro Ser
565 570 575

Glu Gln Gly Thr Leu Val Phe Pro Gly Asn Leu Gly Met Phe Glu Trp
580 585 590

Gly Gly Ile Ser Val Asp Pro Asn Arg Glu Val Ala Ile Ala Asn Pro

613/762

595

600

605

Met Ala Met Pro Phe Val Ser Lys Leu Ile Pro Arg Gly Pro Gly Asn
 610 615 620

Pro Met Glu Gln Pro Lys Asp Ala Lys Gly Thr Gly Thr Glu Ser Gly
 625 630 635 640

Ile Gln Pro Gln Tyr Gly Val Pro Tyr Gly Val Thr Leu Asn Pro Phe
 645 650 655

Leu Ser Pro Phe Gly Leu Pro Cys Lys Glu Pro Ala Trp Gly Tyr Ile
 660 665 670

Ser Ala Leu Asp Leu Lys Thr Asn Glu Val Val Trp Lys Lys Arg Ile
 675 680 685

Gly Thr Pro Glu Asp Ser Met Pro Phe Pro Met Pro Val Pro Val Pro
 690 695 700

Phe Asn Met Gly Met Pro Met Leu Gly Gly Pro Ile Ser Thr Ala Gly
 705 710 715 720

Asn Val Leu Phe Ile Ala Ala Thr Ala Asp Asn Tyr Leu Arg Ala Tyr
 725 730 735

Asn Met Ser Asn Gly Glu Lys Leu Trp Gln Gly Arg Leu Pro Ala Gly
 740 745 750

Gly Gln Ala Thr Pro Met Thr Tyr Glu Val Asn Gly Lys Gln Tyr Val
 755 760 765

Val Ile Ser Ala Gly Gly His Gly Ser Phe Gly Thr Lys Met Gly Asp
770 775 780

Tyr Ile Val Ala Tyr Ala Leu Pro Asp Asp Val Lys
785 790 795

<210> 257

<211> 1332

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1332)

<400> 357

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Met Ser Thr Ser Arg Ser Ile Val Ser Ser Gln Thr Lys Gln Ser Ser
1 5 10 15

tgg cgt aaa taa gac acc tca tgg aag ttc ggc ttg ttt ggt aag gaa 95
Trp Arg Lys Ser Asp Thr Thr Trp Thr Leu Gly Leu Phe Gly Thr Ala
20 25 30

atc ggc acc aag gtc ctg ttc ttc act atc cgc gca ggt ttt ggc gga 144
Ile Gly Ala Gly Val Leu Phe Phe Pro Ile Arg Ala Gly Phe Gly Gly
35 40 45

ctg atc aag att ctt ctg atg ttg gta ttg gca tac ccc atc gcy ttt 192
Leu Ile Pro Ile Leu Leu Met Leu Val Leu Ala Tyr Pro Ile Ala Phe
50 55 60

tat tgc cac agg gag ctg gag cgt ctg tat ctt tct ggc tct aac cct 240
Tyr Cys His Arg Ala Leu Ala Arg Leu Cys Leu Ser Gly Ser Asn Pro
65 70 75 80

tcc ggc aac att aag gaa aag gtc gaa gag cat ttt ggt aaa act ggc 288
Ser Gly Asn Ile Thr Glu Thr Val Glu Glu His Phe Gly Lys Thr Gly

	85	90	95	
ggc ggc gtt atc acg ttc ctg tac ttc ttc ggc att tgc cca ctg ctg				336
Gly Val Val Ile Thr Phe Leu Tyr Phe Phe Ala Ile Cys Pro Leu Leu				
	100	105	110	
tgg att tat ggc gtt act att acc aat acc ttt atg acg ttc tgg gaa				384
Tyr Ile Tyr Gly Val Thr Ile Thr Asn Thr Phe Met Thr Phe Trp Glu				
	115	120	125	
aac cag ctg ggc ttt gca cgg ctg aat cgc ggc ttt gtg gcg ctg ttc				432
Asn Gln Leu Gly Phe Ala Pro Leu Asn Arg Gly Phe Val Ala Leu Phe				
	130	135	140	
ctg tgg ctg ctg atg gct ttc gtc atc tgg ttt ggt aag gac ctg atg				480
Leu Leu Leu Leu Met Ala Phe Val Ile Trp Phe Gly Lys Asp Leu Met				
	145	150	155	160
gll aac gtc atg aac tac ctg gta tgg cgg ttt atc gcc agc ctg gtc				528
Val Lys Val Met Ser Tyr Leu Val Trp Pro Phe Ile Ala Ser Leu Val				
	165	170	175	
ctg att tat tgg tgg ctg atc cct tac tgg aac tat gcc gtt atc gac				576
Leu Ile Ser Leu Ser Leu Ile Pro Tyr Trp Asn Ser Ala Val Ile Asp				
	180	185	190	
cag gtt gac ctg ggt tgg ctg tgg tta acc ggt cat gac ggt atc atg				624
Gln Val Asp Leu Gly Ser Leu Ser Leu Thr Gly His Asn Gly Ile Leu				
	195	200	205	
atc acc gtc tgg ctg ggg att tcc atc atg att ttc tcc ttt aac ttc				672
Ile Thr Val Trp Leu Gly Ile Ser Ile Met Val Phe Ser Phe Asn Phe				
	210	215	220	
tgg cca atc gtc tat tcc ttc gtc gtt tct aag cgt gaa gag tat gag				720
Ser Pro Ile Val Ser Ser Phe Val Val Ser Lys Arg Glu Glu Tyr Glu				
	225	230	235	240
aaa gac ttc ggt cgc gac ttc acc gaa cgt aaa tgt tcc caa atc att				768
Lys Asp Phe Gly Arg Asp Phe Thr Gln Arg Lys Cys Ser Gln Ile Ile				
	245	250	255	

tct cgt gcc agc atg ctg atg gtt gca gtg gtg atg ttc tll gcc ttt	816
Ser Arg Ala Ser Met Leu Met Val Ala Val Val Met Phe Phe Ala Phe	
260 265 270	
agc tgc ctg ttt act ctg tct ccg gcc aac atg gag gaa gcc aaa gag	864
Ser Cys Leu Phe Thr Leu Ser Pro Ala Asn Met Ala Glu Ala Lys Ala	
275 280 285	
ccg aat att cca gtg ctt tct tat ctg gct aac cac tll gcy tcc atg	912
Gln Asn Ile Pro Val Leu Ser Tyr Leu Ala Asn His Phe Ala Ser Met	
290 295 300	
acc ggt acc aaa aca acg ttc gag att aca ctg gaa tat gag gct ttc	960
Thr Gly Thr Lys Thr Phe Ala Ile Thr Leu Glu Tyr Ala Ala Ser	
305 310 315 320	
atc atc gca ctg gty gct atc ttc aaa tct ttc ttc ggt cac tat ctg	1008
Ile Ile Ala Leu Val Ala Ile Phe Lys Ser Phe Phe Gly His Tyr Leu	
325 330 335	
gga acg ctg gaa ggt ctg aat ggc ctg gtc ctg aag ttt ggt lal aaa	1056
Gly Thr Leu Glu Gly Leu Asn Gly Leu Val Leu Lys Phe Gly Tyr Lys	
340 345 350	
ggc gcc aaa acc aca gtg tgg ctg ggt aca ctg aac act atc agc atg	1104
Gly Asp Lys Thr Lys Val Ser Iau Gly Lys Leu Asn Thr Ile Ser Met	
355 360 365	
atc ttc atc atg ggc tcc aac tgg gtt gtt gcc tac gcc aac ccg aac	1152
Ile Phe Ile Met Gly Ser Thr Trp Val Val Ala Tyr Ala Asn Pro Asn	
370 375 380	
ata ctt gac ctg atl gaa gcc atg ggc gca ccg att ala gca tcc ctg	1200
Ile Leu Asp Leu Ile Glu Ala Met Gly Ala Pro Ile Ile Ala Ser Leu	
385 390 395 400	
ctg tga ctg tgg ccg atg tat gcc atc cgt aaa gag ccg tct ctg gag	1248
Leu Cys Leu Leu Pro Met Tyr Ala Ile Arg Lys Ala Pro Ser Leu Ala	
405 410 415	
aaa lac cgt ggt cgt ctg gat aac gtg ttt gtt acc gtg att ggt ctg	1296
Lys Tyr Arg Gly Arg Leu Asp Asn Val Phe Val Thr Val Ile Gly Leu	

617/762

420

425

430

ctg acc atc ctg aac atc gta tac aaa ctg ttt taa

1332

Leu Thr Ile Leu Asn Ile Val Tyr Lys Leu Phe

435

440

<210> 258

<211> 443

<212> PRT

<213> Escherichia coli

<400> 258

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5

10

15

Trp Arg Lys Ser Asp Thr Thr Trp Thr Leu Gly Leu Phe Gly Thr Ala

20

25

30

Ile Gly Ala Gly Val Leu Phe Phe Pro Ile Arg Ala Gly Phe Gly Gly

35

40

45

Leu Ile Pro Ile Leu Leu Met Leu Val Leu Ala Tyr Pro Ile Ala Phe

50

55

60

Tyr Cys His Arg Ala Leu Ala Arg Leu Cys Leu Ser Gly Ser Asn Pro

65

70

75

80

Ser Gly Asp Ile Thr Glu Thr Val Glu Glu His Phe Gly Lys Thr Gly

85

90

95

Gly Val Val Ile Thr Phe Leu Tyr Phe Phe Ala Ile Cys Pro Leu Leu

100

105

110

Trp Ile Tyr Gly Val Thr Ile Thr Asn Thr Phe Met Thr Phe Trp Glu
115 120 125

Asn Gln Leu Gly Phe Ala Pro Leu Asn Arg Gly Phe Val Ala Leu Phe
130 135 140

Leu Leu Leu Leu Met Ala Phe Val Ile Trp Phe Gly Lys Asp Leu Met
145 150 155 160

Val Lys Val Met Ser Tyr Leu Val Trp Pro Phe Ile Ala Ser Leu Val
165 170 175

Leu Ile Ser Leu Ser Leu Ile Pro Tyr Trp Asn Ser Ala Val Ile Asp
180 185 190

Gln Val Asp Leu Gly Ser Leu Ser Leu Thr Gly His Asp Gly Ile Leu
195 200 205

Ile Thr Val Trp Leu Gly Ile Ser Ile Met Val Phe Ser Phe Asn Phe
210 215 220

Ser Pro Ile Val Ser Ser Phe Val Val Ser Lys Arg Glu Glu Tyr Glu
225 230 235 240

Lys Asp Phe Gly Arg Asp Phe Thr Glu Arg Lys Cys Ser Gln Ile Ile
245 250 255

Ser Arg Ala Ser Met Leu Met Val Ala Val Val Met Phe Phe Ala Phe
260 265 270

Ser Cys Leu Phe Thr Leu Ser Pro Ala Asn Met Ala Gln Ala Lys Ala
275 280 285

Gln Asn Ile Pro Val Leu Ser Tyr Leu Ala Asn His Phe Ala Ser Met
 290 335 380

Thr Gly Thr Lys Thr Thr Phe Ala Ile Thr Leu Glu Tyr Ala Ala Ser
 305 310 315 320

Ile Ile Ala Leu Val Ala Ile Phe Lys Ser Phe Phe Gly His Tyr Leu
 325 330 335

Gly Thr Leu Glu Gly Leu Asn Gly Ser Val Leu Lys Phe Gly Tyr Lys
 340 345 350

Gly Asp Lys Thr Lys Val Ser Leu Gly Lys Leu Asn Thr Ile Ser Met
 355 360 365

Ile Phe Ile Met Gly Ser Thr Trp Val Val Ala Tyr Ala Asn Pro Asn
 370 375 380

Ile Leu Asp Leu Ile Glu Ala Met Gly Ala Pro Ile Ile Ala Ser Leu
 385 390 395 400

Leu Cys Leu Leu Pro Met Tyr Ala Ile Arg Lys Ala Pro Ser Leu Ala
 405 410 415

Lys Tyr Arg Gly Arg Leu Asp Asn Val Phe Val Thr Val Ile Gly Leu
 420 425 430

Leu Thr Ile Leu Asn Ile Val Tyr Lys Leu Phe
 435 440

<210> 259
 <211> 2049
 <212> DNA
 <213> *Escherichia coli*

<220>
 <221> CDS
 <222> (1)..(2049)

<400> 259
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 gga ggc cag acc ttc gct gta gaa gal ala aag cgt got gat caa att 96
 Ala Gly Gln Thr Phe Ala Val Glu Asp Ile Thr Arg Ala Asp Gln Ile
 20 25 30
 ccg gta ltu aag gaa gag aag cag cat gcg aag gta agt gag cgc gta 144
 Pro Val Leu Tyr Glu Glu Thr Gln His Ala Thr Val Ser Glu Arg Val
 35 40 45
 aag tog cgc ttc acc cgt tet cat tat cgc cag ltu gac ctc gat cag 192
 Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu Asp Gln
 50 55 60
 gca ttt tog ggc aaa atc ttt gaa cgc tac ctg aat ctg ctc gat tac 240
 Ala Phe Ser Ala Lys Ile Phe Asp Arg Tyr Leu Asn Leu Leu Asp Tyr
 65 70 75 80
 agc cao aac gty dly dty gca agc gat gtt gaa cag ttc gcg aaa aag 288
 Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala Lys Lys
 85 90 95
 aaa acc gag tta ggc gat gaa ctg cgt lta ggc aaa ctc gac gtt ttc 336
 Tyr Thr Glu Leu Gly Asp Gln Leu Arg Ser Gly Lys Ser Asp Val Phe
 100 105 110
 tac gat ctc tac aat ctg gcg caa aag cgc cgt ttt gag cgt ltu aag 384
 Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Glu Arg Tyr Gln
 115 120 125

tac gct ttg tgg gta ctg gaa aac ccc atg gat ttc acc ggc aac gac	432
Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly Asn Asp	
130 135 140	
act tat aac ctt gac cgc acc aaa gcg ccc tgg ccg aac aac gag gct	480
Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn Glu Ala	
145 150 155 160	
gag ttg aac gcg ctg tgg gac agt aaa gtc asa ttc gac gag tta ago	528
Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu Leu Ser	
165 170 175	
ctg aag ctg acc gga aaa acg gat aaa gaa att cgt gaa acc ctg act	576
Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr Leu Thr	
180 185 190	
cgc cgc tac aaa ttt gcc att cgt cgt ctg gcg caa acc aac agc gaa	624
Arg Arg Tyr Lys Phe Ala Ile Arg Leu Ala Cln Thr Asn Ser Glu	
195 200 205	
gat gtt ttc tgg ctg gaa atg acg gcg ttt gcg cgt gaa atc gac ccc	672
Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro	
210 215 220	
cct acc aac tat ctt tcc ccc cgt aat acc gaa cag ttc aac uct gaa	720
His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Glu Phe Asn Thr Glu	
225 230 235 240	
atg agt ttg tgg ctg gaa ggt att ggc gca tgg ctg caa atg gat gat	768
Met Ser Leu Ser Leu Glu Gly Ile Gly Ala Val Leu Glu Met Asp Asp	
245 250 255	
gac tac acc gtt atc aat tgg atg gtg gca ggt ggt ccc gca gcg aag	816
Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala Ala Lys	
260 265 270	
agt aaa gct atc agc gtt ggt gac aaa att gtc ggt gtt ggt cuu uu	864
Ser Lys Ala Ile Ser Val Gly Asp Lys Phe Val Gly Val Gly Cln Thr	
275 280 285	
ggc aag ccg atg gtt gac gtc att ggc tgg cgt ctt gat gat gtg gtt	912

qgt cgt gcg ctg gtt gtg ggt gaa cgg acg ttt ggt aaa ggc acc gtt Gly Arg Ala Leu Val Val Gly Glu Pro Thr Phe Gly Lys Gly Thr Val 465 470 475 480	1440
cag caa tac cgt tca ttg aac cgt att tac gat cag atg tta cgt cct Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu Arg Pro 485 490 495	1488
gaa tgg cca gcg ctg ggt tct gtg cag cac acg atc cag aaa ttc tal Glu Trp Pro Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys Phe Tyr 500 505 510	1536
cgc gtt aac ggc ggc agt acg caa cgt aaa ggc gtu acg cca gac atc Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro Asp Ile 515 520 525	1584
atc atg cgg acg qgt aat gaa gaa acg gaa acg ggt gag aaa ttc gaa Ile Met Pro Thr Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys Phe Glu 530 535 540	1632
gat aac gag ctg cgg tgg gat agc att gat ggc gcg act tat gtg aaa Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr Val Lys 545 550 555 560	1680
tca gga gat tta acg gcc tct gaa cgg gag ctg ctg aag gaa cat aat Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu His Asn 565 570 575	1728
gcg cgt atc gcy aaa gat cct gag ttc cag aac atc acg aag gat atc Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys Asp Ile 580 585 590	1776
gcg cgc ttc aac gct atg aag gac aag cgc aat atc gtt tct ctg aat Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser Leu Asn 595 600 605	1824
tac gct gtg cgt gag aaa gag aat aat gaa gat gat gcg acg cgt ctg Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr Arg Leu 610 615 620	1872
gcg cgt ttg aac gaa cgc ttt aaa cgc gaa ggt aaa cgg gag lly aag 1920	

Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu Leu Lys
 625 630 635 640

aaa ctg qat qat cta ccy aaa gat tac cag gaa ccy gat cct tat atg 1958
 Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro Tyr Leu
 645 650 655

gal gag acg ggg aat atc gca ctc gat ctg gcg aag att gaa aaa gcc 2016
 Asp Glu Thr Val Asn Ile Ala Leu Asp Leu Ala Lys Leu Gln Lys Ala
 660 665 670

aga ccc gcg gaa caa ccc gct ccc gtc aag taa 2049
 Arg Pro Ala Gln Gln Pro Ala Pro Val Lys
 675 680

<210> 260
 <211> 682
 <212> PEST
 <213> Bocharich's cold
 <400> 260

Met Asn Met Phe Phe Arg Leu Thr Ala Leu Ala Gly Leu Leu Ala Ile
 1 5 10 15

Ala Gly Gln Thr Phe Ala Val Glu Asp Ile Thr Arg Ala Asp Gln Ile
 20 25 30

Pro Val Leu Lys Glu Glu Thr Gln His Ala Thr Val Ser Glu Arg Val
 35 40 45

Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu Asp Gln
 50 55 60

Ala Phe Ser Ala Lys Ile Phe Asp Arg Cys Leu Asn Leu Leu Asp Tyr
 65 70 75 80

Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala Lys Lys
85 90 95

Lys Thr Glu Leu Gly Asp Glu Leu Arg Ser Gly Lys Leu Asp Val Phe
100 105 110

Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Glu Arg Tyr Gln
115 120 125

Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly Asn Asp
130 135 140

Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn Glu Ala
145 150 155 160

Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu Leu Ser
165 170 175

Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr Leu Thr
180 185 190

Arg Arg Tyr Lys Phe Ala Ile Arg Arg Leu Ala Gln Thr Asn Ser Glu
195 200 205

Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro
210 215 220

His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Gln Phe Asn Thr Glu
230 235 240

Met Ser Leu Ser Leu Glu Gly Ile Cys Ala Val Leu Gln Met Asp Asp

245

250

255

Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala Ala Lys
260 265 270

Ser Lys Ala Ile Ser Val Gly Asp Pys Ile Val Gly Val Gly Gln Thr
275 280 285

Gly Lys Pro Met Val Asp Val Ile Gly Ser Arg Leu Asp Asp Val Val
290 295 300

Ala Leu Ile Lys Gly Pro Lys Gly Ser Lys Val Arg Leu Glu Ile Leu
305 310 315 320

Pro Ala Gly Lys Gly Thr Lys Thr Arg Thr Val Thr Leu Thr Arg Glu
325 330 335

Arg Ile Arg Leu Glu Asp Arg Ala Val Lys Met Ser Val Lys Thr Val
340 345 350

Gly Lys Glu Lys Val Gly Val Leu Asp Ile Pro Gly Phe Tyr Val Gly
355 360 365

Leu Thr Asp Asp Val Lys Val Gln Leu Gln Lys Leu Glu Lys Gln Asn
370 375 380

Val Ser Ser Val Ile Ile Asp Leu Arg Ser Asn Gly Gly Gly Ala Leu
385 390 395 400

Thr Glu Ala Val Ser Leu Ser Gly Leu Phe Ile Pro Ala Gly Pro Ile
405 410 415

Val Gln Val Arg Asp Asn Asn Gly Lys Val Arg Glu Asp Ser Asp Thr
 420 425 430

Asp Gly Gln Val Phe Tyr Lys Gly Pro Leu Val Val Leu Val Asp Arg
 435 440 445

Phe Ser Ala Ser Ala Ser Glu Ile Phe Ala Ala Ala Met Gln Asp Tyr
 450 455 460

Gly Arg Ala Ser Val Val Gly Glu Pro Val Phe Gly Lys Gly Thr Val
 465 470 475 480

Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu Arg Pro
 485 490 495

Glu Tyr Phe Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys Phe Tyr
 500 505 510

Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro Asp Ile
 515 520 525

Ile Met Pro Val Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys Phe Glu
 530 535 540

Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr Val Lys
 545 550 555 560

Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu His Asn
 565 570 575

Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys Asp Ile

580

585

390

Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser Leu Asn
595 600 605

Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr Arg Leu
610 615 620

Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu Leu Lys
625 630 635 640

Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro Tyr Leu
645 650 655

Asp Gln Thr Val Asn Ile Ala Leu Asp Leu Ala Lys Leu Glu Lys Ala
660 665 670

Arg Pro Ala Glu Gln Pro Ala Pro Val Lys
675 680

<210> 261
<211> 1551
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1551)

<400> 261
ttg ttc atg gca act tat atg act ttt tca tta aag caa tca ggg aga 48
Leu Phe Met Ala Thr Tyr Met Thr Phe Ser Leu Lys Gln Ser Gly Arg
1 5 10 15

gaa atg agt aaa cac gac acc gac act lca gat caa cac ggc gcg aaa	96
Ala Met Ser Lys His Asp Thr Asp Thr Ser Asp Gln His Ala Ala Lys	
20 25 30	
ggc ggc tgg ctt aat gcc cac gaa gag ggg tat cac aaa gag atg ggc	144
Arg Arg Trp Leu Asn Ala His Glu Glu Gly Tyr His Lys Ala Met Gly	
35 40 45	
aat ggc cag gtg cag atg atc gcc att ggc ggc gcg att ggc acc ggc	192
Asn Arg Gln Val Gln Met Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly	
50 55 60	
ttg tll tta ggt gaa gga gcc cga ctg caa atg ggc ggc ccc gca ctg	240
Leu Phe Trp Gly Ala Gly Ala Arg Leu Gln Met Ala Gly Pro Ala Leu	
65 70 75 80	
gaa atg gtt tat tta att tct ggc ttg ttt tgg ttt ttt att ctg cgt	288
Ala Leu Val Tyr Leu Ile Cys Gly Leu Phe Ser Phe Phe Ile Leu Arg	
85 90 95	
gaa ttg ggt gag ctg gtg cta cca ggc cat tcc agt ggc agt ttt gtt	336
Ala Leu Gly Glu Leu Val Leu Ala Arg Pro Ser Ser Gly Ser Phe Val	
100 105 110	
tct tat gcc cgt gag ttt ttg ggt gag aaa gcc gat tat gtt gct ggc	384
Ser Tyr Ala Arg Glu Phe Leu Gly Glu Lys Ala Ala Tyr Val Ala Gly	
115 120 125	
tgg atg tac ttc atc aac tgg gcc atg aag ggg att gtt gat att acc	432
Trp Met Tyr Phe Ile Asn Trp Ala Met Thr Gly Ile Val Asp Ile Thr	
130 135 140	
gcc gtc gct atg tat atg cat tac tgg ggt gcc ttt gcc gcc gtg cgg	480
Ala Val Ala Leu Tyr Met His Tyr Trp Gly Ala Phe Gly Gly Val Pro	
145 150 155 160	
cag tgg gtc ttt gag ctc gct gca att acc atc gtt gcc acc atg aat	528
Glu Trp Val Phe Ala Leu Ala Ala Leu Thr Ile Val Gly Thr Met Asn	
165 170 175	
atg atc ggt gtg aaa tgg ttt gag gag atg gag ttc tgg ttt gcc att	576
Met Ile Gly Val Lys Trp Phe Ala Glu Met Glu Phe Trp Phe Ala Leu	

180	185	190	
att aaa gtg ctg ggc att gtg acc ttg ttg gtc gtg ggt aca gtg ttc			624
Ile Lys Val Leu Ala Ile Val Thr Phe Leu Val Val Gly Thr Val Phe			
195	200	205	
ctc ggt agt ggt cag ccg ctg gat ggc aac acc act ggc ttt cat tta			672
Leu Gly Ser Gly Gln Pro Leu Asp Gly Asn Thr Thr Gly Phe His Leu			
210	215	220	
atc acc gal aat ggc ggc ttc ttc ccc cac ggt ttg ctg cct ggc ctg			720
Ile Thr Asp Asn Gly Gly Phe Phe Pro His Gly Leu Leu Pro Ala Leu			
225	230	235	240
gtg ttg att cag ggc gta gtg ttt gct ttt gcc tcc att gaa ctg gtg			768
Val Leu Ile Glu Gly Val Val Phe Ala Phe Ala Ser Ile Glu Met Val			
245	250	255	
ggt aca gct gcc gga gaa tgt aaa gal ccg cag aca atg gtg cct aaa			816
Gly Thr Ala Ala Gly Glu Cys Lys Asp Pro Gln Thr Met Val Pro Lys			
260	265	270	
gcc att aac agt gtg att tgg cgt att ggc ctg ttt tac gtc ggc tcc			864
Ala Ile Asn Ser Val Ile Trp Arg Ile Gly Leu Phe Tyr Val Gly Ser			
275	280	285	
gtg gtg ttg ctg gtt atg tta ttg ccg tgg agc ggc tat cag cgc ggg			912
Val Val Leu Leu Val Met Leu Leu Pro Trp Ser Ala Tyr Gln Ala Gly			
290	295	300	
caa agt ccg ttc gty ccg ttt ttc tca aaa ctg ggt gtg cca tat atc			960
Gln Ser Pro Phe Val Thr Phe Phe Ser Lys Leu Gly Val Pro Tyr Ile			
305	310	315	320
ggc agc att atg aac att gtg gtg ctg acc gct gcc ctg tcc agc ctg			1008
Gly Ser Ile Met Asn Ile Val Val Leu Thr Ala Ala Leu Ser Ser Leu			
325	330	335	
aat tca ggt ctg tac tgc acc gga cgt att ctg cgc tca atg ccg atg			1056
Asn Ser Gly Leu Tyr Cys Thr Gly Arg Ile Leu Arg Ser Met Ala Met			
340	345	350	

ggc ggt tcc gca cgg agt ttt atg gcg aaa atg agt cgt cag cat gtg Gly Gly Ser Ala Pro Ser Phe Met Ala Lys Met Ser Arg Gln His Val 355 360 365	1104
cgg tat gcc ggg atg ctg gcg aca cta gtt gtg tat gtc gtc ggc gta Pro Tyr Ala Gly Ile Leu Ala Thr Leu Val Val Tyr Val Val Gly Val 370 375 380	1152
ttc ctc aac tat ctg gtg ccg tgg cgc gta ttt gag att gtg ttg aac Phe Leu Asn Tyr Leu Val Pro Ser Arg Val Phe Glu Ile Val Leu Asn 385 390 395 400	1200
lta gcg tgg ctg gga atc atc gct tca tgg ccg ttt atc atc gtg tgc Phe Ala Ser Leu Gly Ile Ile Ala Ser Trp Ala Phe Ile Ile Val Cys 405 410 415	1248
cag atg cgc ctg cgt aca gcg att aaa gaa ggc aac gca gcg gat gtc Gln Met Arg Leu Arg Lys Ala Ile Lys Glu Gly Lys Ala Ala Asp Val 420 425 430	1296
agt ttt aaa ctg cct ggc gcg ccc ttc act tcc tgg ctg aca tta ctg Ser Phe Lys Leu Pro Gly Ala Pro Phe Thr Ser Trp Leu Thr Leu Leu 435 440 445	1344
ttt tta ctg agt gcc att gtg cly atg gcg ttc gat taa ccg aac ggg Phe Leu Leu Ser Val Leu Val Leu Met Ala Phe Asp Tyr Pro Asn Gly 450 455 460	1392
act tat act atc ggg gcc ctg ccg att atc ggt att tgg cly gtt ata Thr Tyr Thr Ile Ala Ala Leu Pro Ile Ile Gly Ile Leu Leu Val Ile 465 470 475 480	1440
ggc tgg ttt ggt gtg cgc aaa cgc gtt gct gaa att caa agc act gcg Gly Trp Phe Gly Val Arg Lys Arg Val Ala Glu Ile His Ser Thr Ala 485 490 495	1488
caa gtc gtc gag gaa gat gaa gaa aaa cgg gaa att gtg ttt aag cct Pro Val Val Glu Asp Glu Glu Lys Gln Glu Ile Val Phe Lys Pro 500 505 510	1536
gaa acg gcg agt taa Glu Thr Ala Ser	1551

515

<210> 262
 <211> 516
 <212> PRT
 <213> Escherichia coli

<400> 262

Leu Phe Met Ala Thr Tyr Met Thr Phe Ser Leu Lys Gln Ser Gly Arg
 1 5 10 15

Ala Met Ser Lys His Asp Thr Asp Thr Ser Asp Gln His Ala Ala Lys
 20 25 30

Arg Arg Trp Leu Asn Ala His Glu Glu Gly Tyr His Lys Ala Met Gly
 35 40 45

Asn Arg Gln Val Gln Met Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly
 50 55 60

Leu Phe Leu Gly Ala Gly Ala Arg Leu Gln Met Ala Gly Pro Ala Leu
 65 70 75 80

Ala Leu Val Tyr Leu Ile Cys Gly Leu Phe Ser Phe Phe Ile Leu Arg
 85 90 95

Ala Leu Gly Glu Leu Val Leu His Arg Pro Ser Ser Gly Ser Phe Val
 100 105 110

Ser Tyr Ala Arg Glu Phe Leu Gly Glu Lys Ala Ala Tyr Val Ala Gly
 115 120 125

Trp Met Tyr Phe Ile Asn Trp Ala Met Thr Gly Ile Val Asp Ile Thr
 130 135 140

Ala Val Ala Leu Tyr Met His Tyr Trp Gly Ala Phe Gly Gly Val Pro
 145 150 155 160

Gln Trp Val Phe Ala Leu Ala Ala Leu Thr Ile Val Gly Thr Met Asn
 165 170 175

Met Ile Gly Val Lys Trp Phe Ala Glu Met Glu Phe Trp Phe Ala Leu
 180 185 190

Ile Lys Val Leu Ala Ile Val Thr Phe Leu Val Val Gly Thr Val Phe
 195 200 205

Leu Gly Ser Gly Gln Pro Leu Asp Gly Asn Thr Thr Gly Phe His Leu
 210 215 220

Ile Thr Asp Asn Gly Gly Phe Phe Pro His Gly Leu Leu Pro Ala Leu
 225 230 235 240

Val Leu Ile Glu Gly Val Val Phe Ala Phe Ala Ser Ile Glu Met Val
 245 250 255

Gly Thr Ala Ala Gly Gln Cys Lys Asp Pro Gln Thr Met Val Pro Lys
 260 265 270

Ala Ile Asn Ser Val Ile Trp Arg Ile Gly Leu Phe Tyr Val Gly Ser
 275 280 285

Val Val Leu Leu Val Met Leu Leu Pro Trp Ser Ala Tyr Gln Ala Gly
 290 295 300

Gln Ser Pro Phe Val Thr Phe Phe Ser Lys Leu Gly Val Pro Tyr Ile
 305 310 315 320

Gly Ser Ile Met Asn Ile Val Val Leu Thr Ala Ala Leu Ser Ser Leu
 325 330 335

Asn Ser Gly Leu Tyr Cys Thr Gly Arg Ile Leu Arg Ser Met Ala Met
 340 345 350

Gly Gly Ser Ala Pro Ser Phe Met Ala Lys Met Ser Arg Gln His Val
 355 360 365

Pro Tyr Ala Gly Ile Leu Ala Thr Leu Val Val Tyr Val Val Gly Val
 370 375 380

Phe Asp Arg Tyr Leu Val Pro Ser Arg Val Phe Glu Ile Val Leu Asn
 385 390 395 400

Phe Ala Ser Leu Gly Ile Ile Ala Ser Trp Ala Phe Ile Ile Val Cys
 405 410 415

Gln Met Arg Leu Arg Lys Ala Ile Lys Glu Gly Lys Ala Ala Asp Val
 420 425 430

Ser Phe Lys Leu Pro Gly Ala Pro Phe Thr Ser Trp Leu Thr Leu Leu
 435 440 445

Phe Leu Leu Ser Val Leu Val Leu Met Ala Phe Asp Tyr Pro Asn Gly
 450 455 460

Thr Tyr Thr Ile Ala Ala Leu Pro Ile Ile Gly Ile Leu Leu Val Ile
465 470 475 480

Gly Trp Phe Gly Val Arg Lys Arg Val Ala Glu Ile His Ser Thr Ala
485 490 495

Pro Val Val Glu Glu Asp Glu Glu Lys Gln Glu Ile Val Phe Lys Pro
500 505 510

Glu Thr Ala Ser
515

<210> 263
<211> 681
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(681)

<400> 263
atg atc agg agt cac acc atg acc att acg tct ctg gat ggc tat cgc 40
Met Ile Arg Ser His Thr Met Thr Ile Thr Ser Leu Asp Gly Tyr Arg
1 5 10 15

tgg ctg aag aac gat att att cgc ggt aat ttt caa cag gat gaa aaa 96
Trp Leu Lys Asn Asp Ile Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys
20 25 30

tta cga atg agt ttg ctg aca tgg cgt tat gca att ggc gtt ggg cag 144
Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro
35 40 45

llu cgg gaa gct ctt tgg caa ctg gtc gcc gaa cgg ctg gtc aag gtc 192
Leu Arg Gln Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
50 55 60

gtg aat cea aaa ggg tat cgg gtg gcg tct atg tca gag cag ga3 ctg	240
Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln Glu Leu	
65 70 75 80	
ctc gat att ttc gac gcc cgc gcc aat atg caa gcg atg tta gta aqt	288
Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Ser	
85 90 95	
ctg gcg att gcc cgc ggt gcc gat gag tgg gag gaa gaa gtt ctc gaa	326
Leu Ala Ile Ala Arg Gly Gly Asp Gln Trp Glu Ala Asp Val Leu Ala	
100 105 110	
caa gcg cat ctg ctg agt aag ctt gag gcc tgt gac gcc agc gag aaa	364
Lys Ala His Leu Leu Ser Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys	
115 120 125	
atg ctt gat gag tgg gat ctg cgt cat cag gcg ttt cat acg gaa att	402
Met Leu Asp Glu Trp Asp Leu Arg His Gln Ala Phe His Thr Ala Ile	
130 135 140	
gtg gcg ggc tyt gat tct cwc tat ttg ctg caa atg cgt gaa cgg ttg	440
Val Ala Gly Cys Gly Ser His Tyr Leu Leu Gln Met Arg Glu Arg Leu	
145 150 155 160	
ttt gat ctg gcg gcg cgt tat cga ttt atc tgg ctg cgg cga acg gtg	528
Phe Asp Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val	
165 170 175	
ctt tcy atg gaa atg ctg gag gat aaa cac gat cag cac cag acc ctg	576
Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Glu His Glu Thr Leu	
180 185 190	
act gcg gcg gta ctg gcg cga gat acc gcg cgc gcc agt gag tta atg	624
Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu Leu Met	
195 200 205	
cgc cag cat tta ctg acg cca att ccc att abc cag cag gcg ctg gct	672
Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala	
210 215 220	
ggc aal lea	681

Gly Asn

225

<210> 264

<211> 226

<212> F32

<213> Escherichia coli

<400> 264

Met Ile Arg Ser His Thr Met Thr Ala Thr Ser Leu Asp Gly Tyr Arg

1 5 10 15

Trp Leu Tyr Asn Asp Val Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys

20 25 30

Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro

35 40 45

Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val

50 55 60

Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln Glu Leu

65 70 75 80

Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Ser

85 90 95

Leu Ala Ile Ala Arg Gly Gly Asp Glu Trp Glu Ala Asp Val Leu Ala

100 105 110

Lys Ala His Leu Leu Ser Lys Leu Glu Ala Cys Asp Ala Ser Gln Lys

115 120 125

Met Leu Asp Glu Trp Asp Leu Arg His Gln Ala Phe His Thr Ala Ile
 130 135 140

Val Ala Gly Cys Gly Ser His Tyr Leu Leu Gln Met Arg Glu Arg Leu
 145 150 155 160

Phe Asp Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val
 165 170 175

Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Gln His Gln Thr Leu
 180 185 190

Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu Leu Met
 195 200 205

Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala
 210 215 220

Gly Ser
 225

<210> 265
 <211> 1152
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1152)

<400> 265
 atg atg got aac aga atg att atg aac gaa acg gaa tgg tut ggt egg
 Met Met Ala Asn Arg Met Ile Leu Asn Glu Thr Ala Trp Phe Gly Arg

639/762

3	5	10	15	
ggg gct gtt ggg gct tta acc gat gag gtg aac cgc cgt ggt tat cag				96
Gly Ala Val Gly Ala Leu Thr Asp Glu Val Lys Arg Arg Gly Tyr Gln				
20	25	30		
aag gcg ctg atc gtc aac gat aac aag ctg gtg caa tgc ggc gtg gtg				144
Lys Ala Leu Ile Val Thr Asp Lys Thr Leu Val Gln Cys Gly Val Val				
35	40	45		
ggg aaa gtg acc gat aag atg gat gct gca ggg ctg gca tgg gcg att				192
Ala Lys Val Thr Asp Lys Met Asp Ala Ala Gly Leu Ala Trp Ala Ile				
50	55	60		
tac gac ggc gta gtg ccc aac cca acc att act gtc gtc aac gaa ggg				240
Tyr Asp Gly Val Val Pro Asn Pro Thr Ile Thr Val Val Lys Gln Gly				
65	70	75	80	
ctc ggt gtc ttc cag aat agc ggc gcg gat tac ctg atc gct att ggt				288
Leu Gly Val Phe Gln Asn Ser Gly Ala Asp Tyr Leu Ile Ala Ile Gly				
85	90	95		
ggg ggt tct cca cag gat act tct aaa gcg att ggc att atc ugc aac				336
Gly Gly Ser Pro Gln Asp Thr Cys Lys Ala Ile Gly Ile Ile Ser Ser				
100	105	110		
aac cca gag ttt gcc gat gtg cgt agc ctg gaa ggc ctt tcc cag aac				384
Asn Pro Glu Phe Ala Asp Val Arg Ser Leu Glu Gly Leu Ser Pro Thr				
115	120	125		
aat aaa ccc agt gta ccg att ctg gca att cct acc aca gca cct act				432
Asn Lys Pro Ser Val Pro Phe Leu Ala Ile Pro Thr Thr Ala Gly Thr				
130	135	140		
ggg gca gaa gtg acc ctt aac tac gtg atc act gac gaa gag aac cgg				480
Ala Ala Glu Val Thr Ile Asn Tyr Val Ile Thr Asp Glu Glu Lys Arg				
145	150	155	160	
cgc aag ttt gtt tgc ctt gat ccg aat gat aac ccg cag gtg gcg ttt				528
Arg Lys Phe Val Cys Val Asp Pro His Asp Ile Pro Gln Val Ala Phe				
165	170	175		

att gac gct gac atg atg gat ggt atg cct cca gcg ctg aaa gct gcg	576
Ile Asp Ala Asp Met Met Asp Gly Met Pro Pro Ala Leu Lys Ala Ala	
130 185 190	
acg ggt gtc gat gcg ctg acg cat gct att gag ggg tat att acc cgt	621
Thr Gly Val Asp Ala Leu Thr His Ala Ile Glu Gly Tyr Ile Thr Arg	
195 200 205	
ggc gcg tgg gcg cta acc gat gca ctg cag att aaa gcg att gaa atc	672
Gly Ala Trp Ala Leu Thr Asp Ala Leu His Ile Lys Ala Ile Glu Ile	
210 215 220	
att gct ggg gcg ctg cga gga tgg gtt gct ggt gat aag gat gcc gga	723
Ile Ala Gly Ala Leu Arg Gly Ser Val Ala Gly Asp Lys Asp Ala Gly	
225 230 235 240	
gaa gaa atg gcg ctg ggg cag tat gtt gcg ggt atg ggc ttc tgg aat	768
Glu Glu Met Ala Leu Gly Glu Tyr Val Ala Gly Met Gly Phe Ser Asn	
245 250 255	
gtt ggg tta gga ttg gta cat ggt atg gcg cct con ctg ggc ggc ttt	815
Val Gly Leu Gly Leu Val His Gly Met Ala His Pro Leu Gly Ala Phe	
260 265 270	
tat acc act cca cag ggt gtt gcg aac gcc atc ctg tta ccg cat gtc	861
Tyr Asn Thr Pro His Gly Val Ala Asn Ala Ile Leu Leu Pro His Val	
275 280 285	
atg cgt tat aac gct gac ttt acc ggt gag aag tac cgc gat atc gcg	912
Met Arg Tyr Asn Ala Asp Phe Thr Gly Glu Lys Tyr Arg Asp Ile Ala	
290 295 300	
cgc gtt atg ggc gtg aaa gtg gaa ggt atg agc ctg gaa gag gcg cgt	960
Arg Val Met Gly Val Lys Val Glu Gly Met Ser Leu Glu Glu Ala Arg	
305 310 315 320	
aat gcc gct gtt gaa gcg ctg ttt gct ctg aac cgt gat gtc ggt att	1008
Asn Ala Ala Val Glu Ala Val Phe Ala Leu Asn Arg Asp Val Gly Ile	
325 330 335	
ccg cca cat ttg cgt gat gtt ggt gta cgc aag gaa gac att ccg gca	1056
Pro Pro His Leu Arg Asp Val Gly Val Arg Lys Glu Asp Ile Pro Ala	

641/762

340	345	350	
ctg gcg cag gcg gca ctg gat gat gtc tgt acc ggt ggc aac ccg cgt	1194		
Leu Ala Gln Ala Ala Leu Asp Asp Val Cys Thr Gly Gly Asn Pro Arg			
355	360	365	
gaa gca acg ctt gag gat att gta gag ctt tac cat acc gcc tgg taa	1152		
Glu Ala Thr Leu Glu Asp Ile Val Glu Leu Tyr His Thr Ala Trp			
370	375	380	
<210> 266			
<211> 383			
<212> F="			
<213> Escherichia coli			
<400> 266			
Met Met Ala Asn Arg Met Ile Leu Asn Glu Thr Ala Trp Phe Gly Arg			
1	5	10	15
Gly Ala Val Gly Ala Leu Thr Arg Gly Val Pys Arg Arg Gly Tyr Gln			
20	25	30	
Lys Ala Leu Ile Val Thr Asp Lys Thr Leu Val Gln Cys Gly Val Val			
35	40	45	
Ala Lys Val Thr Asp Lys Met Asp Ala Ala Gly Leu Ala Thr Ala Ile			
50	55	60	
Tyr Asp Gly Val Val Pro Asn Pro Thr Ile Thr Val Val Lys Glu Gly			
65	70	75	80
Leu Gly Val Phe Gln Asn Ser Gly Ala Asp Tyr Leu Ile Ala Ile Gly			
85	90	95	

Gly Gly Ser Pro Gln Asp Thr Cys Lys Ala Ile Gly Ile Ile Ser Asn
100 105 110

Asn Pro Glu Phe Ala Asp Val Arg Ser Leu Glu Gly Leu Ser Pro Thr
115 120 125

Asn Lys Pro Ser Val Pro Ile Leu Ala Ile Pro Thr Thr Ala Gly Thr
130 135 140

Ala Ala Glu Val Thr Ile Asn Tyr Val Ile Thr Asp Glu Glu Lys Arg
145 150 155 160

Arg Lys Phe Val Cys Val Asp Pro His Asp Ile Pro Gln Val Ala Phe
165 170 175

Ile Asp Ala Asp Met Met Asp Gly Met Pro Pro Ala Leu Lys Ala Ala
180 185 190

Thr Glu Val Asp Ala Leu Thr His Ala Ile Glu Gly Tyr Ile Thr Arg
195 200 205

Gly Ala Trp Ala Leu Thr Asp Ala Leu His Ile Lys Ala Ile Glu Ile
210 215 220

Ile Ala Gly Ala Leu Arg Gly Ser Val Ala Gly Asp Lys Asp Ala Gly
225 230 235 240

Glu Glu Met Ala Leu Gly Glu Tyr Val Ala Gly Met Gly Phe Ser Asn
245 250 255

Val Gly Leu Gly Leu Val His Gly Met Ala His Pro Leu Gly Ala Phe
260 265 270

Tyr Asn Thr Pro His Gly Val Ala Asn Ala Ile Leu Leu Pro His Val
 275 286 285

Met Arg Tyr Asn Ala Asp Phe Thr Gly Glu Lys Tyr Arg Asp Ile Ala
 290 295 300

Arg Val Met Gly Val Lys Val Glu Gly Met Ser Leu Glu Glu Ala Arg
 305 310 315 320

Asn Ala Ala Val Glu Ala Val Phe Ala Leu Asn Arg Asp Val Gly Ile
 325 330 335

Pro Pro His Leu Arg Asp Val Gly Val Arg Lys Glu Asp Ile Pro Ala
 340 345 350

Leu Ala Glu Ala Ala Leu Asp Asp Val Cys Thr Gly Gly Asn Pro Arg
 355 360 365

Glu Ala Thr Leu Glu Asp Ile Val Cys Leu Tyr His Thr Ala Thr
 370 375 380

<210> 267

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1197)

<400> 267

atg aat tac cgc tat cgc gcc atg acc cag gat ggt caa aua ttg caa

644/762

Met	Asn	Tyr	Arg	Tyr	Arg	Ala	Met	Thr	Gln	Asp	Gly	Gln	Lys	Leu	Gln	
1			5					10					15			
ggg	atc	att	gat	gct	aac	gat	gaa	cgt	cag	gca	cga	ctg	cgg	ctg	cgt	55
Gly	Ile	Ile	Asp	Ala	Asn	Asp	Glu	Arg	Gln	Ala	Arg	Leu	Arg	Leu	Arg	
			20					25				30				
gaa	gaa	ggg	ctt	ttc	ctg	ctg	gat	att	cgu	ccc	caa	aaa	agt	tcg	gga	144
Glu	Glu	Gly	Leu	Phe	Leu	Leu	Asp	Ile	Arg	Pro	Gln	Lys	Ser	Ser	Gly	
			35				40					45				
gta	aaa	aca	cgt	cgc	cgg	atc	agc	cat	agt	gaa	ctg	acg	ctt	ttc		192
Val	Lys	Thr	Arg	Arg	Pro	Arg	Ile	Ser	His	Ser	Gln	Leu	Thr	Leu	Phe	
	50				55					60						
acc	cgg	cag	ttg	gca	acc	tta	agc	gca	ggg	gca	tta	ccc	ctg	gaa	gag	240
Thr	Arg	Gln	Leu	Ala	Thr	Leu	Ser	Ala	Ala	Ala	Leu	Pro	Leu	Glu	Glu	
65			70					75				80				
agc	ctt	gcc	gta	atc	ggc	caa	caa	agu	agt	aat	aaa	cga	ctg	ggc	gac	288
Asp	Leu	Ala	Val	Ile	Gly	Gln	Gln	Ser	Ser	Asn	Lys	Arg	Leu	Gln	Asp	
			85					90				95				
gtg	tta	aat	cag	gta	cgc	agc	guc	atc	ctt	gaa	ggg	aat	ccc	ctt	ttc	336
Val	Leu	Asn	Gln	Val	Arg	Ser	Ala	Ile	Leu	Glu	Gly	His	Pro	Leu	Ser	
	100						105					110				
gat	aca	tta	cag	cat	ttt	ccc	acg	ctt	ttc	gat	tcg	ctc	tat	cgt	acu	384
Asp	Ala	Leu	Gln	His	Phe	Pro	Thr	Leu	Phe	Asp	Ser	Leu	Tyr	Arg	Thr	
	115				120					125						
ctg	gta	aaa	gug	ggc	gaa	aag	agc	cgg	ctg	ctg	goc	mcg	gtg	ttg	gaa	432
Leu	Val	Lys	Ala	Gly	Glu	Lys	Ser	Gly	Leu	Leu	Ala	Pro	Val	Leu	Glu	
	130				135					140						
agc	ctg	gct	gat	tac	aat	gaa	aac	cgy	cag	aaa	ala	cgc	agc	asg	ctc	480
Lys	Leu	Ala	Asp	Tyr	Asn	Glu	Asp	Arg	Gln	Lys	Ile	Arg	Ser	Lys	Leu	
145			150					155				160				
att	cag	tca	ctg	atc	tac	ccc	tgt	atg	ctc	act	acg	gtg	guy	att	ggg	528
Ile	Gln	Ser	Leu	Ile	Tyr	Pro	Cys	Met	Leu	Thr	Thr	Val	Ala	Ile	Gly	
			165					170				175				

gtc gtg att att ctc ctc act gct gtc gtg ccc aaa att acc gaa cag	576
Val Val Ile Ile Leu Leu Thr Ala Val Val Pro Lys Ile Thr Glu Glu	
180 185 190	
ttc gtg cat atg aag cag caa ctg cgg ctg agt acc cgc att att tta	624
Phe Val His Met Lys Gln Gln Leu Pro Leu Ser Thr Arg Ile Leu Leu	
195 200 205	
ggc ctg agc gac aag ttg aac cgt acc ggu cgg acc tta tta gag acc	672
Gly Leu Ser Asp Thr Leu Gln Arg Thr Gly Pro Thr Leu Leu Ala Thr	
210 215 220	
gtg ttt att gtc gct gta ggt ttc tgg ctg tgg ttu aac cgc ggc acc	720
Val Phe Ile Val Ala Val Gly Phe Arg Leu Trp Leu Lys Arg Gly Asn	
225 230 235 240	
aac cgc cac cgt ttt cat gcc atg ttg ctg cgc gtt ggc ctc atc ggc	768
Asn Arg His Arg Phe His Ala Met Leu Leu Arg Val Ala Leu Ile Gly	
245 250 255	
cgg ctg att tgc gcc att aac agc gca cgc tat ctc cgt act tta agt	816
Pro Leu Ile Cys Ala Ile Asn Ser Ala Arg Tyr Leu Arg Thr Leu Ser	
260 265 270	
att ttg caa tcc agc ggc glu cct ctg ctg gat ggg atg aat ttg tcc	864
Ile Leu Gln Ser Ser Gly Val Pro Leu Leu Asp Gly Met Asn Leu Ser	
275 280 285	
acc gaa agc ctc aac aac ctc gaa att cgc cag cgt ctg gca aat ggc	912
Thr Glu Ser Leu Asn Asn Leu Glu Ile Arg Gln Arg Leu Ala Asn Ala	
290 295 300	
gca gag aac gtc cgc cag ggt aac agc att cat ctt tcy ctg gaa caa	960
Ala Glu Asn Val Arg Gln Gly Asn Ser Ile His Leu Ser Asn Glu Gln	
305 310 315 320	
acc gca att ttc cgg cgg atg atg ctc aac atg gtc gcc tct ggc gaa	1008
Thr Ala Ile Phe Pro Pro Met Met Leu Tyr Met Val Ala Ser Gly Glu	
325 330 335	
aaa agc ggg cag ctc ggc aca tta atg gtc aga gcc gca gat aac cag	1056

646/762

Lys Ser Gly Glu Leu Gly Thr Leu Met Val Arg Ala Ala Asp Asn Gln
 340 345 350

Gag Adu Cto Caa Caa Aat Cgg Atc Gcg Cta Aag Cto Tcc Atc Ttc Gag 1164
 Glu Thr Leu Gln Gln Asn Arg Ile Ala Leu Thr Leu Ser Ile Phe Glu
 355 360 365

Cca Gca Ctc Att Att Aag Atg Gca Ctg Atc Gtc Cgg Ttt Att Gtc Gtg 1152
 Pro Ala Leu Ile Ile Thr Met Ala Leu Ile Val Leu Phe Ile Val Val
 370 375 380

Cug Gta Cto Caa Cct Ctt Ctt Caa Ctt Aac Tca Alg All Aat Taa 1197
 Ser Val Leu Gln Pro Leu Leu Gln Leu Asn Ser Met Ile Asn
 385 390 395

<210> 268

<211> 398

<212> ERT

<213> Escherichia coli

<400> 268

Met Asn Tyr Arg Tyr Arg Ala Met Thr Gln Asp Gly Gln Lys Leu Gln
 1 5 10 15

Gly Ile Ile Asp Ala Asn Asp Glu Arg Gln Ala Arg Leu Arg Leu Arg
 20 25 30

Glu Glu Gly Leu Phe Leu Leu Asp Ile Arg Pro Gln Lys Ser Ser Gly
 35 40 45

Val Lys Thr Arg Arg Pro Arg Ile Ser His Ser Glu Leu Thr Leu Phe
 50 55 60

Thr Arg Gln Leu Ala Thr Leu Ser Ala Ala Ala Leu Pro Leu Glu Glu
 65 70 75 80

Ser Leu Ala Val Ile Gly Gln Gln Ser Ser Asn Lys Arg Leu Gly Asp
85 90 95

Val Leu Asn Gln Val Arg Ser Ala Ile Leu Glu Gly His Pro Leu Ser
100 105 110

Asp Ala Leu Gln His Phe Pro Thr Leu Phe Asp Ser Leu Tyr Arg Thr
115 120 125

Leu Val Lys Ala Gly Glu Lys Ser Cys Leu Leu Ala Pro Val Leu Glu
130 135 140

Lys Leu Ala Asp Tyr Asn Glu Asn Arg Gln Lys Ile Arg Ser Lys Leu
145 150 155 160

Ile Gln Ser Leu Ile Tyr Pro Cys Met Leu Thr Thr Val Ala Ile Gly
165 170 175

Val Val Ile Ile Leu Leu Thr Ala Val Val Pro Lys Ile Thr Glu Glu
180 185 190

Phe Val His Met Lys Gln Gln Leu Pro Leu Ser Thr Arg Ile Leu Leu
195 200 205

Gly Leu Ser Asp Thr Leu Gln Arg Thr Gly Pro Thr Leu Leu Ala Thr
210 215 220

Val Phe Ile Val Ala Val Gly Phe Trp Leu Trp Leu Lys Arg Gly Asn
225 230 235 240

Asn Arg His Arg Phe His Ala Met Leu Leu Arg Val Ala Leu Ile Gly

245

250

255

Pro Leu Ile Cys Ala Ile Asn Ser Ala Arg Tyr Leu Arg Thr Leu Ser
 260 265 270

Ile Leu Gln Ser Ser Gly Val Pro Leu Leu Asp Gly Met Asn Leu Ser
 275 280 285

Thr Glu Ser Leu Asn Asn Leu Glu Ile Arg Gln Arg Leu Ala Asn Ala
 290 295 300

Ala Glu Asn Val Arg Gln Gly Asn Ser Ile His Leu Ser Leu Glu Gln
 305 310 315 320

Thr Ala Ile Phe Pro Pro Met Met Leu Tyr Met Val Ala Ser Gly Glu
 325 330 335

Lys Ser Gly Gln Leu Gly Thr Leu Met Val Arg Ala Ala Asp Asn Gln
 340 345 350

Glu Thr Leu Gln Gln Asn Arg Ile Ala Leu Thr Leu Ser Ile Phe Glu
 355 360 365

Pro Ala Leu Ile Ile Thr Met Ala Leu Ile Val Leu Phe Ile Val Val
 370 375 380

Ser Val Leu Gln Pro Leu Leu Gln Leu Asn Ser Met Ile Asn
 385 390 395

<210> 269

<211> 660

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(660)

<400> 263

atg gat cgt att gtt agt tct tca cat gac cgt aca tca ctg ctt agc 48
Met Asp Arg Ile Val Ser Ser Ser His Asp Arg Thr Ser Leu Leu Ser

1 5 10 15

acc cat aag gtg ctg cgt aat acc tat ttt ctg ctg agc ctg acg ctg 96
Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu

20 25 30

gcc ttt tgg gag att acc gca act gcc agt acg gtg ctg atg ctg aca 144
Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro

35 40 45

tct cgg ggt ctg att ctg acg ctg gtg ggt atg tat ggt ttg atg ttc 192
Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe

50 55 60

ctg acc tat aac acg gag aat cgg ccg acc gag att atc tcc gca ttc 240
Leu Thr Tyr Lys Thr Ala Asn Lys Pro Thr Gly Ile Ile Ser Ala Phe

65 70 75 80

gcc ttt acc ggt ttt ctg ggt tat atc ctc gga cct att ctg aac acc 288
Ala Phe Thr Gly Phe Leu Gly Tyr Phe Leu Gly Pro Ile Leu Asn Thr

85 90 95

tat ctg tct gcc gga atg ggt gac gta atc gct atg gca ctg ggc gga 336
Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly

100 105 110

acg gag tta gtg ttc ttc tgc tgc tct gca tat gtg ctg acc acc cgc 384
Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg

115 120 125

aac gat atg tgg ttc ctc ggc ggt atg ctg atg gag ggt att gtg gtg 432
Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val

650/762

130	135	140	
gtg ctg att ggt atg gtt gcg aat atc ttc ctg cag ctg cct gct ctg			483
Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Glu Leu Pro Ala Leu			
145	150	155	160
cat ctg gcg atc agc gcg gtc ttc att ctg atc tcc tct ggc gct atc			528
His Leu Ala Ile Ser Ala Val Phe Ile Val Ile Ser Ser Gly Ala Ile			
165	170	175	
ttg ttt gaa acc agc aac atc att cat ggc ggt gag acg aac tat att			576
Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile			
180	185	190	
cgt gcc acg gtt agc ctg tat gtt lcy ctg tac aac atc ttc gtc agc			624
Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser			
195	200	205	
ctg ctg agc att ctg ggc ttc gct agc ccg gat taa			660
Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp			
210	215		
<210> 270			
<211> 219			
<212> PRT			
<213> Escherichia coli			
<400> 270			
Met Asp Arg Ile Val Ser Ser Ser His Asp Arg Thr Ser Leu Leu Ser			
1	5	10	15
Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu			
20	25	30	
Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro			
35	40	45	

Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe
 50 55 60

Leu Thr Tyr Lys Thr Ala Asn Tyr Pro Thr Gly Ile Ile Ser Ala Phe
 65 70 75 80

Ala Phe Thr Gly Phe Leu Gly Tyr Ile Leu Gly Pro Ile Leu Asn Thr
 85 90 95

Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly
 100 105 110

Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg
 115 120 125

Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val
 130 135 140

Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Gln Leu Pro Ala Leu
 145 150 155 160

His Leu Ala Ile Ser Ala Val Phe Ile Leu Ile Ser Ser Gly Asn Ile
 165 170 175

Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile
 180 185 190

Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser
 195 200 205

Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp
 210 215

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 <212> DNA
 <213> *Saccharomyces cerevisiae*

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<400> 271
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 45
 Met Ser Asn Lys Leu Phe Arg Leu Asp Ala Gly Tyr Gln Gln Tyr Asp
 1 5 10 15
 Lys ggt aaa atc ggc tct tct tca gct gtc gct caa ttt gct gac cat
 96
 Trp Gly Lys Ile Gly Ser Ser Ser Ala Val Ala Gln Phe Ala Ala His
 20 25 30
 tct gac ccc tct ggt caa att gaa caa gat aaa caa tat gaa gag tta
 144
 Ser Asp Pro Ser val Gln ile Glu Gln Asp Lys Pro Tyr Ala Glu Leu
 35 40 45
 tgg atg ggt acc cnc agc aag atg ctt tcc tac aac cat gag tct aag
 192
 Trp Met Gly Thr His Ser Tyr Met Pro Ser Tyr Asn His Glu Ser Lys
 50 55 60
 gaa tcc ctg aga gat atc atc tcc aag aac ccc tct gcc atg tta ggt
 240
 Glu Ser Leu Arg Asp ile ile Ser Lys Asn Pro Ser Ala Met Leu Gly
 65 70 75 80
 aag gac att att gat aag ttc cac gcc aca aat gaa ttt ccc ttc att
 288
 Lys Asp ile ile Asp Lys Phe His Ala Thr Asn Glu Leu Pro Phe Leu
 85 90 95

ttc aaa gtl ttg tcc att gaa aca gtc ttg tat att caa gca cat ccc
136

Phe Lys Val Leu Ser Ile Glu Lys Val Leu Ser Ile Gln Ala His Pro
140 145 150

gac aaa gcc ttg ggt aaa ata ttg ccc gct caa gat cct aag aac tat
184

Asp Lys Ala Leu Gly Lys Ile Leu His Ala Gln Asp Pro Lys Asn Tyr
115 120 125

cct gat gat aat cac aaa cct gaa atg gcc atc gct gtg act gac ttt
432

Pro Asp Asp Asn His Lys Pro Glu Met Ala Ile Ala Val Thr Asp Phe
130 135 140

gaa ggt ttc tgc ggg ttc aaa cct ttg caa gag att gca gat gaa ttg
460

Glu Gly Phe Cys Gly Phe Lys Pro Leu Gln Glu Ile Ala Asp Glu Leu
145 150 155 160

aaa cgt att cct gaa tta cgc aac att gtt ggt gaa gaa act tcc agg
528

Lys Arg Ile Pro Glu Leu Arg Asn Ile Val Gly Glu Glu Thr Ser Arg
165 170 175

aat ttt att gag aac aii cca cct tct gct cag aac ggt tcc cca gaa
576

Asn Phe Ile Glu Asn Ile Gln Pro Ser Ala Gln Lys Gly Ser Pro Glu
180 185 190

gat gaa caa aac aaa aag cta ttg caa gct gtc ttc agc agg gtc atg
624

Asp Glu Gln Asn Lys Lys Leu Leu Gln Ala Val Phe Ser Arg Val Met
195 200 205

aac gct tgc gat gac aaa atc aag att caa gct cgc tcc ttg gtc gaa
672

Asn Ala Ser Asp Asp Lys Ile Lys Ile Gln Ala Arg Ser Leu Val Glu
210 215 220

aga tca aag aat tct cca tca gac ttt aac aaa cct gat tta cca gaa
720

Arg Ser Lys Asn Ser Pro Ser Asp Phe Asn Lys Pro Asp Leu Pro Glu
 225 350 235 240

tta att caa aga atg aat aaa caq ttc cct gat gac gtg ggt tgg ttt
 768

Leu Ile Gln Arg Leu Asn Lys Gln Phe Pro Asp Asp Val Gly Leu Thr
 245 250 255

tgt gga tgt tta ttg ttg aat cac tgc aga ttg aat gct ggt gaa ggc
 816

Cys Gly Cys Leu Leu Leu Asn His Cys Arg Leu Asn Ala Gly Glu Ala
 260 265 270

atc ttt tta aga gct aag gat cct cac gcc tat ata agc ggt gat atc
 864

Ile Phe Ileu Arg Ala Lys Asp Pro His Ala Tyr Ile Ser Gly Asp Ile
 275 280 285

atg gaa tgt atg gct gct tct gac aac gta gtt aga ggc ggc ttc atc
 912

Met Glu Cys Met Ala Ala Ser Asp Asn Val Val Arg Ala Gly Phe Thr
 290 295 300

cca aaa ttc aag gat gtt aaa aac ttg gtc tcc atg tta acc tat aca
 360

Pro Lys Phe Lys Asp Val Lys Asn Leu Val Ser Met Leu Thr Tyr Thr
 305 310 315 320

tat gat cct gtg gaa aag cca aaa atg cag cct tta aag ttc gac agg
 1088

Tyr Asp Pro Val Glu Lys Gln Lys Met Gln Pro Leu Lys Phe Asp Arg
 325 330 335

tac tct ggt aac ggt aag tca gtt tta tat aac cct cca atc gaa gaa
 1096

Ser Ser Gly Asn Gly Lys Ser Val Ile Tyr Asn Pro Pro Ile Glu Glu
 340 345 350

ttt gct gta ttg gag act aot ttt gat gag aaa ctt ggt caa agg cat
 1104

Phe Ala Val Leu Glu Thr Thr Phe Asp Glu Lys Leu Gly Gln Arg His
 355 360 365

ttt gaa ggt gtt gat ggt cca agt atc tta atc act aca aaa ggt aat
1152

Phe Glu Gly Val Asp Gly Pro Ser Ile Leu Ile Thr Thr Lys Gly Asn
370 375 380

ggt tac att aaa gca gat ggc caa aaa ttg aaa gct gaa ccc ggt ttt
1200

Gly Tyr Ile Lys Ala Asp Gly Gln Lys Leu Lys Ala Glu Pro Gly Phe
385 390 395 400

gtc ttt ttc atc gct cca cat ttg cct gtt gat ttg gaa gct gaa gat
1248

Val Phe Phe Ile Ala Pro His Leu Pro Val Asp Leu Glu Ala Glu Asp
405 410 415

gag gag ttt act acc tat aga gcc ttt gtg gaa cca aat tag
1290

Glu Ala Phe Thr Thr Tyr Arg Ala Phe Val Glu Pro Asn
420 425

<210> 373

<211> 429

<212> FRT

<213> Zeccharomycetes caravissae

<400> 272

Met Ser Asn Lys Leu Phe Arg Leu Asp Ala Gly Tyr Gln Gln Tyr Asp
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Trp Gly Lys Ile Gly Ser Ser Ser Ala Val Ala Glu Phe Ala Ala His
20 25 30

Ser Asp Pro Ser val Gln ile Glu Gln Asp Lys Pro Tyr Ala Glu Leu
35 40 45

Trp Met Gly Thr His Ser Lys Met Pro Ser Tyr Asn His Glu Ser Lys

50

55

60

Glu Ser Leu Arg Asp Ile Ile Ser Lys Asn Pro Ser Ala Met Leu Gly
 65 70 75 80

Lys Asp Ile Ile Asp Lys Phe His Ala Thr Asn Gln Leu Pro Phe Leu
 85 90 95

Phe Lys Val Leu Ser Ile Glu Lys Val Leu Ser Ile Gln Ala His Pro
 100 105 110

Asp Lys Ala Leu Gly Lys Ile Leu His Ala Gln Asp Pro Lys Asn Tyr
 115 120 125

Pro Asp Asp Asn His Lys Pro Glu Met Ala Ile Ala Val Thr Asp Phe
 130 135 140

Glu Gly Phe Cys Gly Phe Lys Pro Leu Gln Glu Ile Ala Asp Glu Leu
 145 150 155 160

Lys Arg Ile Pro Glu Leu Arg Asn Ile Val Gly Glu Glu Thr Ser Arg
 165 170 175

Asn Phe Ile Glu Asn Ile Gln Pro Ser Ala Gln Lys Gly Ser Pro Gln
 180 185 190

Asp Glu Gln Asn Lys Lys Leu Leu Gln Ala Val Phe Ser Arg Val Met
 195 200 205

Asn Ala Ser Asp Asp Lys Ile Lys Ile Gln Ala Arg Ser Leu Val Glu
 210 215 220

Arg Ser Lys Asn Ser Pro Ser Asp Phe Asn Lys Pro Asp Leu Pro Glu
 225 230 235 240

Leu Ile Gln Arg Leu Asn Lys Gln Phe Pro Asp Asp Val Gly Leu Phe
 245 250 255

Cys Gly Cys Leu Leu Leu Asn His Cys Arg Leu Asn Ala Gly Glu Ala
 260 265 270

Ile Phe Leu Arg Ala Lys Asp Pro His Ala Tyr Ile Ser Gly Asp Ile
 275 280 285

Met Glu Cys Met Ala Ala Ser Asp Asn Val Val Arg Ala Gly Phe Thr
 290 295 300

Pro Lys Phe Lys Asp Val Lys Asn Leu Val Ser Met Leu Thr Tyr Thr
 305 310 315 320

Tyr Asp Pro Val Glu Lys Gln Lys Met Gln Pro Leu Lys Phe Asy Arg
 325 330 335

Ser Ser Gly Asn Gly Lys Ser Val Leu Tyr Asn Pro Pro Ile Glu Glu
 340 345 350

Phe Ala Val Leu Glu Thr Thr Phe Asp Glu Lys Leu Gly Gln Arg His
 355 360 365

Phe Glu Gly Val Asp Gly Pro Ser Ile Leu Ile Thr Thr Lys Gly Asn
 370 375 380

Gly Tyr Ile Lys Ala Asp Gly Gln Lys Leu Lys Ala Glu Pro Gly Phe

385 390 395 400

Val Phe Phe Ile Ala Pro His Leu Pro Val Asn Leu Glu Ala Glu Asp
405 410 415

Glu Ala Phe Thr Thr Tyr Arg Ala Phe Val Glu Pro Asn
420 425

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<211> 1539
<212> DNA
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<221> CDG
<222> (1)..(1539);

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Met Val Ala Thr Ile Met Gln Thr Thr Thr Thr Val Leu Thr Thr Val
1 5 10 15

gcc gca atg tct act acc tta gca tca aat tac ata tct tcg caa gct
96
Ala Ala Met Ser Thr Thr Leu Ala Ser Asn Tyr Ile Ser Ser Gln Ala
20 25 30

agt tcc tcg acg agt gta aca aca gta acg aca atc gag aca tcc ata
144
Ser Ser Ser Thr Ser Val Thr Thr Val Thr Thr Ile Ala Thr Ser Ile
35 40 45

cgc tct aca cgg tct aat cta ctc ttc tct aat gtc gag gct cag cca
192
Arg Ser Thr Pro Ser Asn Leu Leu Phe Ser Asn Val Ala Ala Gln Pro
50 55 60

659/762

aaa tca tct tca gca agc aca att ggg ctt tca atc gga ctt ccc atc
240

Lys Ser Ser Ser Ala Ser Thr Ile Gly Leu Ser Ile Gly Leu Pro Ile
65 70 75 80

gga ata ttc tgt ttc gga lla ctt alc ctt ttg tgt tat ttc tac ctt
280

Gly Ile Phe Cys Phe Gly Leu Leu Ile Leu Leu Cys Tyr Phe Tyr Leu
85 90 95

aaa agg aat tgg gtg tcc att tca aat cca ccc atg tca gct acg att
320

Lys Arg Asn Ser Val Ser Ile Ser Asn Pro Pro Met Ser Ala Thr Ile
100 105 110

cca agg gaa gag gaa tat tgt cgc cgc act aat tgg ttc tca cgg tta
360

Pro Arg Gln Gln Gln Tyr Cys Arg Arg Thr Asn Trp Phe Ser Arg Leu
115 120 125

ttt tgg cag agt aag tgt gag gat cag aat tca tat tct aat cgt gat
400

Phe Trp Gln Ser Lys Cys Gln Asp Gln Asn Ser Tyr Ser Asn Arg Asp
130 135 140

att gag aag tat aac gac acc cag tgg acc tgg ggt gat aac atg tct
440

Ile Gln Lys Tyr Asn Asp Thr Gln Trp Thr Ser Gly Asp Asn Met Ser
145 150 155 160

tca aca ata cag tac aaa att tcc aaa ccc ata ata ccg cag cat ata
480

Ser Lys Ile Gln Tyr Lys Ile Ser Lys Pro Ile Ile Pro Gln His Ile
165 170 175

ctg aca cct aag aaa acg gtg aag aac cca tat gct tgg tct ggt aaa
520

Leu Thr Pro Lys Lys Thr Val Lys Asn Pro Tyr Ala Trp Ser Gly Lys
180 185 190

aac att tgg tta gac cca aaa gtg aac gaa atg gag gaa gag aaa gtt
560

660/762

Asn Ile Ser Leu Asp Pro Lys Val Asn Glu Met Glu Glu Glu Lys Val
 195 200 205

qtg gat gca ttc ctg tat act aaa cca cgg aat att gtc cat att gaa
 672

Val Asp Ala Phe Leu Tyr Thr Lys Pro Pro Asn Ile Val His Ile Glu
 210 215 220

tcg agc atg ccc tcg tat aat gat tta cct tct caa aaa aag gtg tcc
 720

Ser Ser Met Pro Ser Tyr Asn Asp Leu Pro Ser Gln Lys Thr Val Ser
 225 230 235 240

tca aag aaa act gcg tta aaa acg agl gag aaa tgg agt tac gca tct
 758

Ser Lys Lys Thr Ala Leu Lys Thr Ser Glu Lys Trp Ser Tyr Glu Ser
 245 250 255

caa cta tct cga tgg ttc ttg agg ggt tct aca tac ttt aag gat tat
 816

Pro Leu Ser Arg Trp Thr Leu Arg Gly Ser Thr Tyr Phe Lys Asp Tyr
 260 265 270

ggc tta tca aag aac tct tta aag acc cca act ggg gct cca cca ctg
 854

Gly Leu Ser Lys Thr Ser Leu Lys Thr Pro Thr Gly Ala Pro Gln Leu
 275 280 285

aag caa atg aaa atg ctg tcc cgg ata agt aag ggt tac ttc aat gag
 912

Lys Gln Met Lys Met Leu Ser Arg Ile Ser Lys Gly Tyr Phe Asn Glu
 290 295 300

tca gat ata atg cct gac gaa cga tgg ccc atc ttg gag tat aat aac
 960

Ser Asp Ile Met Pro Asp Glu Arg Ser Pro Ile Leu Glu Tyr Asn Asn
 305 310 315 320

acg cct ctg gat gca aat gac agt gtg aat aac ttg ggt aat acc acg
 1008

Thr Pro Leu Asp Ala Asn Asp Ser Val Asn Asn Leu Gly Asn Thr Thr
 325 330 335

cca gat tca aaa atc aca tct tat cgc aac aat aac atc gat cta atc
1056

Pro Asp Ser Gln Ile Thr Ser Tyr Arg Asn Asn Asn Ile Asp Leu Ile
340 345 350

acg gca aga ccc cat tca gtg ata tac ggt act act gca caa caa act
1104

Thr Ala Arg Pro His Ser Val Ile Tyr Gly Thr Thr Ala Gln Gln Thr
355 360 365

ttg gaa acc aac ttc aat gat cat cat gac tgc aat aaa agc act gag
1152

Leu Glu Thr Asn Phe Asn Asp His His Asp Cys Asn Lys Ser Thr Glu
370 375 380

aaa cac gag tgg ata ata ccc acc cca tca aaa cca cta aag aaa agg
1200

Lys His Glu Leu Ile Ile Pro Thr Pro Ser Lys Pro Leu Lys Lys Arg
385 390 395 400

aaa aaa agc aga caa agt aca atc tat cag cat tta caa cat ttg tca
1248

Lys Lys Arg Arg Gln Ser Lys Met Tyr Gln His Leu His His Leu Ser
405 410 415

ogt tct aca cca ttg ccg ctt act cca aac tcc aaa tat aat ggg gag
1296

Arg Ser Lys Pro Leu Pro Leu Thr Pro Asn Ser Lys Tyr Asn Gly Gln
420 425 430

gct agc gtc caa tta ggg aag aca tat aca gtc att cag gat tac gag
1344

Ala Ser Val Gln Leu Gly Lys Thr Tyr Thr Val Ile Gln Asp Tyr Glu
435 440 445

cct aga ttg aca gac gaa ata aga atc tgg ctg ggt gaa aaa gtt aaa
1392

Pro Arg Leu Thr Asp Glu Ile Arg Ile Ser Leu Gly Glu Lys Val Lys
450 455 460

662/762

att ctg gcc act cat acc gat gga tgg tgt ctg gta gaa aag tgt aat
1440

Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu Val Glu Lys Cys Asn
465 470 475 480

aca caa aag ggt tct att caa gtc agt gtt gac gat aaa aga tac ctc
1488

Thr Glu Lys Gly Ser Ile His Val Ser Val Asp Asp Lys Arg Tyr Leu
485 490 495

ast gaa gat aga gcc att gbg cct ggt gac tgt ctc caa gaa tac gac
1516

Asn Glu Asp Arg Gly Ile Val Pro Gly Asp Cys Leu Gln Glu Tyr Asp
500 505 510

tga

1539

<216> 275

<211> 512

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 274

Met Val Ala Thr Ile Met Glu Thr Thr Thr Thr Val Leu Thr Thr Val
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20 25 30

Ser Ser Ser Thr Ser Val Thr Thr Val Thr Thr Ile Ala Thr Ser Ile
35 40 45

Arg Ser Thr Pro Ser Asn Leu Leu Phe Ser Asn Val Ala Ala Gln Pro
50 55 60

Lys Ser Ser Ser Ala Ser Thr Ile Gly Leu Ser Ile Gly Leu Pro Ile
65 70 75 80

Gly Ile Phe Cys Phe Gly Leu Leu Ile Leu Leu Cys Tyr Phe Tyr Leu
85 90 95

Lys Arg Asn Ser Val Ser Ile Ser Asn Pro Pro Met Ser Ala Thr Ile
100 105 110

Pro Arg Glu Glu Glu Tyr Cys Arg Arg Thr Asn Trp Phe Ser Arg Leu
115 120 125

Phe Trp Gln Ser Lys Cys Glu Asn Gln Asn Ser Tyr Ser Asn Arg Asp
130 135 140

Ile Glu Lys Tyr Asn Asp Thr Gln Trp Thr Ser Gly Asn Met Ser
145 150 155 160

Ser Lys Ile Gln Tyr Lys Ile Ser Lys Pro Ile Ile Pro Gln His Ile
165 170 175

Leu Thr Pro Lys Lys Thr Val Lys Asn Pro Tyr Ala Trp Ser Gly Lys
180 185 190

Asn Ile Ser Leu Asp Pro Lys Val Asn Glu Met Glu Gln Glu Lys Val
195 200 205

Val Asp Ala Phe Leu Tyr Thr Lys Pro Pro Asn Ile Val His Ile Glu
210 215 220

Ser Ser Met Pro Ser Tyr Asn Asp Leu Pro Ser Gln Lys Thr Val Ser
225 230 235 240

Ser Lys Lys Thr Ala Leu Lys Thr Ser Glu Lys Trp Ser Tyr Glu Ser
245 250 255

Pro Leu Ser Arg Trp Phe Leu Arg Gly Ser Thr Tyr Phe Lys Asp Tyr
260 265 270

Gly Leu Ser Lys Thr Ser Leu Lys Thr Pro Thr Gly Ala Pro Gln Leu
275 280 285

Lys Gln Met Lys Met Leu Ser Arg Ile Ser Lys Gly Tyr Phe Asn Glu
290 295 300

Ser Asp Ile Met Pro Asp Glu Arg Ser Pro Ile Leu Gln Tyr Asn Asn
305 310 315 320

Thr Pro Leu Asp Ala Asn Asp Ser Val Asn Asn Leu Gly Asn Thr Thr
325 330 335

Pro Asp Ser Gln Ile Thr Ser Tyr Arg Asn Asn Asn Ile Asp Leu Ile
340 345 350

Thr Ala Arg Pro His Ser Val Ile Tyr Gly Thr Thr Ala Gln Gln Thr
355 360 365

Leu Glu Thr Asn Phe Asn Asp His His Asp Cys Asn Lys Ser Thr Glu
370 375 380

Lys His Glu Leu Phe Ile Pro Thr Pro Ser Lys Pro Leu Lys Lys Arg
385 390 395 400

Lys Lys Arg Arg Gln Ser Lys Met Tyr Gln His Leu Gln His Leu Ser
405 410 415

Arg Ser Lys Pro Leu Pro Leu Thr Pro Asn Ser Lys Tyr Asn Gly Gln
420 425 430

Ala Ser Val Gln Leu Gly Lys Thr Tyr Thr Val Ile Gln Asp Tyr Gln
435 440 445

Pro Arg Leu Thr Asp Gln Ile Arg Ile Ser Leu Gly Gln Lys Val Tyr
450 455 460

Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu Val Gln Lys Cys Asn
465 470 475 480

Thr His Tyr Gly Ser Ile His Val Ser Val Asp Asp Lys Arg Tyr Leu
485 490 495

Asn Gln Asp Arg Gly Ile Val Pro Gly Asp Cys Leu Gln Gln Tyr Asp
500 505 510

<210> 275

<211> 2901

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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<400> 275

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1	5	10	15
caa caa caa cag caa caa caa cag cag caa cag cag gaa gaa			
36			
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala			
20	25	30	
ggt cct cag cag caa ctc gaa cca tta aca caa tca act gcg gaa act			
144			
Val Pro Gln Gln Pro Leu Asp Pro Leu Thr Gln Ser Thr Ala Glu Thr			
35	40	45	
egg ctc tcc att gct tct ttg gaa gaa acc ctt ggt gat ggu gac agg			
192			
Tyr Leu Ser Ile Ala Ser Leu Ala Glu Thr Leu Gly Asp Gly Asp Arg			
50	55	60	
gcc gaa atg gaa tat gaa gcc act tta cag ttc aat ccc tca tct gaa			
240			
Ala Ala Met Ala Tyr Asp Ala Thr Leu Gln Phe Asn Pro Ser Ser Ala			
65	70	75	80
aag gct tta aca cct ttg gct cac ttg tac cgt tuc aga gac atg ttc			
288			
Lys Ala Leu Thr Ser Leu Ala His Leu Tyr Arg Ser Arg Asp Met Phe			
85	90	95	
caa aga gct gaa gaa tta tat gaa aga gaa ctt ttg gta aat ouc gaa			
336			
Gln Arg Ala Ala Glu Leu Tyr Glu Arg Ala Leu Leu Val Asn Pro Glu			
106	105	110	
cta tca gat gbg tgg gct act tta ggc cat tgt tat ctg atg ctg gat			
384			
Leu Ser Asp Val Trp Ala Thr Leu Gly His Cys Tyr Leu Met Leu Asp			
115	120	125	
gat ctg cca aga gct tac aat gcc tat caa cag gct ctc tac cac ctc			
432			
Asp Leu Gln Arg Ala Tyr Asn Ala Tyr Gln Gln Ala Leu Tyr His Leu			
130	135	140	

agt aat ccc aac gta ccg aaa tta tgg cat gga atc ggc att ctt tat
480

Ser Asn Pro Asn Val Pro Lys Leu Trp His Gly Ile Gly Ile Leu Tyr
145 150 155 160

gac aga tat ggt tcy ctc gac tat ggc gaa gaa gct ttt gcc aaa gtt
528

Asp Arg Tyr Gly Ser Leu Asp Tyr Ala Glu Gln Ala Phe Ala Lys Val
165 170 175

ttg gaa ttg gac cct cat ttt gaa aag gca aac gaa atc tac ttc aga
576

Leu Glu Leu Asp Pro His Phe Glu Lys Ala Asn Glu Ile Tyr Phe Arg
180 185 190

cta ggt att att tat aaa cat aag ggt aac tgg tct caa gct ttg gaa
624

Leu Gly Ile Ile Tyr Lys His Gln Gly Lys Trp Ser Gln Ala Leu Glu
195 200 205

tgc ttc aga tac att ctc cct caa cct cct gct ccc ttg cag gag tgg
672

Cys Phe Arg Tyr Ile Leu Pro Gln Pro Pro Ala Pro Leu Gln Glu Trp
210 215 220

gac ata tgg ttt cag ttg ggt agt gtt ttg gag agt atg gga gag tgg
720

Asp His Trp Phe Gln Leu Gly Ser Val Leu Glu Ser Met Gly Glu Trp
225 230 235 240

caa ggt gag aag gaa gcc tuc gag cat gtc ttg gct caa aat caa cat
768

Gln Gly Ala Lys Glu Asn Tyr Glu His Val Leu Ala Gln Asn Gln His
245 250 255

cat gcc aaa gta tta caa caa tta ggt tgt ctt tac ggt atg agt aac
816

His Ala Lys Val Leu Gln Gln Leu Gly Cys Leu Tyr Gly Met Ser Asn
260 265 270

gta caa ttt tat gac cct caa aag gca ttg gat tat ctt ata aag tgg
864

Val Gln Phe Tyr Asp Pro Gln Lys Ala Leu Asp Tyr Leu Lau Lys Ser
275 280 285

ttt gaa gaa gat ccc lcc gaa gcc act acc tgg tac cat ctg qgt aga
312

Leu Glu Ala Asp Pro Ser Asp Ala Thr Thr Trp Tyr His Leu Gly Arg
290 295 300

gtg cal atg att aga aca gat tat act gcc gca tat gat get ttc caa
960

Val His Met Ile Arg Thr Asp Tyr Thr Ala Ala Tyr Asp Ala Phe Gln
305 310 315 320

000 gct ggt aat aga gat tca aga aac cct atc ttt tgg tgc tca atc
1000

Gln Ala Val Asn Arg Asp Ser Arg Asn Pro Uic Phe Trp Cys Ser Ile
325 330 335

ggg gtt tta tat tac caa att tct caa tac aga gaa gcc tta gac ggc
1056

Gly Val ~~Val~~ Tyr Tyr ~~Gln~~ Ile Ser Gln Tyr Arg Asp Ala Leu Asp Ala
340 345 350

tac aac aga gcc ata aga tta aat cc. Lal att agt gaa gtt tgg tac
 . 104

Tyr Thr Arg Ala Ile Arg Leu Asn Pro Tyr Ile Ser Glu Val Trp Tyr
 355 360 365

gat ota ggt act ctt tac gaa act tct aac aac caa tta tct gac gcc
1152

Asp Leu Gly Thr Leu Tyr Glu Thr Cys Asn Asn Gln Leu Ser Asp Ala
370 375 380

ctt gat ggg tat aag caa gct gca aga ctg gac gta aat aat gtt cac
1290

Leu Asp Ala Tyr Lys Gln Ala Ala Arg Leu Asp Val Asn Asn Val His
385 390 395 400

ata aga gaa aga tta gaa gct tta aca aag cag tta gaa aac cca ggc
3248

His Arg Glu Arg Leu Glu Ala Leu Thr Lys Gln Leu Gln Asn Pro Gly
405 410 415

aat ata aac aaa tgg aac ggt gog cca acg aat gac tat cct gcc cca
1296

Asp Ile Asn Lys Ser Asn Gly Ala Pro Thr Asn Ala Ser Pro Ala Pro
420 425 430

cct cct gtg att tta cca cct acc tta cca cct aat gat caa gga aat
1344

Pro Pro Val Ile Leu Gln Pro Thr Leu Gln Pro Asn Asp Gln Gly Asn
435 440 445

cct ttg aac act aga att tca gcc caa tct gcc axt gat ucl gat lua
1392

Pro Leu Asn Thr Arg Ile Ser Ala Gln Ser Ala Asn Ala Thr Ala Ser
450 455 460

atg gta caa caa cag cat cct gct caa caa acg cct att aac tat tat
1440

Met Val Gln Gln Gln His Pro Ala Gln Gln Thr Pro Ile Asn Ser Ser
465 470 475 480

gaa caa atg tuc agt aat gga gct tcc cct caa tta caa gct caa gct
1488

Ala Thr Met Tyr Ser Asn Gly Ala Ser Pro Gln Leu Gln Ala Gln Ala
485 490 495

caa gct caa gct caa gaa caa gct caa gca caa gca caa gct caa gaa
1536

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
500 505 510

caa gca caa gca caa gog caa gca caa gca caa gca cag gog caa gca
1584

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
515 520 525

cag gaa caa gca caa gca caa gca cat gca caa gog caa gca caa gca
1632

Gln Ala Gln Ala Gln Ala Gln Ala His Ala Gln Ala Gln Ala Gln Ala
530 535 540

caa gca cag gca caa gca caa gca cag gag cag gca caa caa caa caa
1580

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Gln Gln Gln
545 550 555 560

caa caa cag caa caa caa caa caa caa caa caa caa caa caa caa
1728

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
565 570 575

caa caa caa caa caa caa caa cag cag cag cag caa tta cag ccc cta caa
1776

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Pro Leu Pro
580 585 590

aga caa cag ctg cag caa aag gga gtt tot gtg caa atg tta aat cct
1824

Arg Gln Gln Leu Gln Gln Lys Gly Val Ser Val Gln Met Leu Asn Pro
595 600 605

caa caa gag caa caa tat atc caa cag caa acc gtc ata caa gct caa
1872

Gln Gln Gln Gln Pro Tyr Ile Thr Gln Pro Thr Val Ile Gln Ala His
610 615 620

caa ctg caa caa ttt tct caa caa gct atg gca cat ccg caa cgc tct
1920

Gln Leu Gln Pro Phe Ser Thr Cln Ala Met Gln His Pro Gln Ser Ser
625 630 635 640

caa ctg caa cct caa cag caa caa cta caa tct gtt caa cat cca caa
1968

Gln Leu Pro Pro Gln Gln Gln Gln Leu Gln Ser Val Gln His Pro Gln
645 650 655

caa ctt caa gag cag cct caa gcc caa gct ccc caa cct tta acc cag
2016

Gln Leu Gln Gly Gln Pro Thr Ala Gln Ala Pro Gln Pro Leu Ile Gln
660 665 670

cat aac gtg gaa cag aac gtt tta cct caa aag aga tac atg gaa ggt
2064

His Asn Val Glu Gln Asn Val Leu Pro Gln Lys Arg Tyr Met Glu Gly
675 680 685

gca atc ccc aat tta gta gat gcc gcc gca tcc agt agc acc cac aca
2112

Ala Ile His Thr Leu Val Asp Ala Ala Val Ser Ser Ser Thr His Thr
690 695 700

gag aat aac aca aag tct cct cgt cca cca acc cat gcc att cca acc
2160

Glu Asn Asn Thr Lys Ser Pro Arg Gln Pro Thr His Ala Ile Pro Thr
705 710 715 720

caa gct ccc gca aca gga ata acg aac gct gaa cca cag gta aag acg
2208

Gln Ala Pro Ala Thr Gly Ile Thr Asn Ala Glu Pro Gln Val Lys Lys
725 730 735

caa aag ctg aac tat uca aat tca aac aic aac aca tta gca aat att
2256

Gln Lys Asn Asn Ser Pro Asn Ser Asn Ile Asn Lys Leu Val Asn Thr
740 745 750

gct aat tcc att gaa gaa aat gca aaa tot gag gag agc aac cca tgg
2304

Ala Thr Ser Ile Glu Glu Asn Ala Lys Ser Glu Val Ser Asn Glu Ser
755 760 765

cca gca gla g-g gag tcl aat acc aat aat aat tca caa gaa gaa aaa
2352

Pro Ala Val Val Glu Ser Asn Thr Asn Asn Thr Ser Gln Glu Glu Lys
770 775 780

cct gta aaa gca aac tca ata cct tca gta att gcc gca cag gaa cct
2400

Pro Val Lys Ala Asn Ser Ile Pro Ser Val Ile Gly Ala Gln Glu Pro
785 790 795 800

cca cag gaa gct agt cct gct gaa gaa gct acc aaa gca gct tat gtt
2448

Pro Gln Glu Ala Ser Pro Ala Glu Glu Ala Thr Lys Ala Ala Ser Val
805 810 815

tct cct tct acc aac ccg ctt aat acy gaa cca gag tca tct agt gtc
2496

Ser Pro Ser Thr Lys Pro Leu Asn Thr Glu Pro Glu Ser Ser Ser Val
820 825 830

caa cca act gta tca leu gaa agt tca acc acc aaa gca aat gac caa
2544

Gln Pro Thr Val Ser Ser Gln Ser Ser Thr Thr Lys Ala Asa Asp Gln
835 840 845

agg act gct gag aac ata gaa ctt tct act gct act gtt cct gca gaa
2592

Asn Thr Ala Glu Thr Ile Glu Leu Ser Thr Ala Thr Val Pro Ala Glu
850 855 860

gca agc cct gla gaa gac gaa gta aga cag cat tct aac gag gaa aac
2640

Ala Ser Pro Val Glu Asp Glu Val Arg Gln His Ser Lys Glu Glu Asn
865 870 875 880

ggc acc act gaa gca tct gca cct tct act gaa gag gcg gag cca gca
2688

Gly Thr Thr Glu Ala Ser Ala Pro Ser Thr Glu Glu Ala Glu Pro Ala
885 890 895

gct tcc aga gat gct gaa aac cca cca gat gaa acc gct gct aca acy
2736

Ala Ser Arg Asp Ala Glu Lys Gln Gln Asp Glu Thr Ala Ala Thr Thr
900 905 910

ata act gta atc aac cct act ttg gaa acc atg gaa acc atg aac gag
2784

Ile Thr Val Ile Lys Pro Thr Leu Glu Thr Met Glu Thr Val Lys Glu
915 920 925

gag gcc aac atg cgt gag gaa gag aac acc tct cca gaa aac tcc cca
2832

Glu Ala Lys Met Arg Gln Glu Glu Gln Thr Ser Gln Glu Lys Ser Pro
930 935 940

cag gag aac aca ctt cca aga gaa aat gta gta agg cca gtg gaa gaa
2880

Gln Glu Asn Thr Leu Pro Arg Glu Asn Val Val Arg Gln Val Glu Glu
345 359 355 360

gat gaa aac laa gac gac taa
2901

Asp Gln Asn Tyr Asp Asp
365

<210> 276

<211> 966

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 276

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20 25 30

Val Pro Gln Gln Pro Leu Asp Pro Leu Thr Gln Ser Thr Ala Glu Thr
35 40 45

Tyr Leu Ser Ile Ala Ser Leu Ala Glu Thr Leu Gly Asp Gly Asp Arg
50 55 60

Ala Ala Met Ala Tyr Asp Ala Thr Leu Gln Phe Asn Pro Ser Ser Ala
65 70 75 80

Lys Ala Leu Thr Ser Leu Ala His Leu Tyr Arg Ser Arg Asp Met Phe
85 90 95

Gln Arg Ala Ala Glu Leu Tyr Glu Arg Ala Leu Leu Val Asn Pro Glu
100 105 110

Leu Ser Asp Val Trp Ala Thr Leu Gly His Cys Tyr Leu Met Leu Asp
115 120 125

Asp Leu Gln Arg Ala Tyr Asn Ala Tyr Gln Glu Ala Leu Tyr His Leu
130 135 140

Ser Asn Pro Asn Val Pro Lys Leu Trp His Gly Ile Gly Ile Leu Tyr
145 150 155 160

Asp Arg Tyr Gly Ser Leu Asp Tyr Ala Glu Glu Ala Phe Ala Lys Val
165 170 175

Leu Glu Leu Asp Pro His Phe Glu Lys Ala Asn Glu Ile Tyr Phe Arg
180 185 190

Leu Gly Ile Ile Tyr Lys His Glu Gly Lys Trp Ser Gln Ala Leu Glu
195 200 205

Cys Phe Arg Tyr Ile Leu Pro Gln Pro Pro Ala Pro Leu Gln Gln Trp
210 215 220

Asp Ile Trp Phe Glu Leu Gly Ser Val Leu Glu Ser Met Gly Glu Trp
225 230 235 240

Gln Gly Ala Lys Glu Ala Tyr Glu His Val Leu Ala Gln Asn Gln His
245 250 255

His Ala Lys Val Leu Gln Gln Leu Gly Cys Leu Tyr Gly Met Ser Asn
260 265 270

Val Gln Phe Tyr Asp Pro Gln Lys Ala Leu Asp Tyr Leu Leu Lys Ser
275 280 285

Leu Glu Ala Asp Pro Ser Asp Ala Thr Thr Trp Tyr His Leu Gly Arg
290 295 300

Val His Met Ile Arg Thr Asp Tyr Thr Ala Ala Tyr Asp Ala Phe Gln
305 310 315 320

Gln Ala Val Asn Arg Asp Ser Arg Asn Pro Ile Phe Trp Cys Ser Ile
325 330 335

Gly Val Leu Tyr Tyr Gln Ile Ser Gln Tyr Arg Asp Ala Leu Asp Ala
340 345 350

Tyr Thr Arg Ala Ile Arg Leu Asn Pro Tyr Ile Ser Glu Val Trp Tyr
355 360 365

Asp Leu Gly Thr Leu Tyr Glu Thr Cys Asn Asn Gln Leu Ser Asp Ala
370 375 380

Leu Asp Ala Tyr Lys Gln Ala Ala Arg Leu Asp Val Asn Asn Val His
385 390 395 400

Ala Arg Glu Arg Leu Glu Ala Leu Thr Lys Gln Leu Glu Asn Pro Gly
405 410 415

Asn Ile Asn Lys Ser Asn Gly Ala Pro Thr Asn Ala Ser Pro Ala Pro
420 425 430

Pro Pro Val Ile Leu Gln Pro Thr Leu Gln Pro Asn Asp Gln Gly Asn
 435 440 445

Pro Leu Asn Thr Arg Ile Ser Ala Gln Ser Ala Asn Ala Thr Ala Ser
 450 455 460

Met Val Gln Gln Gln His Pro Ala Gln Gln Thr Pro Ile Asn Ser Ser
 465 470 475 480

Ala Thr Met Tyr Ser Asn Gly Ala Ser Pro Gln Leu Gln Ala Gln Ala
 485 490 495

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
 500 505 510

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
 515 520 525

Gln Ala Gln Ala Gln Ala Gln Ala His Ala Gln Ala Gln Ala Gln Ala
 530 535 540

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Gln Gln Gln
 545 550 555 560

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 565 570 575

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Pro Leu Pro
 580 585 590

Arg Gln Gln Leu Gln Gln Lys Gly Val Ser Val Gln Met Leu Asn Pro
 595 600 605

Gln Gln Gly Gln Pro Tyr Ile Thr Gln Pro Thr Val Ile Gln Ala His
610 615 620

Gln Leu Gln Pro Phe Ser Thr Gln Ala Met Glu His Pro Gln Ser Ser
625 630 635 640

Gln Leu Pro Pro Cln Gln Gln Gln Leu Gln Ser Val Gln His Pro Gln
645 650 655

Gln Leu Gln Gly Gln Pro Gln Ala Gln Ala Pro Gln Pro Leu Ile Gln
660 665 670

His Asn Val Glu Gln Asn Val Leu Pro Gln Lys Arg Tyr Met Glu Gly
675 680 685

Ala Ile His Thr Leu Val Asp Ala Ala Val Ser Ser Ser Thr His Thr
690 695 700

Glu Asn Asn Thr Lys Ser Pro Arg Gln Pro Thr His Ala Ile Pro Thr
705 710 715 720

Gln Ala Pro Ala Thr Gly Ile Thr Asn Ala Glu Pro Gln Val Lys Lys
725 730 735

Gln Lys Leu Asn Ser Pro Asn Ser Asn Ile Asn Lys Leu Val Asn Thr
740 745 750

Ala Thr Ser Ile Glu Glu Asn Ala Lys Ser Glu Val Ser Asn Gln Ser
755 760 765

Pro Ala Val Val Glu Ser Asn Thr Asn Asn Thr Ser Gln Glu Glu Lys
 770 775 780

Pro Val Lys Ala Asn Ser Ile Pro Ser Val Ile Gly Ala Gln Glu Pro
 785 790 795 800

Pro Gln Glu Ala Ser Pro Ala Glu Gln Ala Thr Lys Ala Ala Ser Val
 805 810 815

Ser Pro Ser Thr Lys Pro Leu Asn Thr Gln Pro Glu Ser Ser Ser Val
 820 825 830

Gln Pro Thr Val Ser Ser Glu Ser Ser Thr Thr Lys Ala Asn Asp Gln
 835 840 845

Ser Thr Ala Glu Thr Ile Glu Leu Ser Thr Ala Thr Val Pro Ala Gln
 850 855 860

Ala Ser Pro Val Glu Asp Glu Val Arg Glu His Ser Lys Gly Glu Asn
 865 870 875 880

Gly Thr Thr Glu Ala Ser Ala Pro Ser Thr Glu Glu Ala Glu Pro Ala
 885 890 895

Ala Ser Arg Asp Ala Glu Lys Gln Gln Asp Glu Thr Ala Ala Thr Thr
 900 905 910

Ile Thr Val Ile Lys Pro Thr Leu Glu Thr Met Glu Thr Val Lys Glu
 915 920 925

Glu Ala Lys Met Arg Glu Glu Glu Gln Thr Ser Glu Glu Lys Ser Pro
 930 935 940

Gln Glu Asn Thr Leu Pro Arg Glu Asn Val Val Arg Gln Val Glu Glu
945 950 955 960

Asp Glu Asn Tyr Asp Asp
965

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<210> 377
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<212> DNA
<213> Saccharomyces cerevisiae
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<231> CDS
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36

Ser Trp Glu Glu Lys Tyr Glu Glu Leu Lys Glu Lys Asn Lys Asp Leu
20 25 30

gag caa gag aat gtc gaa aag gag aat gag atc aag tct tta acc gtc
144

Glu Cln Glu Asn Val Glu Lys Cln Asn Cln Ile Lys Ser Leu Thr Val
35 40 45

aaa aac aag caa ttg gag gat gag atc gag aag ctg gaa ggc gga ctt
192

Lys Asn Gln Glu Leu Glu Asp Glu Ile Glu Lys Leu Glu Ala Gly Leu
50 55 60

tct gac tct aag caa aca gaa cag gat aac gtt gaa uuu gaa aat cag
240

Ser Asp Ser Lys Glu Thr Glu Gln Asp Asn Val Glu Lys Glu Asn Gln
65 70 75 80

atc aag tcc ttg acg gtg aag aac cac caa ttg gag gaa gag atc gag
288

Ile Lys Ser Leu Thr Val Lys Asn His Gln Leu Glu Glu Glu Ile Glu
65 80 95

aag ttg gaa gca gaa ttg gct gaa tcc aag caa ttg tcc gag gac tct
336

Lys Leu Glu Ala Glu Leu Ala Glu Ser Lys Gln Leu Ser Glu Asp Ser
100 105 110

cac cac ttg cag tcc aac aac gac aat ttc tcc aag aag aac cag caa
304

His His Leu Gln Ser Asn Asn Asp Asn Phe Ser Lys Lys Asn Gln Gln
115 120 125

ttg gaa gaa gac ttg gag gaa agc gat acc aag cta aag gaa acc acg
432

Leu Glu Glu Asp Leu Glu Glu Ser Asp Thr Lys Leu Lys Glu Thr Thr
130 135 140

gag aca ttg aga gag tcc gac ttg aag gca gat caa ttg gaa aga aga
480

Glu Lys Leu Arg Glu Ser Asp Leu Lys Ala Asp Gln Leu Glu Arg Arg
145 150 155 160

gta gct gcc ttg gaa gaa uuu nga gaa gaa tgg gaa aga aag aac gag
528

Val Ala Ala Leu Glu Gln Gln Arg Glu Glu Trp Glu Arg Lys Asn Glu
165 170 175

gaa ttg acc gtc aag taa gaa gac gca aag cag gaa ctg gac gaa att
576

Glu Leu Thr Val Lys Tyr Glu Asp Ala Lys Lys Glu Leu Asp Glu Ile
180 185 190

gct gca tct ctg gaa aac ttg tga
600

Ala Ala Ser Leu Glu Asn Leu

195

<210> 278

<211> 199

<212> PRT

<213> *Saccharomyces cerevisiae*

<403> 278

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20 25 30

Glu Glu Glu Asn Val Glu Lys Glu Asn Gln Ile Lys Ser Phe Tyr Val

35 40 45

Lys Asn Gln Glu Leu Glu Asp Glu Ile Glu Lys Met Glu Ala Gly Leu

50 55 60

Ser Asp Ser Lys Gln Thr Glu Glu Asp Asn Val Glu Lys Glu Asn Glu

65 70 75 80

Ile Lys Ser Leu Thr Val Lys Asn His Gln Leu Glu Glu Glu Ile Glu

85 90 95

Lys Leu Glu Ala Glu Leu Ala Glu Ser Lys Gln Leu Ser Glu Asp Ser

100 105 110

His His Leu Glu Ser Asn Asn Asp Asn Phe Ser Lys Lys Asn Gln Gln

115 120 125

Leu Glu Glu Asp Leu Glu Glu Ser Asp Thr Lys Leu Lys Glu Thr Thr
 130 135 140

Glu Lys Leu Arg Glu Ser Asp Leu Lys Ala Asp Gln Leu Glu Arg Arg
 145 150 155 160

Val Ala Ala Leu Glu Glu Gln Arg Glu Glu Trp Glu Arg Lys Asn Glu
 165 170 175

Glu Leu Thr Val Lys Tyr Glu Asp Ala Lys Lys Glu Leu Asp Glu Ile
 180 185 190

Ala Ala Ser Leu Glu Asn Leu
 195

<210> 279
 <211> 603
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(603)

<400> 279
 atg gca ggt atc aag ttg acg cat aag ctt tat cag tat tat caa tta
 48
 Met Ala Gly Ile Lys Leu Thr His Lys Leu Tyr Gln Tyr Tyr Gln Leu
 1 5 10 15
 gcc aca agc ttt ttg tat gct gca tta ttg ata cgg tgg ctg ata tta
 36
 Ala Thr Ser Phe Leu Tyr Ala Ala Leu Leu Ile Arg Trp Leu Ile Leu
 20 25 30

atg cca ctg gta ggg tct cgg ttt tta ccg gga gga atc cao gaa ttc
144

Met Pro Leu Val Gly Ser Arg Phe Leu Pro Gly Gly Ile His Glu Phe
35 40 45

ttg ata tat ttg atg ttt tat tcc ags atc atg gaa gtt att tgg ttg
192

Leu Ile Tyr Leu Met Phe Tyr Ser Ser Ile Met Glu Val Ile Trp Leu
50 55 60

ctt aga ttc ccc ggg ttc aaa tat ggt ttg ctt tca aga acg ttt ttg
240

Leu Arg Phe His Gly Phe Lys Tyr Gly Leu Leu Ser Arg Thr Phe Leu
65 70 75 80

aaa gac cta aat ttt atc tat tta gtc agc gtg atc cat ttt tat gac
288

Iys Asp Leu Asn Phe Ile Tyr Leu Val Ser Val Ile His Phe Tyr Asp
85 90 95

gat tat gag cat gca ttg atc ctc aag aat gca tca tat tct agt ttc
336

Asp Tyr Glu His Ala Leu Ile Leu Lys Asn Ala Ser Tyr Ser Ser Phe
100 105 110

att att tcc tta tct tta tca cag gca tat tgc cat tgg tgc aaa ctt
360

Ile Ile Ser Leu Ser Leu Ser Glu Ala Tyr Cys His Trp Cys Lys Leu
115 120 125

ttt aaa cgt aag ggc gta aag gaa aga aca ctt gta tgg aag gtt aac
432

Phe Lys Arg Lys Gly Val Lys Glu Arg Thr Leu Val Trp Lys Val Asn
130 135 140

aca ttt gtt aca ttg cca att ctc tat ctg agt gaa ttt gca ttg cta
480

Thr Phe Val Thr Leu Pro Ile Leu Tyr Leu Ser Glu Phe Ala Leu Leu
145 150 155 160

cta tta aat atc cag gtt aag aac tat cat tct acc ccg act ttg gac
528

Leu Leu Asn Ile Gln Val Lys Asn Tyr His Ser Thr Pro Thr Leu Asp
165 170 175

ate atc aac agg gtg gll LLu cta gca tac ttc cct gca cta cta aca
576

Ile Ile Asn Arg Val Val Leu Leu Ala Tyr Phe Pro Val Leu Leu Thr
180 185 190

gca cac aac aac cta cta aca aac tga
603

Ala Tyr Lys Lys Leu Leu Thr Lys
195 200

<210> 280

<211> 200

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 280

Met Ala Gly Ile Lys Leu Thr His Lys Leu Tyr Gln Tyr Trp Gln Leu
1 5 10 15

Ala Thr Ser Phe Leu Tyr Ala Ala Leu Leu Ile Arg Trp Leu Ile Leu
20 25 30

Met Pro Leu Val Gly Ser Arg Phe Leu Pro Gly Gly Ile His Gln Phe
35 40 45

Leu Ile Tyr Leu Met Phe Tyr Ser Ser Ile Met Gln Val Ile Trp Leu
50 55 60

Leu Arg Phe His Gly Phe Lys Tyr Gly Leu Leu Ser Arg Thr Phe Leu
65 70 75 80

Lys Asp Leu Asn Phe Ile Tyr Leu Val Ser Val Ile His Phe Tyr Asp

83

90

95

Asp Tyr Gln His Ala Leu Ile Leu Lys Asn Ala Ser Tyr Ser Ser Phe
 100 105 110

Ile Ile Ser Leu Ser Leu Ser Gln Ala Tyr Cys His Trp Cys Lys Leu
 115 120 125

Phe Lys Arg Lys Gly Val Lys Glu Arg Thr Leu Val Trp Lys Val Asn
 130 135 140

Thr Phe Val Thr Leu Pro Ile Leu Tyr Leu Ser Glu Phe Ala Leu Leu
 145 150 155 160

Leu Leu Asn Ile Gln Val Lys Asn Tyr His Ser Thr Pro Thr Leu Asp
 165 170 175

Ile Ile Asn Arg Val Val Leu Leu Ala Tyr Phe Pro Val Leu Leu Thr
 180 185 190

Ala Tyr Lys Lys Leu Leu Thr Lys
 195 200

<210> 281
 <211> 447
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> (76)
 <222> (1)..(447)

<100> 281

atg tgt gaa tca tca aet aag aot gaa nat gat ata gtc aga ttg tca
48

Met Cys Glu Ser Ser Asn Lys Thr Glu Asn Asp Ile Val Arg Leu Ser
1 5 10 15

caa gct atg gat gtc ctg gct aag ttg atc att tca aag caa aaa gac
96

Gln Ala Met Asp Val Leu Ala Lys Leu Ile Ile Ser Lys Gln Lys Asp
20 25 30

gga tca caa tta caa gtt gag tac gag cat aag ttg aaa gaa tta gag
144

Gly Ser Gln Leu Gln Val Glu Tyr Glu His Lys Leu Lys Glu Leu Glu
35 40 45

aaa ttc att aac cta cta ctg gga ttg aat gaa agn aot gtg gga agt
192

Lys Phe Ile Asn Leu Leu Leu Gly Leu His Glu Ser Thr Val Gly Ser
50 55 60

atg atg aat aot agt gll att gac atg gta ctg cgg aat gga ata gag
240

Met Met Asn Thr Ser Val Leu Asp Met Val Leu Arg Asn Gly Ile Glu
65 70 75 80

atc atg aaa aaa gac gat caa cau tat gcc ctg ata cog att aaa gcc
188

Ile Met Glu Cys Asp Asp Gln Lys Tyr Ala Leu Ile Pro Ile Lys Ala
85 90 95

aag gaa gag gca gat aaa aot aag ago aul all auy gga gta acc ago
336

Lys Glu Glu Ala Asp Lys Thr Thr Ser Thr Ile Gln Gly Val Thr Ser
100 105 110

aaa aag agt agt aaa aag aaa aat aag ata aaa tgt tca ttt tgt
384

Lys Lys Ser Ser Lys Lys Lys Lys Asn Lys Ile Lys Cys Ser Phe Cys
115 120 125

caa gag aat aac cac aca agg gca cac tgc ggt gcg aga cag aca gtt
432

His Glu Ala Gly His Thr Arg Ala His Cys Gly Ala Arg Leu Thr Val
 130 135 140

ala ser arg asn thr

447

ile pro lys lys

145

<210> 282

<211> 148

<212> PRT

<213> saccharomyces cerevisiae

<400> 282

Met Cys Glu Ser Ser Asn Lys Thr Glu Asn Asp Ile Val Arg Leu Ser
 1 5 10 15

Gln Ala Met Asp Val Leu Ala Lys Leu Ile Ile Ser Lys Gln Lys Asp
 20 25 30

Gly Ser Gln Leu Gln Val Glu Tyr Gln His Lys Leu Lys Glu Leu Glu
 35 40 45

Lys Phe Ile Asn Leu Leu Leu Gly Leu His Glu Ser Thr Val Gly Ser
 50 55 60

Met Met Asn Thr Ser Val Leu Asp Met Val Leu Arg Asn Gly Ile Glu
 65 70 75 80

Ile Met Glu Lys Asp Asp Gln Lys Tyr Ala Leu Ile Pro Ile Lys Ala
 85 90 95

Lys Glu Glu Ala Asp Lys Thr Thr Ser Thr Ile Gln Gly Val Thr Ser
 100 105 110

Lys Lys Ser Ser Lys Lys Lys Lys Asn Lys Ile Lys Cys Ser Phe Cys
 115 120 125

His Glu Ala Gly His Thr Arg Ala His Cys Gly Ala Arg Leu Thr Val
 130 135 140

Ile Pro Lys Lys
 145

<210> 283

<211> 1545

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1545)

<400> C92

atg gag gaa caa cgt gaa ata ctg gaa caa ttg aag aaa act ctg cag
 48

Met Glu Glu Gln Arg Glu Ile Leu Glu Gln Leu Lys Lys Thr Leu Glu
 1 5 10 15

atg cta aat ytu gag cca tct aaa aat aac caa atc gcc aac gaa gaa
 56

Met Leu Thr Val Glu Pro Ser Lys Asn Asn Gln Ile Ala Asn Glu Glu
 20 25 30

aag gaa aag aaa gaa aat gaa aat tgg tgg tgg atc ctc gag cac aat
 144

Lys Glu Lys Lys Glu Asn Glu Asn Ser Trp Cys Ile Leu Glu His Asn
 35 40 45

tat gag gat att gcc dag gaa ttc att gat ttc att tac aag aac cgt
 192

689/762

Tyr Glu Asp Ile Ala Glu Glu Phe Ile Asp Phe Ile Tyr Lys Asn Pro
 50 55 60

Asu Asl Lue Cui gta gta tca ttt ttc gcg gag ctg Lla gat aag cat
 240

Thr Thr Tyr His Val Val Ser Phe Phe Ala Glu Leu Leu Asp Lys His
 65 70 75 80

aac ttc aaa tac ttg agc gag aaa tcc aat tgg cag gac tcc att ggc
 288

Asn Phe Lys Tyr Leu Ser Glu Lys Ser Asn Trp Glu Asp Ser Ile Gly
 85 90 95

gaa gat ggt ggg aaa ttc tac act ata aga aat gga acL auc cta tct
 336

Glu Asp Gly Gly Lys Phe Tyr Thr Ile Arg Asn Gly Thr Asn Leu Ser
 100 105 110

gac ttt atc ctg ggc aaa aac tgg aga gac gaa aag ggt gtc ggt glu
 384

Ala Phe Ile Leu Gly Lys Asn Thr Arg Ala Glu Lys Gly Val Gly Val
 115 120 125

att gga tct cat ctg gac gct ttg acg gtc aaa ttg aag ccc gtc tcc
 432

Ile Gly Ser His Val Asp Ala Leu Thr Val Lys Leu Lys Pro Val Ser
 130 135 140

ttt aaa gac aca gac caa ggt tac gga aga att gct gtt gct ccc tat
 480

Phe Lys Asp Thr Ala Glu Gly Tyr Gly Arg Ile Ala Val Ala Pro Tyr
 145 150 155 160

gga ggt aca ctg aat gaa ttg tgg cta gac aga gac cta ggt att ggt
 528

Gly Gly Thr Leu Asn Glu Leu Trp Leu Asp Arg Asp Leu Gly Ile Gly
 165 170 175

ggt cgc att att tac aag aag aag ggc act aac gaa att aaa agc gcc
 576

Gly Arg Leu Leu Tyr Lys Lys Lys Gly Thr Asn Glu Ile Lys Ser Ala
 180 185 190

ttg gtt gat tct aca ccc cta cct gtc tgt cga att cct tca ttg gct
824

Leu Val Asp Ser Thr Pro Leu Pro Val Cys Arg Ile Pro Ser Leu Ala
195 200 205

ccc ccc ttc cgt aca cct gct gaa ggc cca ttt gat cca gag gac caa
872

Pro His Phe Gly Lys Pro Ala Glu Gly Pro Phe Asp Lys Glu Asp Gln
210 215 220

act atc ccc gtc atc ggc ttc ccc acc ccc gat gag gaa ggt act gaa
720

Thr Ile Pro Val Ile Gly Phe Pro Thr Pro Asp Glu Glu Gly Asn Glu
125 230 235 240

cct ccc acc gat gat gaa aag aac tgc ccc tta ttt ggc aac cac tgc
768

Pro Pro Thr Asp Asp Glu Lys Lys Ser Pro Leu Phe Gly Lys His Cys
245 250 255

atc cac ctg tta agg tac gtt gcc aac tca gcc ggt gtc gaa gtc tcc
816

Ile His Leu Leu Arg Tyr Val Ala Lys Leu Ala Gly Val Glu Val Ser
260 265 270

gaa ttg att cca atg gat tta gac tta ttc gat gtc caa aag ggt acc
864

Glu Leu Ile Gln Met Asp Leu Asp Leu Phe Asp Val Gln Lys Gly Thr
275 280 285

att gga ggt att ggt aca cac ttc ctt ttt gcc cca cgt cta gat gaa
912

Ile Gly Gly Ile Gly Lys His Phe Leu Phe Ala Pro Arg Leu Asp Asp
290 295 300

agg ttg tgt agt ttc gca gca atg att gct ttg att tgc taa gnt aag
960

Arg Leu Lys Ser Phe Ala Ala Met Ile Ala Leu Ile Cys Tyr Ala Lys
305 310 315 320

guc gtc aat acc gag gaa tcc gat tta ttc tct act gtc aat ttg tat
1008

Asp Val Asn Thr Glu Glu Ser Asp Leu Phe Ser Thr Val Thr Leu Tyr
325 330 335

gat aat gaa gaa atc gga tgg ttg aca aga caa ggc gaa aaa ggt ggc
1056

Asp Asn Glu Glu Ile Gly Ser Leu Thr Arg Gln Gly Ala Lys Gly Gly
340 345 350

ttg ttg gag tca gtg gtg gaa cgc agt tct tct gca ttc act aag aaa
1104

Leu Leu Glu Ser Val Val Glu Arg Ser Ser Ser Ala Phe Thr Lys Lys
355 360 365

ccg gtc gat ttg cat acg gtt tgg gct aat tcc atc atc ttg tcc gca
1152

Pro Val Asp Leu His Thr Val Trp Ala Asn Ser Ile Ile Leu Ser Ala
370 375 380

gac gtc aac cac glu taa aac cca aac ttt cct gaa gtc tat ttg aag
1200

Asp Val Asn His Leu Tyr Asn Pro Asn Phe Pro Glu Val Tyr Leu Lys
385 390 395 400

aat cat ttt cca gtg cct aat gtc gga atc act tta tca dtg gat cat
1248

Asn His Phe Pro Val Pro Asn Val Gly Ile Thr Leu Ser Leu Asp Pro
405 410 415

aac ggt cat atg gcc aca gat gtc gta gga aat gcc cta gta gaa gaa
1296

Asn Gly His Met Ala Thr Asp Val Val Gly Thr Ala Leu Val Glu Glu
420 425 430

tta gca cgc cgc aat gga gac aaa gtg caa tat ttc caa atc aaa aac
1344

Leu Ala Arg Arg Asn Gly Asp Lys Val Gln Tyr Phe Gln Ile Lys Asn
435 440 445

cac tca aga tca ggt ggt act atc ggc cca tca ttg gct tct caa aaa
1392

692/762

Asn Ser Arg Ser Gly Gly Thr Ile Gly Pro Ser Leu Ala Ser Gln Thr
 450 455 460

ggc gct cgt acc ata gac ctg gga att gca cag ttg tcc atg cac agc
 1440

Gly Ala Arg Thr Ile Asp Leu Gly Ile Ala Gln Leu Ser Met His Ser
 465 470 475 480

atc aga gct gct aca ggg tcc aag gat gtc gga tta ggt gtt aag ttc
 1488

Ile Arg Ala Ala Thr Gly Ser Lys Asp Val Gly Leu Gly Val Lys Phe
 485 490 495

ttc aac gga ttt ttc aag cac tgg aga tca gtc tac gat gaa ttc ggc
 1536

Phe Asn Gly Phe Phe Lys His Trp Arg Ser Val Tyr Asp Glu Phe Gly
 500 505 510

gag ttg tga

1548

Gln Leu

<210> 284

<211> 514

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 294

Met Glu Glu Gln Arg Gln Ile Leu Glu Gln Leu Lys Lys Thr Leu Gln
 1 3 10 15

Met Leu Thr Val Glu Pro Ser Lys Asn Asn Gln Ile Ala Asn Glu Glu
 20 25 30

Lys Glu Lys Lys Glu Asn Glu Asn Ser Trp Cys Ile Leu Glu His Asn
 35 40 45

Tyr Glu Asp Ile Ala Gln Glu Phe Ile Asp Phe Ile Tyr Lys Asn Pro
50 55 60

Thr Thr Tyr His Val Val Ser Phe Phe Ala Glu Leu Leu Asp Lys His
65 70 75 80

Asn Phe Lys Tyr Leu Ser Glu Lys Ser Asn Trp Glu Asp Ser Ile Gly
85 90 95

Glu Asp Gly Gly Lys Phe Tyr Thr Ile Arg Asn Gly Thr Asn Leu Ser
100 105 110

Ala Phe Ile Leu Gly Lys Asn Trp Arg Ala Glu Lys Gly Val Gly Val
115 120 125

Ile Gly Ser His Val Asp Ala Leu Thr Val Lys Leu Lys Pro Val Ser
130 135 140

Phe Lys Asp Thr Ala Glu Gly Tyr Gly Arg Ile Ala Val Ala Pro Tyr
145 150 155 160

Gly Gly Thr Leu Asn Glu Leu Trp Leu Asp Arg Asp Leu Gly Ile Gly
165 170 175

Gly Arg Leu Leu Tyr Lys Lys Lys Gly Thr Asn Glu Ile Lys Ser Ala
180 185 190

Leu Val Asp Ser Thr Pro Leu Pro Val Cys Arg Ile Pro Ser Leu Ala
195 200 205

Pro His Phe Gly Lys Pro Ala Glu Gly Pro Phe Asp Lys Glu Asp Glu

210

215

220

Thr Ile Pro Val Ile Gly Phe Pro Thr Pro Asp Glu Glu Gly Asn Glu
 225 230 235 240

Pro Pro Thr Asp Asp Glu Lys Lys Ser Pro Leu Phe Gly Lys His Cys
 245 250 255

Ile His Leu Leu Arg Tyr Val Ala Lys Leu Ala Gly Val Glu Val Ser
 260 265 270

Glu Leu Ile Gln Met Asp Leu Asp Leu Phe Asp Val Gln Lys Gly Thr
 275 280 285

Ile Gly Gly Ile Gly Lys His Phe Leu Phe Ala Pro Arg Leu Asp Asp
 290 295 300

Arg Leu Cys Ser Phe Ala Ala Met Ile Ala Leu Ile Cys Tyr Ala Lys
 305 310 315 320

Asp Val Asn Thr Glu Glu Ser Asp Leu Phe Ser Thr Val Thr Leu Tyr
 325 330 335

Asp Asn Glu Glu Ile Gly Ser Leu Thr Arg Gln Gly Ala Lys Gly Gly
 340 345 350

Leu Leu Glu Ser Val Val Glu Arg Ser Ser Ser Ala Phe Thr Lys Lys
 355 360 365

Pro Val Asp Leu His Thr Val Tyr Ala Asn Ser Ile Ile Leu Ser Ala
 370 375 380

Arg Val Asn His Leu Tyr Asn Pro Asn Phe Pro Glu Val Tyr Leu Lys
385 390 395 400

Asn His Phe Pro Val Pro Asn Val Gly Ile Tyr Leu Ser Leu Asp Pro
405 410 415

Asn Gly His Met Ala Thr Asp Val Val Gly Thr Ala Leu Val Glu Glu
420 425 430

Leu Ala Arg Arg Asn Gly Asp Lys Val Gln Tyr Phe Gln Ile Lys Asn
135 440 445

Asn Ser Arg Ser Gly Gly Thr Ile Gly Pro Ser Leu Ala Ser Gln Thr
450 455 460

Gly Ala Arg Thr Ile Asp Leu Gly Ile Ala Gln Leu Ser Met His Ser
465 470 475 480

Ile Arg Ala Val Thr Gly Ser Lys Asp Val Gly Leu Gly Val Lys Phe
485 490 495

Phe Asn Gly Phe Phe Lys His Trp Arg Ser Val Tyr Asp Glu Phe Gly
500 505 510

Glu Leu

•210• 205

<211> 579

<312> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1) .. (579)

<400> 285

atg tct gaa aag gcu gtt aga agg aaa ctt gtt att att ggt gat ggt
48

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly Asp Gly
5 10 15

ggt tgt ggc aag aac tct tta cta tat gta ttt aca tta gga aca ttc
96

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Lys Phe
20 25 30

cct gaa caa tat cat ccg aca gtg ttc gag aat tat gtc act gat tgc
144

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp Cys
35 40 45

aga gtt gac gga ata aaa gtg taa tta acg cta tgg gat aca gcg gga
192

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr Ala Gly
50 55 60

caa gag gaa tat gaa cgt tta cgt cca ttc taa tat tca aca gaa gat
240

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys Ala Asp
65 70 75 80

ata ata tta att ggg ttt gct gta gaa aat ttt gaa taa cta att aac
288

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu Ile Asn
85 90 95

gca agg acg aaa tgg gcg gat gag gca tta cga tat tgt cct gac gca
336

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro Asp Ala
100 105 110

cca atc gct ctt gta gcc ttg aaa aaa gat ccg agg caa gaa gcc cat
384

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu Ala His
115 120 125

ttt aaa gag aat gct acc gat gaa atg gtt ccc att gaa gat gca aaa
432

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp Ala Lys
130 135 140

caa gct gca agg gcc att ggg gcc aag aaa tac atg gaa tgt agt gca
480

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala
145 150 155 160

atg aat ggt gag ggt gtg gat gat gtc ttt gaa gta gct aca aga acc
528

Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr
165 170 175

agt ttg ott atg aag aag gca cca ggg gct aac tgt tgc ata att tta
576

Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile Ile Leu
180 185 190

tta

579

<210> 286

<211> 192

<212> CRET

<213> Saccharomyces cerevisiae

<400> 286

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly Asp Gly
1 5 10 15

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Lys Phe
20 25 30

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp Cys
 35 40 45

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr Ala Gly
 50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys Ala Asp
 65 70 75 80

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu Ile Asn
 85 90 95

Ala Arg Thr Iys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro Asp Ala
 100 105 110

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu Ala His
 115 120 125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp Ala Iys
 130 135 140

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala
 145 150 155 160

Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr
 165 170 175

Ser Leu Leu Met Lys Lys Gln Pro Gly Ala Asn Cys Cys Ile Ile Leu
 180 185 190

<210> 287
 <211> 792
 <213> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(792)

<400> 287
 atg atc gct acc tdc cga gcc gta aac atg aat aaa gag tca aaa cdc
 48
 Met Ile Ala Thr Ser Arg Ala Val Asn Met Asn Lys Glu Ser Lys His
 1 5 10 15
 aag aag gct gtt gcc aaa cca tgc aga gag aga caa act tca gtt aca
 36
 Lys Lys Ala Val Ala Lys Pro Cys Arg Glu Arg Gln Thr Ser Val Thr
 20 25 30
 aga gcc atg aga cca gct gta gca cgt gat cct' cgc aga ctt tca acg
 144
 Arg Ala Met Arg Pro Ala Val Ala Arg Asp Pro Arg Arg Leu Ser Thr
 35 40 45
 tog tog tct cct tct tog tca cca atg tca gca cag aga agg ctt tog
 122
 Ser Ser Ser Pro Ser Ser Ser Pro Met Ser Ala Gln Arg Arg Leu Ser
 50 55 60
 agg gaa gaa tta ata aac gaa atg gaa aag gag caa gac gct att gta
 240
 Arg Glu Glu Ile Ile Asn Gln Met Gln Lys Glu Gln Asp Ala Ile Val
 65 70 75 80
 gta aga ctt cta ogg gaa att gaa act tta aaa gaa gaa aac tct agg
 288
 Val Arg Leu Leu Arg Glu Ile Glu Thr Leu Lys Glu Glu Asn Ser Arg
 85 90 95

tta aaa aat aua atg cac cat ccc gtc ccc gct aga agg tog tct cca
336

Leu Lys Asn Gln Leu His His Pro Val Pro Ala Arg Arg Ser Ser Pro
100 105 110

Utt ttc gaa ggc gag tct gcc atc cta gat gat gac gcc tgc aat tat
364

Phe Phe Gln Gly Glu Ser Ala Ile Leu Asp Asp Asp Asp Cys Asn Tyr
115 120 125

ggc tuc acc ctc gac act cca aag cta aag ctc aca gat ggt gca tcc
432

Gly Tyr Thr Leu Asp Thr Pro Lys Leu Lys Leu Thr Asp Gly Ala Ser
130 135 140

aga cac acc gta ctt ccc tta aca ccu uag gcc tcc atg acc cac att
480

Arg His Thr Val Leu Pro Leu Thr Pro Lys Asp Ser Met Thr His Ile
145 150 155 160

tcc cat tcc gcc aga ayy tca ago cgg aac gct tcc ata tct aac gga
528

Ser His Ser Ala Arg Arg Ser Ser Arg Asn Ala Ser Ile Ser Asn Gly
165 170 175

aca ago atc tca gac acy att ttc ccc att gag act aac atc cac tca
576

Thr Ser Ile Ser Asp Thr Ile Phe Pro Ile Glu Thr Lys Ile His Ser
180 185 190

aca cca cca ata aac aga aac ctt uuu tcc guc gat ctt cca cat cac
624

Ala Pro Thr Thr Asn Arg Asn Leu Pro Ser Ala Asp Leu Pro His His
195 200 205

act ctt ctt cca cgt tct cta ago gcc att tgg tct ago gat tta acc
672

Thr Leu Leu Pro Arg Ser Leu Ser Gly Ile Ser Ser Ser Asp Leu Thr
210 215 220

gaa tcc ggt gct ctt ctt cat gac agg aga agg cgt tcc tcc aat tac
720

Glu Ser Gly Ala Leu Leu His Asp Arg Arg Arg Arg Ser Ser Asn Tyr
 225 230 235 240

ugt ctg gat ggt tca aac tct tta aaq gct qat ctg atg gca aag aga
 245

Ser Leu Asp Gly Ser Asn Ser Leu Lys Ala Asp Leu Met Ala Lys Arg
 245 250 255

ttc csa act ggt tca ttg aaa tag
 260

Phe Gln Thr Gly Ser Leu Lys
 260

<210> 288

<211> 263

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 289

Met Ile Ala Thr Ser Arg Ala Val Asn Met Asn Lys Glu Ser Lys His
 1 5 10 15

Lys Lys Ala Val Ala Lys Pro Cys Arg Glu Arg Gln Thr Ser Val Thr
 20 25 30

Arg Ala Met Arg Pro Ala Val Ala Arg Asp Pro Arg Arg Leu Ser Thr
 35 40 45

Ser Ser Ser Pro Ser Ser Ser Pro Met Ser Ala Gln Arg Arg Leu Ser
 50 55 60

Arg Glu Glu Ile Ile Asn Glu Met Glu Lys Glu Gln Asp Ala Ile Val
 65 70 75 80

Val Arg Leu Leu Arg Glu Ile Glu Thr Leu Lys Glu Glu Asn Ser Arg

85

90

95

Leu Lys Asn Glu Glu His His Pro Val Pro Ala Arg Arg Ser Ser Pro
 100 105 110

Phe Phe Glu Gly Glu Ser Ala Ile Leu Asp Asp Asp Asp Cys Asn Tyr
 115 120 125

Gly Tyr Thr Leu Asp Thr Pro Lys Leu Lys Leu Thr Arg Gly Ala Ser
 130 135 140

Arg His Thr Val Leu Pro Leu Thr Pro Lys Asp Ser Met Thr His Trp
 145 150 155 160

Ser His Ser Ala Arg Arg Ser Ser Arg Asn Ala Ser Ile Ser Asn Gly
 165 170 175

Thr Ser Ile Ser Asp Thr Ile Phe Pro Ile Glu Thr Lys Ile His Ser
 180 185 190

Ala Pro Thr Thr Asn Arg Asn Leu Pro Ser Ala Asp Leu Pro His His
 195 200 205

Thr Leu Leu Pro Arg Ser Leu Ser Gly Ile Ser Ser Ser Asp Thr Thr
 210 215 220

Glu Ser Gly Ala Leu Leu His Asp Arg Arg Arg Arg Ser Ser Asn Tyr
 225 230 235 240

Ser Leu Asp Gly Ser Asn Ser Leu Lys Ala Asp Leu Met Ala Lys Arg
 245 250 255

Phe Gln Thr Gly Ser Leu Lys
260

<210> 289

<211> 576

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(576)

<400> 289

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48

Met Ala Ser Ser Ser Ser Thr Leu Pro Leu His Met Tyr Ile Arg Pro
1 5 10 15

tta atc att gaa gat tta aag cag att ttg aac ttg gaa agc cca ggt
96

Leu Ile Ile Glu Asp Leu Lys Gln Ile Leu Asn Leu Glu Ser Gln Gly
20 25 30

ttc cca ccc aac gaa aga ggt tca gaa gaa att atc agc ttt cgt ttg
144

Phe Pro Pro Asn Glu Arg Ala Ser Glu Glu Ile Ile Ser Phe Arg Leu
35 40 45

atc aat tgt cca gag cta tgc tca ggt ctt ttc atc aga gag atc gag
192

Ile Asn Cys Pro Glu Leu Cys Ser Gly Leu Phe Ile Arg Glu Ile Glu
50 55 60

ggc aaa gaa gtt aaa aag gag aca cta att ggt cat att atg ggt act
240

Gly Lys Glu Val Lys Lys Glu Thr Leu Ile Gly His Ile Met Gly Thr
65 70 75 80

aag ata cct cat gaa tac att act atc gaa agc atg ggc aaa tta caa
288

Lys Ile Pro His Glu Tyr Ile Thr Ile Glu Ser Met Gly Lys Leu Gln
85 90 95

gtg gaa tgg agt aat ca. att ggt att cac tct gta gta atc aag cca
336

Val Glu Ser Ser Asn His Ile Gly Ile Ile Ser Val Val Ile Lys Pro
100 105 110

gaa tac cag aac aaa aac ctg gct act tta ctt tta act gac tac att
384

Glu Tyr Gln Lys Lys Asn Leu Ala Thr Leu Leu Leu Thr Asp Tyr Ile
115 120 125

cag aaa ttg agt aat cag gaa att ggt aac aaa att gtc ctt att gct
432

Gln Lys Leu Ser Asn Gln Glu Ile Gly Asn Lys Ile Val Leu Ile Ala
130 135 140

cac gag cca ttg ata cca ttt tat gaa aga gtt ggt ttc aag atc at.
480

His Glu Pro Leu Ile Pro Phe Tyr Glu Arg Val Gly Thr Lys Ile Trp
145 150 155 160

gct gag aac acc aat gtt gct aag gac aua uac ltc gaa gaa cag aaa
528

Ala Glu Asn Thr Asn Val Ala Lys Arg Lys Asn Phe Ala Glu Gln Lys
165 170 175

Lys ala gat atg gag aga gaa cta att aag gaa gaa tac gac aac tag
576

Trp Ala Asp Met Gln Arg Glu Leu Ile Lys Glu Glu Tyr Asp Asn
180 185 190

<210> 290

<211> 191

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 290

Met Ala Ser Ser Ser Ser Thr Leu Pro Leu His Met Tyr Ile Arg Pro
1 5 10 15

Leu Ile Ile Glu Asp Leu Lys Glu Ile Leu Asn Leu Glu Ser Gln Gly
20 25 30

Phe Pro Pro Asn Glu Arg Ala Ser Glu Glu Ile Ile Ser Phe Arg Leu
35 40 45

Ile Asn Cys Pro Gln Leu Cys Ser Gly Leu Phe Ile Arg Glu Ile Glu
50 55 60

Gly Lys Glu Val Lys Lys Glu Thr Leu Ile Gly His Ile Met Gly Thr
65 70 75 80

Lys Ile Pro His Glu Tyr Ile Thr Ile Glu Ser Met Gly Lys Leu Gln
85 90 95

Val Glu Ser Ser Asn His Ile Gly Ile His Ser Val Val Ile Lys Pro
100 105 110

Gln Tyr Gln Cys Lys Asn Leu Ala Thr Leu Leu Leu Thr Asp Tyr Ile
115 120 125

Gln Lys Leu Ser Asn Gln Glu Ile Gly Asn Lys Ile Val Leu Ile Ala
130 135 140

His Glu Pro Leu Ile Pro Phe Tyr Glu Arg Val Gly Phe Lys Phe Ile
145 150 155 160

Ala Glu Asn Thr Asn Val Ala Lys Asp Lys Asn Phe Ala Glu Gln Lys

165

170

175

Trp Ile Asp Met Glu Arg Glu Leu Ile Lys Glu Glu Tyr Asp Asn

180

185

190

Homologs to YDR101C (ORF368), SEQ. ID No. 17

>GM48929802

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 ggattcalacattcgagagcacaactggaaattgtgtacaaagaattgaaagggaagattgagagagggtgtgtcttcccta
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>GM48929802

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Homologs to YBR025C (ORF96), SEQ. No. 31

>BN42370798 DNA: putative GTP-binding protein

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BN42370798 protein: putative GTP-binding protein

Mppkalkakdagpverpilgrfsshkigivglpnvgkstlfnltldspaanfpctiepnearvnipddrfkwlqlykpkse
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rgficars*

>BN44233997 DNA: Similar to GTP-binding protein

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>BN44233997 protein: Similar to GTP-binding protein

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salgrigcaild/kparsvalndkdkdvkhllcllmpkmi/yvanvøetcladpdknefvqqvkalsddqsgshvvsaqv
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fvsagslaaarkilgfssegkeyivkgevdmlfnfr*

>BN46708845 DNA: putative GTP-binding protein

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tggcaatgaacgcagtcgaaggcgccgagaaataacagcaggagggggaacacataatgtgttcaggatggagat
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>BN46708845 protein: putative GTP-binding protein

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>GM50231578 DNA: GTP-binding protein

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ggtatgtgagtcagctggaagcctctggaaagtataaaacaggaagggaagaaacogataitggttccagatgtgagacaft
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>GM 50231578 protein: GTP-binding protein

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ggeltipfsgalermadnppdeaakyceenklqsalpnikdgsainliyfttagpdvkcwqlnqskapqaagailhdf
ergfcaevmlfedkfelgseavkaagkyrqegktyvvqgdilfklfnvsgggkk*

>GM51934822 DNA: Similar to GTP-binding protein

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>OS35840251 putative histone H3

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cgcccgccgcatccgttggcgagggcgtag

>OS40216588 histone H3

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>OS41565420 histone H3.3

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agagggccttaa

>BN42032886 histone H3.3

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>BN42118630 histone H3.3

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agaatcagagcggaagagcttga

>BN47900015 putative histone H3

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>BN51269917 putative histone H3

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gaatcagagcggaagagagcttga

>OS32404891 histone H3.3

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havlaqeaeeaylvlgfcdnlcaihakrvtmpkdiqlamirgera*

>OS32795441 putative histone H3

marfkqlarkstggkcpkqlatkaarksapctggvkkphyrpgtvalreirkyqkstellirklpqrivrelaqdtktdlrfqs
savaaqeaeeaylvlgfcdnlcaihakrvtmpkdiqlamirgera*

>OS34693911 histone H3 protein

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havlaqeaeeaylvlgfcdnlcaihakrvtmpkdiqlamirgera*

>OS35840251 putative histone H3

marfkqlarkstggkcpkqlatkaarksapctggvkkphyrpgtvalreirkyqkstellirklpqrivrelaqdtktdlrfqs
savaaqeaeeaylvlgfcdnlcaihakrvtmpkdiqlamirgera*

>OS40216588 histone H3

marfkqlarkstasmvpkklvmkvarksapctmaglkkphrikpgtvalreirkyqkstellirklpqrivrelaqdvsvyr/q
ssavvaqeaeeaylvlgfcdnlcviahakrvtmpkdiqlamirgera*

>ÖS41585420 histone H3.3

marfkqlarkstggkprkqlatkaarksapitggvkkphyrpgtvalreikyqketellirklpqrtrveiaqdiktdlrfs
havlalqeaaeaylvglfednlcalhakrvtmpkdiqlamirgera*

>BN42032866 histone H3.3

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>BN42113630 histone H3.3

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>BN42307928 putative GTP-binding protein

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>BN42421819 putative histone H3

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>BN45384195 putative histone H3

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>BN45384583 histone H3.3

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>BN47900015 putative histone H3

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>OS3522056 putative signal peptidase subunit

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>OS3505381 putative signal peptidase subunit

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Homologs to YHR113W (ORF1827), SEQ. ID No. 107

>OS3522056 putative signal peptidase subunit

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>OS3505381 putative signal peptidase subunit

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>OS32522056 putative signal peptidase subunit

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>OS32894796 putative clathrin assembly protein
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>OS34902237 AP-1 Golgi-related complex component, clathrin assembly protein
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>OS32684329 clathrin assembly protein AP17-like protein
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>GM53036028 putative clathrin coat assembly protein
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Homologs to YGR180c (ORF1964), SEQ. ID No. 115

5-BN43093876

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>BN51425457 multicatalytic endopeptidase complex, proteasome precursor, beta subunit

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[illegible]

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>BN43154133 Putative S-phase-specific ribosomal protein

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>GI50098495 ribosomal protein S3a

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>OS34661717 ribosomal protein S3a

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>BN46971595 Putative S-phase-specific ribosomal protein

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>OS30932534 S-phase-specific ribosomal protein

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>OS32589884 S-phase-specific ribosomal protein

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>BN41956449 Putative S-phase-specific ribosomal protein

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>BN43154133 Putative S-phase-specific ribosomal protein

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>GM50096495 ribosomal protein S3a

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>GM59622253 translation initiation factor

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>GM52851017 translation initiation factor-like protein

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>GM52699053 translation initiation factor

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>BN44219936 translation initiation factor

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>CM53677364 translation initiation factor-like protein

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>OS40418529 translational initiation factor eIF1

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>OS32568448 translational initiation factor eIF1

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>GM59605347 translational initiation factor eIF1

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>OS34684287 translational initiation factor eIF1
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>OS34073720 translation initiation factor
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>GM59676621 translational initiation factor eIF1
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>GM52851017 translation initiation factor-like protein
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>GM52699053 translation initiation factor
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>BN44219936 translation initiation factor
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>Q153677364 translation initiation factor-like protein
mvsvglvqlptafdpfaeanaedsgagakeyvhvrlvqqmrgkslttvqgllkkeysynkilldlkkefcngtvtvqdpelgq
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>OS40418529 translational initiation factor eIF1
msdlddqiaptafdpfaanaedsgagakeyvhvrlvqqmrgkslttvqgllkkeysynkilldlkkefcngtvtvqdpelgq
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>GM59622253 translation initiation factor
mseldddqiptafdpfaanaedsgagakeyvhvrlvqqmrgkslttvqgllkkeysynkilldvkkfcngtvtvqdpelgq
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Homologs to YNL334C (ORF3578), SEQ. ID No. 175

>OS32585690 imidazoleglycerol-phosphate synthase subunit H-like

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>BN51277788 chaperonin CPN10

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>BN42876571 10 kDa chaperonin

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>GI50703949 putative 10kd chaperonin

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>GM52366459 cp10-like protein

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ails*

>OS32631203 chaperonin

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>GM59730390 protein: sugar transporter

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Homologs to YPL079W (ORF4425), SEQ. ID No. 207

>BN44798833 60S ribosomal protein L21

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>BN44798833 60S ribosomal protein L21

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Homologs to YPR052C (ORF4130), SEQ. ID No. 221

>GM59623606 high mobility group protein 2-related

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>OS36010716 unknown protein

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>OS34825203 HMG protein

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>BN51295208 putative HMG protein

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>GM59623606 high mobility group protein 2-related

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>OS36010716 unknown protein

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>OS34825203 HMG protein

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>BN51295209 putative HMG protein

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Homologs to YLR275W (ORF2923), SEQ. ID No. 225

>BN42537749 small nuclear ribonucleo protein D2 -related

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>OS37525380 small nuclear ribonucleo protein D2 -related

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ga

>BN42537749 small nuclear ribonucleo protein D2 -related

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>OS37525380 small nuclear ribonucleo protein D2 -related

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Homologs to YGL106W (ORF 283) SEQ. ID No. 239

>BN42003647 calmodulin-3

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>BN45450720 calmodulin 2

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>BN42306806 putative calmodulin protein

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>OS34266853 calmodulin

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>OS34824439 calmodulin

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>OS41802485 calmodulin

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>GM47065673 calmodulin

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>OS34028983 calmodulin

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>BN42063347 calmodulin-S

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>BN45450720 calmodulin 2

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>BN42308806 putative calmodulin protein

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>OS34266856 calmodulin

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>OS34824439 calmodulin

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>OS41802485 calmodulin

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>GM47065673 calmodulin

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>OS34028983 calmodulin

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>BN45407352 calmodulin-3

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im⁴

Homologs to YIL023c (ORF1717). SEQ. No. 243

>BN45773929 metal transporter family

[illegible]

>OS32877780 metal transporter family

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> BN51401271

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Homologs to YH103c (ORF1523), SEQ. No. 283

> BH51473779

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> BN51473779

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Homologs to YNL090W (ORF3165), SEQ. ID No. 285

>OS32558796 small GTP-binding protein RAB5B
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 aeknmnmvltetsekldcchinqveelaknprtas*

>OS83960403 putative Rop family GTPase ROP4
 massasrflkcvrvgdgavglctcmlicytsnkplidyvptvfdnfsanvvdgttnlghwdtaggedynrlpsyrgadvf
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>BN42135981 GTP-binding protein
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 vdaaikvvlqppkpkkkkkknkrvll*

>BN45412825 Rho1Ps homolog/ Rac-like protein
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 vskasyenlkkwlpelrhyagpgvpilvgtklldrdkqffidhpgavpistaqgeelkkvigapayiecsaktqgnvka
 vdaaikvvlqppkpkkkkkknkrvll*

>GM47124407 Rac-like gtp binding protein ARAC2
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 aalkvalkppkpkkkpkkrktetll*

>GM47172047 Rac-like GTP binding protein

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daaikvvlqppksekktgkknlpavfi*

>GM48914268 small G protein

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fdaaikvvlqppkklkkrktgkacsi*

>GM50693526 small G-protein ROP9

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daainrvlqppkqkklkgkqkacsi*

>GM52260563 rac-type small GTP-binding protein

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daaikvvlqppkqkklkgkqkacsi*

>GM50189916 rac-type small GTP-binding protein

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daaikvvlqppkqkklkgkqkacsi*

>GM49741826 putative rac protein

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vlfafsvrasayonvkkwipelrhyagvpilivgtikdlrddkqfmdhpgavpittaggeelrkligapayleccssktqq
nvkavfdaaimvlpkppkqnekklkkgkqkshgclenlvcgrlvtrh*

>BN4381801 putative GTP binding protein Arac10

masfaskikcvtvgdgavgktdmliysntfptdyvptvdrfsanvvdgstnlgwtdagqedynrlrplsyrgadvf
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nvkavfdaaikvkvkqkqkqkqkshgclenlvcgrlvtrh*

>BN42385898 putative ROP family GTPase

msasrfikcvtvgdgavgktdliysntfptdyvptvdrfsanvvdgstnlgwtdagqedynrlrplsyrgadvllaf
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gvfdaainrvlqppkqkklkgkqkacsi*

>BN44062474 putative GTP binding protein Arac10

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>BN42519337 Rac-like protein

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fdtalvalrppkakkkkikpnlkrstcfff"

>BN42557868 putative GTP-binding protein

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>BN44504217 GTP-binding protein

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>BN41992996 putative ROP family GTPase

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>OS37907380 small GTP-binding protein

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>CS30348846 small GTP-binding protein

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>OS35505384 GTP-binding protein RAB21

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>OS32558796 small GTP-binding protein RAB5B

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>BN44062474 putative GTP binding protein Arac10

[illegible]

BN42519337 Rec-like protein

[illegible]

>BN42557868 putative GTP-binding protein

[illegible]

>BN44504217 GTP-binding protein

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>BN41992896 putative ROP family GTPase

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>OS37807380 small GTP-binding protein

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>OS30846846 small GTP-binding protein

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>OS35505384 GTP-binding protein RAB21

[illegible]

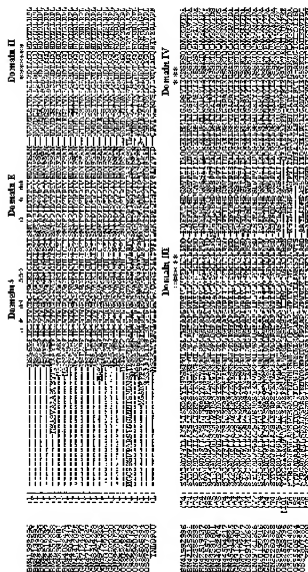


Figure 2 Protein alignment of Ebo small GTPases from *Opuntia stricta* cv. Nipple-Share (a isoprenoid), *Brassica napus* cv. "AC Excel" "Quantum" and "Jesse" (canola), and *Opuntia max* cv. Result (cyclopent). End represents the identical amino acid. Ebo 1 stands for Ebo 1 in a set of sequences. Green shows that an amino acid shows the similar feature.

Figure 2.1



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